

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:40:39 ; Search time 57.74 Seconds
(without alignments)
8.038 Million cell updates/sec

Title: US-09-821-726-1

Perfect score: 90

Sequence: 1 VKEXKXGKGGPGXPPK 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AR.*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	50.0	133	1	US-07-917-722-3
2	45	50.0	878	4	US-09-141-212-8
3	45	50.0	878	4	US-09-561-138-8
4	45	50.0	879	4	US-09-141-212-6
5	45	50.0	879	4	US-09-561-138-6
6	45	50.0	880	2	US-08-916-917-12
7	45	50.0	880	3	US-09-225-170-12
8	45	50.0	880	4	US-09-378-255-6
9	45	50.0	880	4	US-09-141-212-2
10	45	50.0	880	4	US-09-141-212-4
11	45	50.0	880	4	US-09-552-351-4
12	45	50.0	880	4	US-09-251-372-6
13	45	50.0	880	4	US-09-561-138-2
14	45	50.0	880	4	US-09-561-138-4
15	45	50.0	880	4	US-09-715-336-6
16	45	50.0	880	4	US-09-811-241-6
17	45	50.0	880	4	US-09-802-839-4
18	44	48.9	298	3	US-08-767-942A-25
19	43.5	48.3	821	1	US-07-935-311A-4
20	43.5	48.3	821	1	US-08-368-079-4
21	43.5	48.3	821	5	PCT-US93-07996-4
22	42.5	47.2	402	2	US-08-709-979A-3
23	42.5	47.2	402	3	US-08-709-979A-1
24	42.5	47.2	402	3	US-08-709-974A-1
25	42.5	47.2	415	2	US-08-833-642A-5
26	42.5	47.2	415	3	US-08-709-974A-4
27	42.5	47.2	415	4	US-09-069-632-1

28	42.5	47.2	435	1	US-08-361-920-27
29	42.5	47.2	435	1	US-08-479-939-27
30	42.5	47.2	435	1	US-08-483-432-27
31	42.5	47.2	435	4	US-09-069-632-3
32	42	46.7	18	3	US-08-630-916A-9
33	42	46.7	99	4	US-09-314-268-133
34	41	45.6	311	2	US-08-318-837-9
35	41	45.6	738	4	US-08-989-385-1
36	40	44.4	147	4	US-09-347-833-10
37	40	44.4	377	4	US-09-342-681C-4
38	40	44.4	391	4	US-09-342-681C-2
39	40	44.4	1912	4	US-08-913-832A-2
40	39	43.3	59	2	US-08-469-412A-5
41	39	43.3	59	4	US-09-021-715-5
42	39	43.3	269	2	US-07-857-224B-14
43	39	43.3	269	2	US-07-857-224B-16
44	39	43.3	356	2	US-08-700-607-6
45	39	43.3	369	2	US-08-424-224-2

ALIGNMENTS

RESULT 1
US-07-917-722-3
; Sequence 3, Application US/07917722
; Patent No. 5534525
; GENERAL INFORMATION:
; APPLICANT: Sondermeyer, Paulus Jacobus Antonius
; APPLICANT: Claessens, Johannes Antonius Joseph
; TITLE OF INVENTION: Chicken Anemia Virus vaccine and
; TITLE OF INVENTION: diagnostic
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Organon Teknika Corporation
; ADDRESSEE: Biotechnology Research Institute
; STREET: 1330-A Piccard Drive
; CITY: Rockville
; STATE: Maryland
; COUNTRY: U.S.A.
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION NUMBER: US/07/917,722
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/605,881
; FILING DATE: October 31, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Donna Bobrowicz
; REGISTRATION NUMBER: 32,196
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301)258-5200
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-917-722-3

Query Match 50.0%; Score 45; DB 1; Length 133;
Best Local Similarity 41.2%; Pred. No. 13;
Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
Qy 2 KEXKXGKGGPGXPPK 18
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Db 9 RDSKAGRRPPGPP 25

RESULT 2

US-09-141-212-8
; Sequence 8, Application US/09141212
; Patent No. 6200777
; GENERAL INFORMATION:
; APPLICANT: MACPHEE, COLIN
; APPLICANT: PATEL, LISA
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/141,212
; FILING DATE: 27-AUG-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 97306807.5
; FILING DATE: 01-SEP-1997
; APPLICATION NUMBER: EP 98300687.5
; FILING DATE: 30-JAN-1998
; APPLICATION NUMBER: GB 9807720.9
; FILING DATE: 08-APR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-30012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 878 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-141-212-8

Query Match 50.0%; Score 45; DB 4; Length 878;
Best Local Similarity 46.7%; Pred. No. 70;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 KXXKGKGGXPPK 19

Db 562 KRSHGTSPGACPPR 576

RESULT 3

US-09-561-138-8
; Sequence 8, Application US/09561138
; Patent No. 6258580
; GENERAL INFORMATION:
; APPLICANT: MACPHEE, COLIN
; APPLICANT: PATEL, LISA
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30012-D1
; CURRENT APPLICATION NUMBER: US/09/561,138
; CURRENT FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 09/141,212
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: EP 97306807.5
; PRIOR FILING DATE: 1997-09-01
; PRIOR APPLICATION NUMBER: EP 98300687.5
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: GB 9807720.9
; PRIOR FILING DATE: 1998-04-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 878
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-561-138-8

Query Match 50.0%; Score 45; DB 4; Length 878;
Best Local Similarity 46.7%; Pred. No. 70;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 KXXKGKGGXPPK 19

Db 562 KRSHGTSPGACPPR 576

RESULT 4
US-09-141-212-6
; Sequence 6, Application US/09141212
; Patent No. 6200777
; GENERAL INFORMATION:
; APPLICANT: MACPHEE, COLIN
; APPLICANT: PATEL, LISA
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/141,212
; FILING DATE: 27-AUG-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 97306807.5
; FILING DATE: 01-SEP-1997
; APPLICATION NUMBER: EP 98300687.5
; FILING DATE: 30-JAN-1998
; APPLICATION NUMBER: GB 9807720.9
; FILING DATE: 08-APR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-30012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 879 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-141-212-6

Query Match 50.0%; Score 45; DB 4; Length 879;
Best Local Similarity 46.7%; Pred. No. 70;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 KXXGKGGGXPXPPK 19
I: | | | | |

Db 562 KRSHGTSPGACPPPR 576

RESULT 5

US-09-561-138-6

; Sequence 6, Application US/09561138

; Patent No. 6258580

; GENERAL INFORMATION:

; APPLICANT: MACPHEE, COLIN

; APPLICANT: PATEL, LISA

; TITLE OF INVENTION: NOVEL COMPOUNDS

; FILE REFERENCE: GP-30012-D1

; CURRENT APPLICATION NUMBER: US/09/561,138

; CURRENT FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 09/141,212

; PRIOR FILING DATE: 1998-08-27

; PRIOR APPLICATION NUMBER: EP 97306807.5

; PRIOR FILING DATE: 1997-09-01

; PRIOR APPLICATION NUMBER: EP 98300687.5

; PRIOR FILING DATE: 1998-01-30

; PRIOR APPLICATION NUMBER: GB 9807720.9

; PRIOR FILING DATE: 1998-04-08

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 6

; LENGTH: 879

; TYPE: PRT

; ORGANISM: HOMO SAPIENS

US-09-561-138-6

Query Match 50.0%; Score 45; DB 4; Length 879;
Best Local Similarity 46.7%; Pred. No. 70;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 KXXGKGGGXPXPPK 19
I: | | | | |

Db 562 KRSHGTSPGACPPPR 576

RESULT 6

US-09-916-917-12

; Sequence 12, Application US/08916917

; Patent No. 5856132

; GENERAL INFORMATION:

; APPLICANT: Stephens, Len

; APPLICANT: Hawkins, Phillip Thomas

; APPLICANT: Braselmann, Sylvia

; TITLE OF INVENTION: G-BETA-GAMMA REGULATED

; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3', KINASE

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds, LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036-2811

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows

; SOFTWARE: FastSeq for Windows Version 2.0b

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/916,917
; FILING DATE: 15-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/672,211
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel B
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 8549-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 880 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5856132e
US-08-916-917-12

Query Match

50.0%; Score 45; DB 2; Length 880;

Best Local Similarity 46.7%; Pred. No. 70;

Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 KXXGKGGGXPXPPK 19
I: | | | | |

Db 562 KRSHGTSPGACPPPR 576

RESULT 7

US-09-225-170-12

; Sequence 12, Application US/09225170

; Patent No. 6017763

; GENERAL INFORMATION:

; APPLICANT: Stephens, Len

; APPLICANT: Hawkins, Phillip Thomas

; APPLICANT: Braselmann, Sylvia

; TITLE OF INVENTION: G-BETA-GAMMA REGULATED

; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3', KINASE

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds, LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036-2811

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows

; SOFTWARE: FastSeq for Windows Version 2.0b

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/225,170

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/916,917

; FILING DATE: 15-AUG-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Abrams, Samuel B

; REGISTRATION NUMBER: 30,605

; REFERENCE/DOCKET NUMBER: 8549-0006-999

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-493-4935

; TELEFAX: 650-493-5556

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

Query Match 50.0%; Score 45; DB 4; Length 880;
Best Local Similarity 46.7%;
Pred. No. 70;
2. Misatches
6: Indels
0: Gaps

RESULT 10
US-09-141-212-4
; Sequence 4, Application US/09141212
Patent No. 6200777

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US-09-141-212-4
; Sequence 4, Application US/09141212
; Patent No. 6200777
; GENERAL INFORMATION:
; APPLICANT: MACPHER, COLIN
; APPLICANT: PATEL, LISA
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Ver
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/141, 212
; FILING DATE: 27-AUG-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 97306807.5
; FILING DATE: 01-SEP-1997
; APPLICATION NUMBER: EP 98300687.5
; FILING DATE: 30-JAN-1998
; APPLICATION NUMBER: GB 9807720.9
; FILING DATE: 08-APR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-30012
; TELECOMMUNICATION INFORMATION:

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COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/141.212
FILING DATE: 27-AUG-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 97306807.5
FILING DATE: 01-SEP-1997
APPLICATION NUMBER: EP 98300687.5
FILING DATE: 30-JAN-1998
APPLICATION NUMBER: GB 9807720.9
FILING DATE: 03-APR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23.031
REFERENCE/DOCKET NUMBER: GP-30012
TELECOMMUNICATION INFORMATION:

0% 5% 10% 15% 20% 25% 30% 35% 40% 45% 50% 55% 60% 65% 70% 75% 80% 85% 90% 95% 100%

TELEPHONE: 610-407-0700
 TELEFAX: 610-407-0700
 TELEX: 846169
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 880 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-141-212-4

Query Match 50.0%; Score 45; DB 4; Length 880;
 Best Local Similarity 46.7%; Pred. No. 70;
 Matches 7; Conservative 2; Mismatches 6; Indels 6; Gaps 0;

QY 5 KXXGKGGGXPXPPK 19
 I: | | | | |
 Db 562 KRSRGTSPGACPPPR 576

RESULT 11
 US-09-552-351-4
 ; Sequence 4, Application US/09552351
 ; Patent No. 6225090
 ; GENERAL INFORMATION:
 ; APPLICANT: Lisa Patel
 ; TITLE OF INVENTION: No. 6225090el Compounds
 ; FILE REFERENCE: GP-30203
 ; CURRENT APPLICATION NUMBER: US/09/552,351
 ; CURRENT FILING DATE: 2000-04-19
 ; PRIOR APPLICATION NUMBER: UK 9908897.3
 ; PRIOR FILING DATE: 1999-04-19
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 880
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIENS
 US-09-552-351-4

Query Match 50.0%; Score 45; DB 4; Length 880;
 Best Local Similarity 46.7%; Pred. No. 70;
 Matches 7; Conservative 2; Mismatches 6; Indels 6; Gaps 0;

QY 5 KXXGKGGGXPXPPK 19
 I: | | | | |
 Db 562 KRSRGTSPGACPPPR 576

RESULT 12
 US-09-251-372-6
 ; Sequence 6, Application US/09251372
 ; Patent No. 623886
 ; GENERAL INFORMATION:
 ; APPLICANT: PATEL, LISA
 ; TITLE OF INVENTION: NOVEL COMPOUNDS
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Ratner & Prestia
 ; STREET: P.O. Box 980
 ; CITY: Valley Forge
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19482
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/251,372
 FILING DATE: 16-FEB-1999
 CLASSIFICATION:
 PRIOR APPLICATION NUMBER: 9900823.7
 FILING DATE: 14-JAN-1999
 APPLICATION NUMBER: 9803290.7
 FILING DATE: 16-FEB-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Prestia, Paul F
 REGISTRATION NUMBER: 23,031
 REFERENCE/DOCKET NUMBER: GP-30012A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-407-0700
 TELEFAX: 610-407-0700
 TELEX: 846169
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 880 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-251-372-6

Query Match 50.0%; Score 45; DB 4; Length 880;
 Best Local Similarity 46.7%; Pred. No. 70;
 Matches 7; Conservative 2; Mismatches 6; Indels 6; Gaps 0;

QY 5 KXXGKGGGXPXPPK 19
 I: | | | | |
 Db 562 KRSRGTSPGACPPPR 576

RESULT 13
 US-09-561-138-2
 ; Sequence 2, Application US/09561138
 ; Patent No. 6258580
 ; GENERAL INFORMATION:
 ; APPLICANT: MACPHEE, COLIN
 ; TITLE OF INVENTION: NOVEL COMPOUNDS
 ; FILE REFERENCE: GP-30012-D1
 ; CURRENT APPLICATION NUMBER: US/09/561,138
 ; CURRENT FILING DATE: 2000-04-28
 ; PRIOR APPLICATION NUMBER: 09/141,212
 ; PRIOR FILING DATE: 1998-08-27
 ; PRIOR APPLICATION NUMBER: EP 97306807.5
 ; PRIOR FILING DATE: 1997-09-01
 ; PRIOR APPLICATION NUMBER: EP 98300687.5
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: GB 9807720.9
 ; PRIOR FILING DATE: 1998-04-08
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 880
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIENS
 US-09-561-138-2

Query Match 50.0%; Score 45; DB 4; Length 880;
 Best Local Similarity 46.7%; Pred. No. 70;
 Matches 7; Conservative 2; Mismatches 6; Indels 6; Gaps 0;

QY 5 KXXGKGGGXPXPPK 19
 I: | | | | |
 Db 562 KRSRGTSPGACPPPR 576

RESULT 14

Thu Sep 5 11:23:23 2002

Job time: 326 sec

US-09-561-138-4
; Sequence 4, Application US/09561138
; Patent No. 6258580
; GENERAL INFORMATION:
; APPLICANT: MACPHEE, COLIN
; APPLICANT: PATEL, LISA
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30012-D1
; CURRENT APPLICATION NUMBER: US/09/561,138
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/141,212
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: EP 97306807.5
; PRIOR FILING DATE: 1997-09-01
; PRIOR APPLICATION NUMBER: EP 98300687.5
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: GB 9807720.9
; PRIOR FILING DATE: 1998-04-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 880
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-561-138-4

Query Match 50.0%; Score 45; DB 4; Length 880;
Best Local Similarity 46.7%; Pred. No. 70;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 KXXGKGGXPPPK 19
I: | |||
DB 562 KRSRGTSPGACPPPR 576

RESULT 15
US-09-715-336-6
; Sequence 6, Application US/09715336
; Patent No. 6261819
; GENERAL INFORMATION:
; APPLICANT: Colin Houston MacPhee
; APPLICANT: Lisa Patel
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30173-D1
; CURRENT APPLICATION NUMBER: US/09/715,336
; CURRENT FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: UK 9818435.1
; PRIOR FILING DATE: 1998-08-24
; PRIOR APPLICATION NUMBER: UK 9903414.2
; PRIOR FILING DATE: 1999-02-15
; PRIOR APPLICATION NUMBER: 09/378,255
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 880
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-715-336-6

Query Match 50.0%; Score 45; DB 4; Length 880;
Best Local Similarity 46.7%; Pred. No. 70;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 KXXGKGGXPPPK 19
I: | |||
DB 562 KRSRGTSPGACPPPR 576

Search completed: September 4, 2002, 16:46:05

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:42:19 ; Search time 124.34 seconds
(without alignments)
26.435 Million cell updates/sec

Title: US-09-821-726-1
Perfect score: 90
Sequence: 1 VREXKXKXGKPGXPPPK 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_19.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mmc.*
 - 8: sp_organelle.*
 - 9: sp_phase.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp Vertebrate.*
 - 14: sp Unclassified.*
 - 15: sp_rvirus.*
 - 16: sp_bacteriap.*
 - 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	58.9	706	16 Q97E35	Q97e35 clostridium
2	49	54.4	1677	11 070373	070373 mus musculus
3	48	53.3	501	10 Q9FHM0	Q9fhm0 arabidopsis
4	48	53.3	1194	5 Q9W485	Q9w485 drosophila
5	48	53.3	1284	5 Q960F1	Q960f1 drosophila
6	47	52.2	338	10 Q9C9S8	Q9c9s8 arabidopsis
7	47	52.2	355	4 Q9UKR6	Q9ukr6 homo sapien
8	47	52.2	355	4 Q9UJS5	Q9ujjs homo sapien
9	47	52.2	653	10 Q9XEW2	Q9xew2 oryza sativ
10	47	52.2	668	10 Q9FRE1	Q9frf1 oryza sativ
11	47	52.2	774	5 Q9V620	Q9v620 drosophila
12	47	52.2	813	5 Q95TY2	Q95ty2 drosophila
13	47	52.2	941	10 Q9AYJ3	Q9ayj3 oryza sativ
14	47	52.2	1016	10 Q9AUX7	Q9aux7 oryza sativ
15	47	52.2	1073	10 Q9XEQ1	Q9xeq1 sorghum bic
16	46	51.1	998	5 Q21301	Q21301 caenorhabdi

17	46	51.1	1283	4	O95451	O95451 homo sapien
18	46	51.1	1289	10	Q9FLQ7	Q9flq7 arabidopsis
19	46	51.1	1300	12	O36421	O36421 alcelaphine
20	46	51.1	1321	4	O95291	O95291 homo sapien
21	46	51.1	1594	4	Q9HC84	Q9hc84 homo sapien
22	46	51.1	1994	10	Q9LP19	Q9lp19 arabidopsis
23	45	50.0	118	2	O934B5	O934b5 aeromonas s
24	45	50.0	133	12	O90704	O90704 chicken ane
25	45	50.0	494	5	O76941	O76941 drosophila
26	45	50.0	705	4	Q9H624	Q9h624 homo sapien
27	45	50.0	880	4	Q9X2Y2	Q9x2y2 homo sapien
28	45	50.0	889	11	Q9CUD6	Q9cud6 mus musculu
29	45	50.0	914	5	Q22715	Q22715 caenorhabdi
30	45	50.0	983	4	Q9C0A4	Q9c0a4 homo sapien
31	45	50.0	986	4	Q9H0N3	Q9h0n3 homo sapien
32	45	50.0	1209	4	Q9V4D3	Q9v4d3 homo sapien
33	45	50.0	1518	5	Q9VN58	Q9vn58 drosophila
34	45	50.0	1932	5	O01483	O01483 caenorhabdi
35	45	50.0	2061	5	Q9V0H9	Q9v0h9 drosophila
36	45	50.0	2301	10	Q9ATK5	Q9atk5 chlamydomon
37	44.5	49.4	543	5	Q9W852	Q9w852 drosophila
38	44.5	49.4	1134	4	Q96JH1	Q96jhl homo sapien
39	44	48.9	101	2	Q9FBP0	Q9fbp0 streptomyce
40	44	48.9	377	16	O69559	O69559 mycobacteri
41	44	48.9	389	3	Q96039	Q96u39 neurospora
42	44	48.9	495	5	Q95YB0	Q95yb0 caenorhabdi
43	44	48.9	551	4	O16630	O16630 homo sapien
44	44	48.9	588	4	Q9BW18	Q9bw18 homo sapien
45	44	48.9	639	4	Q9NV29	Q9nv29 homo sapien

ALIGNMENTS

RESULT	1		
Q97E35	PRELIMINARY;	PRT;	706 AA.
ID	Q97E35;		
AC	O1-OCT-2001 (TREMBlrel. 18, Created)		
DT	O1-OCT-2001 (TREMBlrel. 18, Last sequence update)		
DT	O1-DEC-2001 (TREMBlrel. 19, Last annotation update)		
DE	ABC-TYPE MULTIDRUG/PROTEIN/LIPID TRANSPORT SYSTEM, ATPASE COMPONENT.		
DE	COMPONENT.		
GN	CAC3281.		
OS	Clostridium acetobutylicum.		
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;		
OC	Clostridium.		
OX	NCBI_TaxID=1488;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=ATCC 824 / DSM 792 / VKM B-1787;		
RX	MEDLINE=21359325; PubMed=11466286;		
RA	Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,		
RA	Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,		
RA	Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,		
RA	Bennett G.N., Koonin E.V., Smith D.R.;		
RT	"Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";		
RT	J. Bacteriol. 183:4823-4838(2001).		
RL	EMBL; AE007824; AAK81215.1; -.		
DR	InterPro; IPR003593; AAA.		
DR	InterPro; IPR001140; ABC_transporter_tmem.		
DR	InterPro; IPR003439; ABC_transporter.		
DR	InterPro; IPR001687; ATP_GTP-A.		
DR	Pfam; PF00664; ABC_membrane; 1.		
DR	Pfam; PF00005; ABC_tran; 1.		
DR	SMART; SM00382; AAA; 1.		
DR	PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.		
KW	Complete proteome.		
SQ	SEQUENCE 706 AA; 78003 MW; 14A1B3F2285332DD CRC64;		

Query Match

58.9%; Score 53; DB 16; Length 706;

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Best Local Similarity 57.9%; Pred. No. 2;
Matches 11; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY 1 VKEXKXG--KGPGGXPP 17
   : ||| | ||||| ||
Db 1 MSERKKSTGMSKGGGPP 19

RESULT 2
ID 070373 PRELIMINARY; PRT; 1677 AA.
AC 070373; 1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE XIN.
GN XIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN RP SEQUENCE FROM N.A.
RC TISSUE=HEART MUSCLE;
RX PubMed-9159189;
RA Wang D.-Z., Hu X., Lin J.L.-C., Kitten G.T., Solursh M., Lin J.J.-C.;
RT "Differential display of mRNAs from the atrioventricular region of
RT developing chicken hearts at stages 15 and 21.";
RL Front. Biosci. 1:a1-a15(1996).
[2]
RN RP SEQUENCE FROM N.A.
RC TISSUE=HEART MUSCLE;
RX MEDLINE=99145891; PubMed=10021346;
RA Wang D.-Z., Reiter R.S., Lin J.L.-C., Wang Q., Williams H.S.,
RA Krob S.L., Schultheiss T.M., Evans S., Lin J.J.-C.;
RT "Requirement of a novel gene, Xin, in cardiac morphogenesis.";
RL Development 126:1281-1294(1999).
DR EMBL; AF051945; AAC06023.1; -.
DR MGD; MGI:1333878; Xin.
SQ SEQUENCE 1677 AA; 182085 MW; A201CFC9A710C7FF CRC64;

Query Match 54.4%; Score 49; DB 11; Length 1677;
Best Local Similarity 76.9%; Pred. No. 21;
Matches 10; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 9 GRGPGGXPP--PK 19
   ||||| ||| ||
Db 575 GRGPGGPPPELPK 587

RESULT 3
ID Q9FHM0 PRELIMINARY; PRT; 501 AA.
AC Q9FHM0;
DT 01-NAR-2001 (TrEMBLrel. 16, Created)
DT 01-NAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE LEAF-SENESCENCE-RELATED PROTEIN.
GN YLS7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20181125; PubMed=10718197;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC

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clones.";
RL DNA Res. 7:31-63(2000).
[2]
RN RP SEQUENCE FROM N.A.
RA Yoshida S., Masaki I., Nishida I., Watanabe A.;
RT "Isolation and expression analysis of molecular markers for leaf
RT senescence in Arabidopsis thaliana.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB018109; BAB08680.1; -.
DR EMBL; AB047810; BAB32887.1; -.
SQ SEQUENCE 501 AA; 56525 MW; 7AB4739CBF50FD98 CRC64;

Query Match 53.3%; Score 48; DB 10; Length 501;
Best Local Similarity 53.3%; Pred. No. 9.2;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 KXXKXGPGGXPPPK 19
   || :||| |||:
Db 452 KKITRKGPDGQPPQ 466

RESULT 4
ID Q9W485 PRELIMINARY; PRT; 1194 AA.
AC Q9W485;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE CG3125 PROTEIN.
GN CG3125.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blasej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Prannkoc C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Smith H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

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RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.W., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003435; AAF46073.1;
 DR FlyBase: FBgn0029797; CG3125.
 SQ SEQUENCE 1194 AA; 127551 MW; F0F2D3A55C7F6C59 CRC64;

Query Match 53.3%; Score 48; DB 5; Length 1194;
 Best Local Similarity 52.9%; Pred. No. 22;
 Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 VKEXKXXGKGGGXP 17
 Db | | | | | | | | | |
 610 VAPMKSPNGPGGAPP 626

RESULT 5
 ID Q960F1 PRELIMINARY; PRT; 1284 AA.
 AC Q960F1;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE SD04165P.
 GN CG3125.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nuno J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celnikier S.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY052093; AAK93517.1;
 SQ SEQUENCE 1284 AA; 137152 MW; E322BE35961525A1 CRC64;

Query Match 53.3%; Score 48; DB 5; Length 1284;
 Best Local Similarity 52.9%; Pred. No. 23;
 Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 VKEXKXXGKGGGXP 17
 Db | | | | | | | | | |
 654 VAPMKSPNGPGGAPP 670

RESULT 6
 ID Q9C9S8 PRELIMINARY; PRT; 338 AA.
 AC Q9C9S8;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE PUTATIVE PROLINE-RICH PROTEIN PRECURSOR.
 GN F25P22.26.
 OS *Arabidopsis thaliana* (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=CV. COLOMBIA;
 RC MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
 RA Dunn P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Mafti R., Marziani A.,
 RA Miličeski J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Taiton L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant *Arabidopsis thaliana*."
 RL Nature 408:816-820(2000).
 DR EMBL: AC012679; AAG52077.1;
 DR InterPro: IPR002965; P-rich.extensn.
 DR PRINTS: PR01217; PRICHEXTENS.
 SQ SEQUENCE 338 AA; 36412 MW; 64362CC1146F09AB CRC64;

Query Match 52.2%; Score 47; DB 10; Length 338;
 Best Local Similarity 77.8%; Pred. No. 9;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 GPGGXPPPK 19
 Db | | | | | | | | | |
 286 GPGGGPPPR 294

RESULT 7
 ID Q9UKR6 PRELIMINARY; PRT; 355 AA.
 AC Q9UKR6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE KRUPPEL-LIKE FACTOR LKLF.
 OS *Homo sapiens* (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG;
 RX MEDLINE=99389728; PubMed=10458913;
 RA Wani M.A., Konkright M.D., Jeffries S., Hughes M.J., Lingrel J.B.;
 RT "cDNA isolation, genomic structure, regulation, and chromosomal
 RT localization of human lung kruppel-like factor."
 RL Genomics 60:78-86(1999).
 DR EMBL: AF134053; AAD55891.1;
 DR HSSP: P08047; 1SP2.
 DR InterPro: IPR002965; P-rich.extensn.
 DR InterPro: IPR000822; Znf-C2H2.
 DR Pfam: PF00096; ZF-C2H2; 3.
 DR PRINTS: PR01217; PRICHEXTENS.
 DR SMART: SM00355; Znf_C2H2; 3.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 3.
 DR PROSITE: PS0157; ZINC_FINGER_C2H2_2; 3.
 KW DNA-binding; Metal-binding; Zinc-finger.
 SQ SEQUENCE 355 AA; 37454 MW; CDD1735CC516DE24 CRC64;

Query Match 52.2%; Score 47; DB 4; Length 355;
 Best Local Similarity 77.8%; Pred. No. 9.5;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 KPGGXPPP 18
 Db | | | | | | | | | |
 161 RGPGRPPPP 169

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RESULT 8
Q9UJSS ID Q9UJSS PRELIMINARY; PRT; 355 AA.
AC Q9UJSS;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE KRUPPEL-LIKE FACTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.J., Kim M.K., Kim Y.H., Seo J.M., Lee H.M., Chung H.J.,
RA Sohn M.Y., Hwang S.Y., Im S.U., Jung E.J., Kim J.C.;
RT "A catalogue of genes in the human dermal papilla cells as identified
RT by expressed sequence tags.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF205849; AAF13295.1; -.
DR HSSP; P08047; ISP2.
DR InterPro; IPR002965; P-rich_extensn.
DR InterPro; IPR000822; Znf-C2H2.
DR Pfam; PF00096; zf-C2H2; 3.
DR PRINTS; PR01217; PRICHEXTENS.
DR SMART; SM00355; ZnfC2H2; 3.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 3.
KW DNA-binding; Metal-binding; Zinc-finger.
SQ SEQUENCE 355 AA; 37419 MW; D5849C831D676AE1 CRC64;

Query Match 52.2%; Score 47; DB 4; Length 355;
Best Local Similarity 77.8%; Pred. No. 9.5;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 KPGGXP 18
Db 161 KPGGXP 169

RESULT 9
Q9XEW2 ID Q9XEW2 PRELIMINARY; PRT; 653 AA.
AC Q9XEW2;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE RIM2 PROTEIN.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Dong H., Dong J., He Z., Li D.;
RT "A Rice Transposon Protein-like cDNA Is Induced by Magnaporthe grisea
RT (Accession No. AF121139). (PGR99-042).";
RL Plant Physiol. 119:1149-1149(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA He Z., Dong H., Dong J., Li D.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF121139; AAD24042.2; -.
DR InterPro; IPR002203; Intein.
DR InterPro; IPR004242; Transposase_21.
DR Pfam; PF02992; Transposase_21; 1.
DR PROSITE; PS00881; PROTEIN_SPLICING; UNKNOWN_1.
SQ SEQUENCE 653 AA; 75811 MW; 8639D15235005C20 CRC64;

Query Match 52.2%; Score 47; DB 10; Length 653;
Best Local Similarity 56.2%; Pred. No. 18;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 VEXKXKXKGGPGXP 16
Db 303 VKDLKVVFGKPGSQP 318

RESULT 11
Q9V620 ID Q9V620 PRELIMINARY; PRT; 774 AA.
AC Q9V620;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CG8991 PROTEIN.
GN CG8991.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; Pubmed=10731132;
RA Adams M.D., Gelniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Fandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,

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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny L., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003824; AAF58619.1;
DR FlyBase; FBgn0033654; CG8991.
DR InterPro; IPR002965; P-rich_extensions.
DR PRINTS; PR01217; PRICHEXTENS.
SQ SEQUENCE 774 AA; 83718 MW; 04A64D97952CF90D CRC64;

Query Match 52.2%; Score 47; DB 5; Length 774;
Best Local Similarity 57.1%; Pred. No. 20;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 KXXGKGGGKXPPP 18
:| | | | | | | |
Db 366 QKSPGPGGAPPPP 379

RESULT 12
ID Q95TY2 PRELIMINARY; PRT; 813 AA.
AC Q95TY2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE GH22790P.
GN CG8991.
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y; CN BW SP;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phoumenavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY058444; AAL13673.1;
SQ SEQUENCE 813 AA; 88199 MW; 9B9F9571EA08308C CRC64;

Query Match 52.2%; Score 47; DB 5; Length 813;
Best Local Similarity 57.1%; Pred. No. 21;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 KXXGKGGGKXPPP 18
:| | | | | | | |
Db 405 QKSPGPGGAPPPP 418

RESULT 13
ID Q9AYJ3 PRELIMINARY; PRT; 941 AA.
AC Q9AYJ3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PUTATIVE TAM1 TRANSPONOSON PROTEIN TNP2.
GN OSJNBA0071K19.5.
OS *Oryza sativa* (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Wing R.A., Frisch D., Presting G., Wood T., Yu Y., Soderlund C.,
RA Kim H., Rambo T., Henry D., Simmons J., Willson R., Johnson D.,
RA Bradshaw H., Du H.;
RT "Rice Genomic Sequence";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC069324; AAK00419.1;
SQ SEQUENCE 941 AA; 107815 MW; 6CD3DD2E0EAB31D CRC64;

Query Match 52.2%; Score 47; DB 10; Length 941;
Best Local Similarity 56.2%; Pred. No. 25;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 VKEXKXKXGKGGXP 16
||:| | | | | | | |
Db 442 VKDLKVVFGKPGSQP 457

RESULT 14
ID Q9AUX7 PRELIMINARY; PRT; 1016 AA.
AC Q9AUX7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PUTATIVE TRANSPONOSON PROTEIN.
GN OSJNBB0028C01.11.
OS *Oryza sativa* (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,
RA Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T.,
RA Riggs F., Hsiao J., Zismann V., Blunt S., Pal G., VanAken S.E.,
RA Utterback T.R., Feldblum T.V., Quackenbush J., Salzberg S.L.,
RA White O., Fraser C.M.;
RT "Oryza sativa chromosome 10 BAC OSJNBB0028C01 genomic sequence";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC079029; AAK38319.1;
SQ SEQUENCE 1016 AA; 116605 MW; A3CE9E26A82C5C71 CRC64;

Query Match 52.2%; Score 47; DB 10; Length 1016;

Thu Sep 5 11:23:25 2002

Best Local Similarity 56.2%; Pred. No. 27;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 VKEXKXXGKGGGXP 16
||:| ||||| |
Db 421 VKDLKVVFGKGGSQP 436

RESULT 15

O9XEQ1 PRELIMINARY; PRT: 1073 AA.
AC O9XEQ1;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE TNP2-LIKE PROTEIN.
OS Sorghum bicolor (Sorghum) (Sorghum vulgare).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoidae; Andropogoneae; Sorghum.
OX NCBI_TaxID=4558;
RN [1]
RP SEQUENCE FROM N.A.
RA Llaca V., Lou A., Young S., Messing J.;
RT "Retrotransposable elements of Sorghum bicolor.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF114171; AAD27566.1; -
DR InterPro; IPR004242; Transposase_21.
DR Pfam; PF02992; Transposase_21; 1.
SQ SEQUENCE 1073 AA; 123055 MW; B46A38EC3882B197 CRC64;

Query Match 52.2%; Score 47; DB 10; Length 1073;

Best Local Similarity 52.6%; Pred. No. 28;
Matches 10; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 VKEXKXXGKGGGXP 19
||:| ||||| |
Db 617 VKDLKVVFGKGGSEPIPK 635

Search completed: September 4, 2002, 17:01:31
Job time: 1152 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:41:24 ; Search time 75.48 Seconds
(without alignments)
24.188 Million cell updates/sec

Title: US-09-821-726-1
Perfect score: 90
Sequence: 1 VREXKXKXGKGGPGXPPK 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	53	58.9	706	D97303	ABC-type multidrug
2	49	54.4	1677	T14267	Xin protein, stage
3	47	52.2	338	H96765	hypothetical prote
4	47	52.2	687	T34082	hypothetical prote
5	46	51.1	998	T23427	hypothetical prote
6	46	51.1	1300	T03166	probable immediate
7	46	51.1	1321	JE0352	mucin MUC5B, trach
8	46	51.1	1994	D86452	protein F6N18.13 [
9	45	50.0	914	T25220	hypothetical prote
10	45	50.0	1209	T20073	hypothetical prote
11	45	50.0	1922	T25525	hypothetical prote
12	44	48.9	298	A49630	ubiquitin conjugat
13	44	48.9	377	E87022	probable conserved
14	44	48.9	551	S57447	HPBRII-7 protein -
15	44	48.9	669	A97443	hypothetical prote
16	44	48.9	669	A26661	hypothetical prote
17	44	48.9	719	T52510	hypothetical prote
18	44	48.9	1323	PN0568	connectin 3B - chl
19	43.5	48.3	821	C39983	eps8 protein - mou
20	43	47.8	118	C43256	hypothetical prote
21	43	47.8	533	T10216	hypothetical prote
22	43	47.8	810	T13861	TRPC1 protein - hu
23	43	47.8	3124	A40020	collagen alpha 1(X
24	42	46.7	76	T09262	glycine-rich cell
25	42	46.7	152	S46272	another-specific pr
26	42	46.7	161	S12246	basic proline-rich
27	42	46.7	188	TJH0481	hypothetical prote
28	42	46.7	326	T29810	collagen col-14 -
29	42	46.7	326	TJ0169	

ALIGNMENTS

RESULT 1

D97303

ABC-type multidrug/protein/lipid transport system, ATPase component CAC3281 [imported
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: D97303

R:Noiling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L
J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: D97303

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-706 <KUR>

A:Cross-references: GB:AE001437; PIDN:AAK81215.1; PID:gl5026358; GSPDB:GN00168

A:Experimental source: Clostridium acetobutylicum ATCC824

A:Genetics:

A:Gene: CAC3281

Query Match 58.9%; Score 53; DB 2; Length 706;

Best Local Similarity 57.9%; Pred. No. 5.4;

Matches 11; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY 1 VREXKXKXG--KGPGGXPP 17

Db 1 MSERKKSTGMSKGGPGGP 19

RESULT 2

T14267

Xin protein, stage early embryo - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T14267

R:Wang, D.Z.; Lin, J.J.C.

submitted to the EMBL Data Library, March 1998

A:Description: Involvement of a novel gene, Xin, in cardiac looping.

A:Reference number: Z17948

A:Accession: T14267

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1677 <WAN>

A:Cross-references: EMBL:AF051945; NID:q2970645; PID:q2970646; PIDN:AAC06023.1

A:Experimental source: cardiac muscle; stage early embryo

Query Match

Best Local Similarity 54.4%; Score 49; DB 2; Length 1677;

Matches 10; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

```

QY 9 GKGGGXPP--PK 19
Db 575 GKGGGXPPPELPK 587

RESULT 3
H96765
hypothetical protein F25p22.26 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: H96765
R:Theologias, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maity, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: H96765
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-338 <STO>
A:Cross-references: GB:AF005173; NID:g6692747; PIDN:AAF24853.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

QY 11 GPGGXPPP 18
Db 286 GPGGGPPPR 294

Query Match 52.2%; Score 47; DB 2; Length 338;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 4
T34082
hypothetical protein C02F12.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jun-2000
C:Accession: T34082
R:Miller, N.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid C02F12.
A:Reference number: Z21473
A:Accession: T34082
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-687 <MIL>
A:Cross-references: EMBL:U41545; PIDN:AAA83191.1; CESP:C02F12.8
C:Genetics:
A:Gene: CESP:C02F12.8
A:Introns: 34/3; 118/3; 288/3; 445/2; 548/1; 634/3
C:Superfamily: Caenorhabditis elegans hypothetical protein C02F12.8

Query Match 52.2%; Score 47; DB 2; Length 687;
Best Local Similarity 52.9%; Pred. No. 37;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 KEXKXXKGGPGGXPPP 18
Db 545 KDOKKRGKRPVSNPPP 561

Query Match 52.2%; Score 47; DB 2; Length 687;
Best Local Similarity 52.9%; Pred. No. 37;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

RESULT 5
T23427
hypothetical protein K07G5.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T23427
R:McMurray, A.
submitted to the EMBL Data Library, April 1996
A:Reference number: Z19739
A:Accession: T23427
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-998 <WIL>
A:Cross-references: EMBL:Z71264; PIDN:CAA95828.1; GSPDB:GN00019; CESP:K07G5.1
A:Experimental source: clone K07G5
C:Genetics:
A:Gene: CESP:K07G5.1
A:Map position: 1
A:Introns: 17/1; 56/2; 131/1; 264/2; 297/1; 335/2; 360/3; 551/3; 775/3; 943/2

Query Match 51.1%; Score 46; DB 2; Length 998;
Best Local Similarity 87.5%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GPGGXPPP 18
Db 945 GPGGAPPP 952

Query Match 51.1%; Score 46; DB 2; Length 998;
Best Local Similarity 87.5%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 6
T03166
probable immediate early protein - alcelaphine herpesvirus 1
C:Species: alcelaphine herpesvirus 1
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Nov-1999
C:Accession: T03166
R:Ensser, A.; Pflanz, R.; Fleckenstein, B.
J. Virol. 71, 6517-6525, 1997
A:Title: Primary structure of the alcelaphine herpesvirus 1 genome.
A:Reference number: Z14840; MUID:97404659
A:Accession: T03166
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-1300 <ENS>
A:Cross-references: EMBL:AF005370; NID:g2337967; PIDN:AAC58118.1; PID:g2338034
C:Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homolo

Query Match 51.1%; Score 46; DB 2; Length 1300;
Best Local Similarity 47.1%; Pred. No. 92;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 KEXKXXKGGPGGXPPP 18
Db 65 KKKRKVTGEGPGGEGP 81

Query Match 51.1%; Score 46; DB 2; Length 1300;
Best Local Similarity 47.1%; Pred. No. 92;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

RESULT 7
JE0352
mucin MUC5B, tracheobronchial - human
C:Species: Homo sapiens (man)
C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
C:Accession: JE0352
R:Offner, G.D.; Nunes, D.P.; Keates, A.C.; Afshar, N.H.; Troxler, R.F.
Biochem. Biophys. Res. Commun. 251, 350-355, 1998
A:Title: The amino-terminal sequence of MUC5B contains conserved multifunctional D do
A:Reference number: JE0352; MUID:99009274
A:Accession: JE0352
A:Molecule type: mRNA
A:Residues: 1-1321 <OFF>
A:Cross-references: GB:AF086604; NID:g3789926; PIDN:AAC67545.1; PID:g3789927
C:Comment: This protein is large multimeric glycoproteins which is secreted by epithe
C:Genetics:
A:Gene: MUC5B

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Query Match 51.1%; Score 46; DB 2; Length 1321;
 Best Local Similarity 57.1%; Pred. No. 94;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 6 KXXGKGGGXPPPK 19
 | : |||| | |

Db 971 KAVARGGGPPPK 984

RESULT 8

D86452

protein P6N18.13 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: D86452

R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Hulzar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: D86452

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1994 <STO>

A:Cross-references: GB:A8005172; NID:96714281; PIDN:AAF25977.1; GSPDB:GN00141

C:Genetics:

A:Gene: P6N18.13

A:Map position: 1

Query Match

Best Local Similarity 51.1%; Score 46; DB 2; Length 1994;

Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 KXXKXXGKGGGXPPPK 19
 | : | | | | | |

Db 1367 KKKKGVGGMGSPPPR 1384

RESULT 9

T25220

hypothetical protein T24B8.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T25220

R:Percy, C.

submitted to the EMBL Data Library, January 1996

A:Reference number: Z19999

A:Accession: T25220

A:Molecule type: DNA

A:Residues: 1-914 <WIL>

A:Cross-references: EMBL:Z68338; PIDN:CAA92756.1; GSPDB:GN00020; CESP:T24B8.4

A:Experimental source: clone T24B8

C:Genetics:

A:Gene: CESP:T24B8.4

A:Map position: 2

A:Introns: 30/3; 218/2; 261/2; 336/1; 468/3; 551/2; 606/3; 796/3

Query Match

Best Local Similarity 50.0%; Score 45; DB 2; Length 914;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GPGGXPPP 18
 |||| |

Db 100 GPGGIPPP 107

RESULT 10

T00373

hypothetical protein KIAA0649 - human

C:Species: Homo sapiens (man)

C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000

C:Accession: T00373

R:Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura,

DNA Res. 5, 169-176, 1998

A:Title: Prediction of the coding sequences of unidentified human genes. X. The compl

A:Reference number: Z14142; MUID:98403880

A:Accession: T00373

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1209 <ISH>

A:Cross-references: EMBL:AB014549; NID:g3327111; PIDN:BAA31624.1; PID:g3327112

A:Experimental source: brain

C:Genetics:

A:Note: KIAA0649

Query Match

Best Local Similarity 50.0%; Score 45; DB 2; Length 1209;

Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 VKEXKXXGKGGGXPP 17
 : : | : || |

Db 754 LSKSKRDSGEGGKKPP 770

RESULT 11

T25525

hypothetical protein C06A5.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000

C:Accession: T25525

R:Davidson, S.; Wohldmann, P.

submitted to the EMBL Data Library, April 1997

A:Description: The sequence of C. elegans cosmid C06A5.

A:Reference number: Z20044

A:Accession: T25525

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1932 <DAV>

A:Cross-references: EMBL:U97193; PIDN:AAB52443.1; GSPDB:GN00019; CESP:C06A5.1

A:Experimental source: strain Bristol N2; clone C06A5

C:Genetics:

A:Gene: CESP:C06A5.1

A:Map position: 1

A:Introns: 66/1; 153/3; 275/2; 497/3; 531/3; 798/2; 902/1; 929/3; 1039/3; 1133/3; 120

C:Superfamily: Caenorhabditis elegans hypothetical protein C06A5.1

Query Match

Best Local Similarity 50.0%; Score 45; DB 2; Length 1932;

Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 KXXGKGGGXPPPK 19
 | : | | | | |

Db 1725 KRSAGDRGGGPPPK 1739

RESULT 12

A49630

ubiquitin conjugating enzyme - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 05-Nov-1999

C:Accession: A49630

R:Plon, S.E.; Leppig, K.A.; Do, H.N.; Groudine, M.

Proc. Natl. Acad. Sci. U.S.A. 90, 10484-10488, 1993

A:Title: Cloning of the human homolog of the CDC34 cell cycle gene by complementation

A:Reference number: A49630; MUID:94068425

A:Accession: A49630

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-298 <RES>

A:Cross-references: GB:I22005; NID:g388308; PIDN:AAC37534.1; PID:g388309

C:Superfamily: human ubiquitin-protein ligase E2

Query Match 48.9%; Score 44; DB 2; Length 298;

Best Local Similarity 53.8%; Pred. No. 45;

Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 KXXGKGPGGXP 17

DB 21 EEEAGGGPGGSP 33

RESULT 13

E87022

probable conserved membrane protein ML0907 [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C:Accession: E87022

R: Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho

R: Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,

cam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S

A:Title: Massive gene decay in the leprosy bacillus.

A:Reference number: A86909; MUID:21128732; PMID:11234002

A:Accession: E87022

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-377 <STO>

A:Cross-references: GB:AL450380; NID:g13092977; PIDN:CAC31288.1; GSPDB:GN00147

C:Genetics:

A:Gene: ML0907

Query Match 48.9%; Score 44; DB 2; Length 377;

Best Local Similarity 87.5%; Pred. No. 56;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GPGGXPPP 18

DB 254 GPGGPPPP 261

RESULT 14

S57447

HPBRII-7 protein - human

N:Alternate names: HPBRII-4 protein

C:Species: Homo sapiens (man)

C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 24-Sep-1999

C:Accession: S57447; S57489

R: Fleischhauer, K.L.

submitted to the EMBL Data Library, June 1992

A:Reference number: S57447

A:Accession: S57447

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-551 <FLE>

A:Cross-references: EMBL:X67336; NID:g871300; PIDN:CAA47751.1; PID:g871301

A:Accession: S57489

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-551 <FL2>

A:Cross-references: EMBL:X67337; NID:g871298; PIDN:CAA47752.1; PID:g871299

C:Genetics:

A:Introns: 231/3

C:Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprotei

F: 82151/Domain: ribonucleoprotein repeat homology <RRM4>

Query Match 48.9%; Score 44; DB 2; Length 551;

Best Local Similarity 87.5%; Pred. No. 79;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GPGGXPPP 18

DB 222 GPGGPPPP 229

RESULT 15

A97443

hypothetical protein AGR_C1238 [imported] - Agrobacterium tumefaciens (strain C58, C

C:Species: Agrobacterium tumefaciens

C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002

C:Accession: A97443

R: Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldm

A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,

Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium

A:Reference number: A97359; PMID:11743194

A:Accession: A97443

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-669 <KUR>

A:Cross-references: GB:AE007869; PIDN:AAK86498.1; PID:g15155650; GSPDB:GN00169

C:Genetics:

A:Gene: AGR_C1238

A:Map position: circular chromosome

Query Match 48.9%; Score 44; DB 2; Length 669;

Best Local Similarity 72.7%; Pred. No. 95;

Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 KXXGKGPGGXP 16

DB 645 KPGKGPGGKP 655

Search completed: September 4, 2002, 16:47:29

Job time: 365 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2002, 16:38:44 : Search time 158.52 Seconds
(without alignments)
13.313 Million cell updates/sec

Title: US-09-821-726-1

Perfect score: 90

Sequence: 1 VKEXKXXGKPGGXPXPPK 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802.*
1: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
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14: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
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20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	63	70.0	185	20	AAW99667 Human secreted pro
2	63	70.0	185	21	AA24067 Human PRO1005 prot
3	63	70.0	185	21	AA58727 Human signal pepti
4	63	70.0	185	21	AA56686 Membrane-bound pro
5	63	70.0	185	22	AA65209 Human PRO1005 (UNQ
6	63	70.0	185	22	AA650957 Human PRO1005 prot
7	63	70.0	186	21	AA638329 Human secreted pro
8	63	70.0	194	19	AA669974 Cancer associated
9	63	70.0	194	20	AA576591 Human ovarian tumo
10	55	61.1	140	22	AA008289 Human polypeptide
11	55	61.1	147	22	AA006887 Human polypeptide

12	54	60.0	52	21	AA59108 Breast and ovarian
13	51	56.7	106	22	AA002086 Human polypeptide
14	51	56.7	107	22	AA004646 Human polypeptide
15	48	53.3	108	22	AA004166 Human polypeptide
16	48	53.3	354	21	AA64874 Arabidopsis thalia
17	48	53.3	503	21	AA64874 Arabidopsis thalia
18	48	53.3	536	21	AA64874 Arabidopsis thalia
19	48	53.3	1194	22	AA59646 Arabidopsis thalia
20	47	52.2	120	22	AA000290 Drosophila melanog
21	47	52.2	774	22	AA64148 Human polypeptide
22	46	51.1	59	21	AA653249 Drosophila melanog
23	46	51.1	106	22	ABG14653 Human colon cancer
24	46	51.1	122	22	AA000825 Novel human diagno
25	46	51.1	150	22	AA010242 Human polypeptide
26	46	51.1	223	21	AA643835 Human polypeptide
27	45	50.0	62	21	AA59111 Human cancer assoc
28	45	50.0	96	22	AA004073 Breast and ovarian
29	45	50.0	109	22	AA009868 Human polypeptide
30	45	50.0	133	13	AA23830 Human polypeptide
31	45	50.0	245	21	AA643357 Chicken anaemia vi
32	45	50.0	281	22	ABG13340 Human ORFX ORF3121
33	45	50.0	600	22	AA64233 Novel human diagno
34	45	50.0	878	20	AA697850 Human protein sequ
35	45	50.0	879	20	AA697849 Human p101/P13 kin
36	45	50.0	880	20	AA697847 Human p101/P13 kin
37	45	50.0	880	20	AA697848 Human p101/P13 kin
38	45	50.0	880	20	AA697848 Human p101/P13 kin
39	45	50.0	880	20	AA697848 Human p101/P13 kin
40	45	50.0	880	21	AA697848 Human p101/P13 kin
41	45	50.0	880	21	AA697848 Human p101/P13 kin
42	45	50.0	880	21	AA697848 Human p101/P13 kin
43	45	50.0	880	21	AA697848 Human p101/P13 kin
44	45	50.0	1518	22	AA64829 Human p101/P13 kin
45	45	50.0	2061	22	AA64829 Human p101/P13 kin

ALIGNMENTS

RESULT 1
ID AAW99667 standard; Protein: 185 AA.
XX AAW99667;
AC AC
DT DT
XX 07-JUN-1999 (first entry)
DE Human secreted protein clone ej90_5 protein.
XX Human; secreted protein; nutritional; cytokine; cell proliferation;
KW differentiation; immune stimulating; vaccine; haematopoiesis regulation;
KW tissue growth; chemotactic; chemokinetic; haemostatic; thrombolytic;
KW anti-inflammatory; cadherin; tumour invasion suppressor;
KW tumour inhibition; gene therapy.
XX Homo sapiens.
OS XX
PN WO9907840-A1.
XX PD
PD 18-FEB-1999.
XX PF
PF 06-AUG-1998; 98WO-US16318.
XX PR
PR 04-AUG-1998; 98US-0130189.
XX PR
PR 06-AUG-1997; 97US-0906708.
XX PA
PA (GEWY) GENETICS INST INC.
XX PI
PI Agostino MJ, Evans C, Jacobs K, Lavallie ER, McCoy JM;
PI Merberg D, Racie LA, Steininger RJ, Treacy M;
XX WPI; 1999-167419/14.
DR N-PSDB; AAX19493.

XX New polynucleotides encoding secreted human proteins - derived from
 PT fetal kidney, adult testes, adult brain, adult heart, adult placenta
 PT or adult retina cDNA libraries
 XX
 PS Claim 34; Page 98-99; 107pp; English.
 XX
 CC The present sequence represents a human secreted protein. The secreted
 CC protein can have activities such as: nutritional activity, cytokine and
 CC cell proliferation/differentiation activity, immune stimulating (e.g. as
 CC vaccines) or suppressing activity, haematopoiesis regulating activity,
 CC tissue growth activity, activin/inhibin activity, chemotactic/
 CC chemokinetic activity, haemostatic and thrombolytic activity, receptor/
 CC ligand activity, anti-inflammatory activity, cadherin/tumour invasion
 CC suppressor activity, and tumour inhibition activity. The secreted
 CC protein polynucleotides and proteins are predicted to have biological
 CC activities which would make them suitable for treating, preventing or
 CC ameliorating medical conditions in humans and animals. The
 CC polynucleotides are also stated to be useful for gene therapy.
 XX
 XX Sequence 185 AA;
 SQ
 Query Match 70.0%; Score 63; DB 20; Length 185;
 Best Local Similarity 78.9%; Pred. No. 0.18;
 Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
 QY 1 VKEXKXKXGKGGXPPPK 19
 ||| || ||||| ||||
 Db 101 vke-kklgkpgg-pppk 117
 RESULT 2
 AAB24067
 ID AAB24067 standard; Protein: 185 AA.
 AC AAB24067;
 XX
 DT 29-JAN-2001 (first entry)
 DE Human PRO1005 protein sequence SEQ ID NO:34.
 XX
 KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
 KW proliferation; tumorigenesis; identification; cancer; cytostatic;
 KW neutropic; neuroprotective; antiinflammatory; immunosuppressive;
 KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
 KW neuronal disorder; glial disorder; astrocytal disorder; angiogenic;
 KW hypothalamic disorder; glandular disorder; macrophagal disorder;
 KW epithelial disorder; stromal disorder; blastocoeic disorder;
 KW inflammatory disorder; immunologic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200053755-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 06-JAN-2000; 2000WO-US00376.
 XX
 PR 08-MAR-1999; 99WO-US05028.
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 07-JUL-1999; 99US-0143048.
 PR 26-JUL-1999; 99US-0145698.
 PR 20-NOV-1999; 99WO-US28313.
 PR 20-DEC-1999; 99WO-US30911.
 PR 05-JAN-2000; 2000WO-US00219.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
 PI Watanabe CK, Wood WI;
 XX

DR WPI; 2000-572270/53.
 DR N-PSDB; AAC58377.
 XX Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
 PT treatment, diagnosis and prevention of cancer.
 XX
 XX Claim 61; Fig 22; 286pp; English.
 PS
 XX The present invention describes an isolated antibody that binds to
 CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO335,
 CC PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,
 CC PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,
 CC PRO1187, PRO1281, PRO23, PRO39, PRO334, PRO1317, PRO1710, PRO2094,
 CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell
 CC growth. The PRO polypeptides and nucleotides are useful in the
 CC treatment, diagnosis and prevention of cancer. The antibodies and other
 CC anti-tumour compounds may be used to treat various conditions, including
 CC those characterised by overexpression and/or activation of the amplified
 CC PRO genes. Exemplary conditions or disorders to be treated with such
 CC antibodies and other compounds include benign or malignant tumours
 CC (e.g., renal, liver, kidney, bladder, lung, vulva, thyroid, hepatic
 CC colorectal, prostate, pancreatic, lung, various head and neck tumours),
 CC carcinomas, sarcomas, glioblastomas, and other disorders such as neuronal,
 CC leukaemias and lymphoid malignancies, other disorders such as neuronal,
 CC glial, astrocytal, hypothalamic and other glandular, macrophagal,
 CC epithelial, stromal and blastocoeic disorders, and inflammatory,
 CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR
 CC primers and hybridisation probes used in the isolation of the human PRO
 CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human
 CC PRO polynucleotide and protein sequences given in the exemplification of
 CC the present invention.
 XX
 XX Sequence 185 AA;
 SQ
 Query Match 70.0%; Score 63; DB 21; Length 185;
 Best Local Similarity 78.9%; Pred. No. 0.18;
 Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
 QY 1 VKEXKXKXGKGGXPPPK 19
 ||| || ||||| ||||
 Db 101 vke-kklgkpgg-pppk 117
 RESULT 3
 AAY87272
 ID AAY87272 standard; Protein: 185 AA.
 XX
 AC AAY87272;
 XX
 DT 11-MAY-2000 (first entry)
 DE Human signal peptide containing protein HSPP-49 SEQ ID NO:49.
 XX
 KW Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
 KW antimicrobial; neutropic; neuroprotective; cardiovascular; hepatotropic;
 KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
 KW reproductive disorder; developmental disorder; arteriosclerosis;
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
 KW Parkinson's disease; Huntington's diseases; ovulatory defect;
 KW muscular dystrophy.
 XX
 OS Homo sapiens.
 XX
 PN WO200000610-A2.
 XX
 PD 06-JAN-2000.
 XX
 PF 25-JUN-1999; 99WO-US14484.
 XX
 PR 26-JUN-1998; 98US-0090762.

PR	31-JUL-1998;	98US-0094983.
PR	01-OCT-1998;	98US-0102686.
PR	11-DEC-1998;	98US-0112129.
XX	(INCY-)	INCYTE PHARM INC..
XX	Lal P,	Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
PI	Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;	
PI	Bandman O;	
XX	XX	
DR	WIPI: 2000-160673/14.	
XX	N-PSDB; AA298157.	
XX		
PT	New human signal peptide-containing proteins useful in treatment,	
PT	prevention and diagnosis of e.g. cancer, inflammation and	
XX	cardiovascular disease -	
XX	Claim 1; Page 193-194; 327pp; English.	
XX		
CC	AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the	
CC	human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have	
CC	anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,	
CC	neuroprotective, cardiovascular and antiasthmatic activities, and can	
CC	be used in gene therapy. HSPPs can be used to treat or prevent disorders	
CC	associated with decreased activity or function of HSPP. Antagonists of	
CC	HSPP are used to treat or prevent disorders associated with increased	
CC	activity or function of HSPP. Such diseases include cell proliferation	
CC	(including cancer), inflammation, cardiovascular, neurological,	
CC	reproductive or developmental disorders. (e.g. arteriosclerosis,	
CC	cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,	
CC	asthma, Crohn's disease, microbial or other infections, congestive or	
CC	ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's	
CC	diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP	
CC	nucleic acids can be used for the recombinant production of HSPP, for	
CC	detecting HSPP in standard hybridisation and amplification assays (for	
CC	diagnosis and monitoring), in gene therapy, as antisense,	
CC	triplex-forming or ribozyme therapeutics, for detecting related sequences	
CC	or genetic variations, and for chromosomal mapping. HSPP are also used to	
CC	raise specific antibodies (Ab) and to screen for agonists and	
CC	antagonists (potential therapeutic agents). Ab are used to diagnose, or	
CC	monitor, HSPP-related diseases (in usual immunoassays), as therapeutic	
CC	antagonists, in competitive drug screens, and for purification of HSPP	
CC	from natural sources.	
XX		
SQ	Sequence 185 AA;	
	Query Match 70.0%; Score 63; DB 21; Length 185;	
	Best Local Similarity 78.98; Pred.No. 0.18; Mismatches 2; Gaps 2;	
	Matches 15; Conservative 0;	
QY	1 VKEXKXKGGGKGGXPPPK 19	
Db	101 vke-kklggkgpgg-pppk 117	
RESULT 4		
AAF66686		
ID	AAF66686 standard; protein; 185 AA.	
XX		
AC	AAF66686;	
XX		
DT	05-APR-2000 (first entry)	
DE		
DE	Membrane-bound protein PRO1005.	
XX		
KW	Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;	
KK	pharmaceutical; receptor immunoadhesin; gene mapping.	
OS	Homo sapiens.	
XX		
PN	WO9963088-A2.	
XX		

PR 25-JUN-1998; 98US-0090691.
 PR 25-JUN-1998; 98US-0090694.
 PR 25-JUN-1998; 98US-0090695.
 PR 25-JUN-1998; 98US-0090696.
 PR 26-JUN-1998; 98US-0090862.
 PR 26-JUN-1998; 98US-0090863.
 PR 01-JUL-1998; 98US-0091358.
 PR 01-JUL-1998; 98US-0091360.
 PR 01-JUL-1998; 98US-0091478.
 PR 02-JUL-1998; 98US-0091478.
 PR 02-JUL-1998; 98US-0091519.
 PR 02-JUL-1998; 98US-0091626.
 PR 02-JUL-1998; 98US-0091628.
 PR 02-JUL-1998; 98US-0091633.
 PR 02-JUL-1998; 98US-0091646.
 PR 02-JUL-1998; 98US-0091673.
 PR 07-JUL-1998; 98US-0091978.
 PR 07-JUL-1998; 98US-0091982.
 PR 09-JUL-1998; 98US-0092182.
 PR 10-JUL-1998; 98US-0092472.
 PR 20-JUL-1998; 98US-0093339.
 PR 30-JUL-1998; 98US-0094651.
 PR 04-AUG-1998; 98US-0095282.
 PR 04-AUG-1998; 98US-0095285.
 PR 04-AUG-1998; 98US-0095301.
 PR 04-AUG-1998; 98US-0095302.
 PR 04-AUG-1998; 98US-0095318.
 PR 04-AUG-1998; 98US-0095321.
 PR 04-AUG-1998; 98US-0095325.
 PR 10-AUG-1998; 98US-0095916.
 PR 10-AUG-1998; 98US-0095929.
 PR 10-AUG-1998; 98US-0096012.
 PR 11-AUG-1998; 98US-0096143.
 PR 11-AUG-1998; 98US-0096146.
 PR 12-AUG-1998; 98US-0096329.
 PR 17-AUG-1998; 98US-0096757.
 PR 17-AUG-1998; 98US-0096766.
 PR 17-AUG-1998; 98US-0096768.
 PR 17-AUG-1998; 98US-0096773.
 PR 17-AUG-1998; 98US-0096791.
 PR 17-AUG-1998; 98US-0096867.
 PR 17-AUG-1998; 98US-0096891.
 PR 17-AUG-1998; 98US-0096894.
 PR 17-AUG-1998; 98US-0096895.
 PR 17-AUG-1998; 98US-0096897.
 PR 18-AUG-1998; 98US-0096949.
 PR 18-AUG-1998; 98US-0096950.
 PR 18-AUG-1998; 98US-0096959.
 PR 18-AUG-1998; 98US-0096960.
 PR 18-AUG-1998; 98US-0097022.
 PR 19-AUG-1998; 98US-0097141.
 PR 20-AUG-1998; 98US-0097218.
 PR 24-AUG-1998; 98US-0097661.
 PR 26-AUG-1998; 98US-0097951.
 PR 26-AUG-1998; 98US-0097952.
 PR 26-AUG-1998; 98US-0097954.
 PR 26-AUG-1998; 98US-0097955.
 PR 26-AUG-1998; 98US-0097971.
 PR 26-AUG-1998; 98US-0097974.
 PR 26-AUG-1998; 98US-0097978.
 PR 26-AUG-1998; 98US-0097979.
 PR 26-AUG-1998; 98US-0097986.
 PR 26-AUG-1998; 98US-0098014.
 PR 31-AUG-1998; 98US-0098525.
 PR 16-SEP-1998; 98US-0100634.
 PR 12-JAN-1999; 99US-0115565.
 XX (GETH) GENENTECH INC.
 PA Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
 PI Wood WI, Yuan J;
 XX

DR WPI; 2000-072883/06.
 DR N-PSDB; AAZ65023.
 XX Membrane-bound proteins and related nucleotide sequences -
 PT claim 12; Fig 139; 822pp; English.
 PS The invention provides membrane-bound PRO polypeptides and
 CC polynucleotides encoding them. The PRO sequences of the invention were
 CC identified based on extracellular domain homology screening. The PRO
 CC sequences have homology with proteins including LDL receptors, TIE
 CC ligands and various enzymes. The membrane-bound proteins and receptor
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
 CC immunoadhesins, for instance, can be used as therapeutic agents to block
 CC receptor-ligand interactions. The membrane-bound proteins can also be
 CC employed for screening of potential peptide or small molecule inhibitors
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences
 CC are useful as hybridization probes, in chromosome and gene mapping and in
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
 CC will also be useful for the preparation of PRO polypeptides, especially
 CC by recombinant techniques.
 XX Sequence 185 AA;
 SQ

Query Match 70.0%; Score 63; DB 21; Length 185;
 Best Local Similarity 78.9%; Pred. No. 0.18; Mismatches 2; Gaps 2;
 Matches 15; Conservative 0;

QY 1 VKEXKXKXGKGGGPPPK 19
 ||| || ||||| ||||
 Db 101 vke-kk1qgkpgg-pppk 117

RESULT 5
 AAB65209
 ID AAB65209 standard; Protein; 185 AA.
 XX
 AC AAB65209;
 XX
 DT 02-APR-2001 (first entry)
 XX Human PRO1005 (UNQ489) protein sequence SEQ ID NO:211.
 DE
 XX Human; secreted and transmembrane protein; PRO: cytostatic;
 KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
 KW diagnostic assay.
 XX Homo sapiens.
 OS
 XX WO200073454-A1.
 PN
 XX 07-DEC-2000.
 PD
 XX 30-MAR-2000; 2000WO-US08439.
 PF
 XX 02-JUN-1999; 99WO-US12252.
 XX 23-JUN-1999; 99US-0141037.
 PR 07-JUL-1999; 99US-0143048.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 28-JUL-1999; 99US-0146222.
 PR 17-AUG-1999; 99US-0149396.
 PR 15-SEP-1999; 99WO-US21090.
 PR 13-SEP-1999; 99WO-US21547.
 PR 08-OCT-1999; 99US-0158663.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;
 XX
 DR WPI: 2001-032160/04.
 DR N-PSDB; AAF44169.
 XX
 PT PRO polynucleotides used to produce polypeptides used to target
 PT bioactive molecules such as toxins, radiolabels or antibodies, to
 PT specific cells, to cause targeted cell death -
 XX
 PS Claim 12; Fig 139; 935pp; English.
 XX
 CC The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
 CC can be used for targeted delivery of bioactive molecules, such as
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA
 CC and DNA. They may also be used to produce transgenic animals which are
 CC used to develop and screen therapeutically useful reagents. The PRO
 CC nucleotide and protein sequence can be used for tissue typing and in
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
 CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 XX
 SQ Sequence 185 AA;
 CC
 Query Match 70.0%; Score 63; DB 22; Length 185;
 Best Local Similarity 78.9%; Pred. No. 0.18;
 Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
 Oy 1 VKEXKXKXGKGGXPPPK 19
 ||| || ||||| |||||
 Db 101 vke-kklgkpgg-pppk 117
 XX
 RESULT 6
 AAB50957
 ID AAB50957 standard; Protein; 185 AA.
 XX
 AC AAB50957;
 XX
 DT 21-MAR-2001 (first entry)
 XX
 DE Human PRO1005 protein.
 XX
 KW Human; PRO; cytostatic; neurotropic; neuroprotective; respiratory general;
 KW antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
 KW PRO agonist; cancer; inflammatory disorder; immunological disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200073348-A2.
 XX
 PD 07-DEC-2000.
 XX
 PF 30-MAY-2000; 2000WO-US14941.

XX
 PR 02-JUN-1999; 99WO-US12252.
 PR 22-JUN-1999; 99US-0140650.
 PR 23-JUN-1999; 99US-0141037.
 PR 20-JUL-1999; 99US-0144758.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30999.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 03-MAR-2000; 2000US-0187202.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
 PI Shelton DL, Smith V, Watanabe CK, Wood WI;
 XX
 DR WPI: 2001-016509/02.
 DR N-PSDB; AAC91559.
 XX
 PT Twenty eight nucleic acids encoding PRO polypeptides which are useful
 PT for treating various tumors, e.g. breast cancer, and other
 PT inflammatory, angiogenic and immunological disorders -
 XX
 PS Claim 31; Fig 14; 188pp; English.
 XX
 CC The present sequence is one of twenty eight novel PRO polypeptides. The
 CC PRO polypeptides and their agonists, including antibodies, peptides, and
 CC small molecule agonists, may be used to treat various tumours, e.g.,
 CC cancers such as breast cancer, ovarian cancer, renal cancer, colorectal
 CC cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,
 CC central nervous system cancer, melanoma or leukaemia. They are also
 CC useful for treating other disorders such as neuronal, glial, astrocytal,
 CC hypothalamic and other glandular, macrophagal, epithelial, stromal and
 CC blastocoealic disorders, and inflammatory, angiogenic and immunological
 CC disorders.
 XX
 SQ Sequence 185 AA;

Query Match 70.0%; Score 63; DB 22; Length 185;
 Best Local Similarity 78.9%; Pred. No. 0.18;
 Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
 Oy 1 VKEXKXKXGKGGXPPPK 19
 ||| || ||||| |||||
 Db 101 vke-kklgkpgg-pppk 117
 XX
 RESULT 7
 AAB38329
 ID AAB38329 standard; Protein; 186 AA.
 XX
 AC AAB38329;
 XX
 DT 31-JAN-2001 (first entry)
 XX
 DE Human secreted protein encoded by gene 9 clone HNSAD53.
 XX
 KW Immunosuppressive; antiarthritic; antirheumatic; antiproliferative;
 KW cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective;

KW neotropic; antibacterial; virucide; fungicide; ophthalmological; human;
 KW vulnary; gene therapy; infection; secreted protein.
 XX Homo sapiens.
 XX W0200061623-A1.
 XX 19-OCT-2000.
 XX 06-APR-2000; 2000WO-US08979.
 XX 09-APR-1999; 99US-0128693.
 XX 26-APR-1999; 99US-0130991.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Ruben SM, Ni J, Komatsoulis GA, Rosen CA, Soppet DR, Shi Y;
 PI Lafleur DW, Olsen HS, Ebner R, Florence KA, Moore PA, Birse CE;
 PI Young PE;
 XX WPI; 2000-647418/62.
 XX New nucleic acid molecules encoding 62 human secreted proteins for
 PT diagnosing, preventing, treating or ameliorating medical conditions and
 PT used as food additives or preservatives -
 XX Claim 11: Page 598; 716pp; English.
 XX Sequences AAB38321-B38396 represent the amino acid sequences of 62
 CC human secreted proteins encoded by the genes AAC69512-C69587. The genes
 CC and proteins are useful for preventing, ameliorating or treating medical
 CC conditions, e.g. by protein or gene therapy. The genes are isolated from
 CC a range of human tissues disclosed in the specification. The nucleic
 CC acids, proteins, antibodies and (ant)agonists are useful in the
 CC diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.
 CC rheumatoid arthritis; (b) hyperproliferative disorders e.g. cardiac
 CC of the breast or liver; (c) cardiovascular disorders e.g. cerebral ischemia; (e)
 CC angiotensin; (f) nervous system disorders e.g. Alzheimer's disease; (g)
 CC infections caused by bacteria, viruses and fungi; and (h) ocular
 CC disorders e.g. corneal infection. The polypeptides can also be used to
 CC aid wound healing and epithelial cell proliferation, to prevent skin
 CC aging due to sunburn, to maintain organs before transplantation, for
 CC supporting cell culture of primary tissues, to regenerate tissues and in
 CC chemotaxis.
 XX Sequence 186 AA;
 Query Match 70.0%; Score 63; DB 21; Length 186;
 Best Local Similarity 78.9%; Pred. No. 0.18;
 Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
 QY 1 VKEXKXKXGKGGXPPPK 19
 Db 101 vke-kklgkgpgg-pppk 117
 RESULT 8
 AAW69974
 ID AAW69974 standard; Protein; 194 AA.
 AC AAW69974;
 DT 16-NOV-1998 (first entry)
 DE Cancer associated protein.
 DE Cancer; PCR; Northern blotting; ribonuclease protection assay;
 KW diagnosis; metastatic cancer.
 XX Synthetic.
 XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;

PN W09837187-A1.
 XX 27-AUG-1998.
 XX 18-FEB-1998; 98WO-JP00667.
 XX 21-FEB-1997; 97JP-0052508.
 XX (TAKI) TAKARA SHUZO CO LTD.
 XX Asada K, Hino F, Kato I, Mukai H, Yoshikawa Y;
 PI WPI; 1998-467552/40.
 XX Detection of cancer cells in tissue samples - by changes in mRNA
 PT expression compared to normal tissue of specific cancer-associated
 PT gene sequences
 XX Claim 14; Page 64-65; 92pp; Japanese.
 XX The cancer associated proteins AAW69974-W69976 where used in the method
 CC of the invention to detect cancer cells in tissue samples or biological
 CC fluids. They are detected by monitoring the change in mRNA expression
 CC as compared to normal tissue of one or more cancer-associated genes
 CC whose cDNA stringently hybridises to cancer associated gene nucleic acid
 CC fragments. The change in expression may be an increase or a decrease
 CC compared to normal tissue. The mRNA expression may be determined by
 CC PCR, Northern blotting or ribonuclease protection assay, or by
 CC determining the change in the amount of protein encoded by the gene(s) as
 CC compared to normal tissue, for example by using a labelled antibody
 CC recognising the protein. Detection of cancer cells for cancer diagnosis,
 CC including detection of metastatic cancer cells in tissues other than the
 CC primary tumour site.
 XX Sequence 194 AA;
 Query Match 70.0%; Score 63; DB 19; Length 194;
 Best Local Similarity 78.9%; Pred. No. 0.19;
 Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
 QY 1 VKEXKXKXGKGGXPPPK 19
 Db 110 vke-kklgkgpgg-pppk 126
 RESULT 9
 AAY76591
 ID AAY76591 standard; Protein; 194 AA.
 AC AAY76591;
 DT 10-APR-2000 (first entry)
 DE Human ovarian tumor EST fragment encoded protein 87.
 DE Expressed sequence tag; EST; human; ovarian tumor; anticancer;
 KW gene therapy; treatment.
 XX Homo sapiens.
 XX DEL9817557-A1.
 XX 21-OCT-1999.
 XX 09-APR-1998; 98DE-1017557.
 XX 09-APR-1998; 98DE-1017557.
 XX (META-) METAGEN GES GENOMFORSCHUNG MBH.
 XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;

CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 147 AA;

Query Match 61.1%; Score 55; DB 22; Length 147;
 Best Local Similarity 58.8%; Pred. NO. 1.9;
 Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 2 KEXKXXGKGGXPPP 18
 I: || || || || ||
 Db 20 kkkkkkgknppggppp 36

RESULT 12

AA059108
 ID AAB59108 standard; Protein: 52 AA.

XX AAB59108;

DT 27-MAR-2001 (first entry)

XX Breast and ovarian cancer associated antigen protein sequence SEQ ID 816.

XX Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
 KW neutropic; neuroprotective; antiviral; antiallergic; hepatotropic;
 KW antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant;
 KW antibacterial; antifungal; antiparasitic; cardiac; immune disorder;
 KW Addison's disease; allergy; autoimmune haemolytic anaemia;
 KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
 KW cardiovascular disorder; wound healing; neurological disease.

XX Homo sapiens.

XX WO200055173-A1.

XX 21-SEP-2000.

XX 08-MAR-2000; 2000WO-US05881.

XX 12-MAR-1999; 99US-0124270.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI: 2000-611515/58.

XX N-PSDB; AAF22011.

XX New human breast and ovarian cancer associated gene sequences and the
 PT polypeptides encoded by these genes, useful in the prevention,
 PT treatment and diagnosis of cancer, immune disorders, cardiovascular
 PT disorders and neurological diseases -

XX Claim 11; Page 1276; 1299pp; English.

XX Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
 CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
 CC associated with breast and ovarian cancer. Included in the invention are
 CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
 CC isolation and characterisation of the DNA and protein sequences of the

CC

CC invention. The breast and ovarian cancer associated DNA, protein, agonist
 CC or antagonist sequences exhibit cytostatic; immunosuppressive;
 CC neutropic; neuroprotective; antiviral; antiallergic; hepatotropic;
 CC antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant;
 CC antibacterial; antifungal; antiparasitic and cardiac activity. The
 CC polynucleotide and protein sequences are used in the diagnosis of cancer,
 CC particularly breast and ovarian cancer. The nucleic acid sequences,
 CC proteins, agonists and antagonists may also be used in the diagnosis,
 CC prevention and treatment of immune disorders e.g. Addison's disease,
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
 CC arthritis and ulcerative colitis; cardiovascular disorders such as
 CC myocardial ischaemias; wound healing; neurological diseases such as
 CC cerebral anoxia and epilepsy; and infectious diseases.

XX Sequence 52 AA;

Query Match 60.0%; Score 54; DB 21; Length 52;
 Best Local Similarity 64.7%; Pred. NO. 1;
 Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 KEXKXXGKGGXPPP 18
 I: || || || || ||

Db 32 kkkkkkxpggxppp 48

RESULT 13

AA02086

ID AAO02086 standard; Protein: 106 AA.

XX AAO02086;

XX 06-NOV-2001 (first entry)

XX Human polypeptide SEQ ID NO 15978.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

XX Homo sapiens.

XX WO200164835-A2.

XX 07-SEP-2001.

XX 26-FEB-2001; 2001WO-US04927.

XX 28-FEB-2000; 2000US-0515126.

XX 18-MAY-2000; 2000US-0577409.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI: 2001-514838/56.

XX N-PSDB; AAI82017.

XX Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -

XX Claim 20; SEQ ID NO 15978; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO00010-AAO3910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating

Qy 9 GKPGGXPPP 18
| | | | |
Db 57 gggpggpppp 66

Search completed: September 4, 2002, 16:45:01
Job time: 377 sec

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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:45:09 ; Search time 166.13 Seconds
(without alignments)
28.128 Million cell updates/sec

Title: US-09-821-726-1
Perfect score: 90
Sequence: 1 VKEXKXXGKGGXPPPK 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 763338 seqs, 245939087 residues

Total number of hits satisfying chosen parameters: 763338

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_patents_AA_New.*

- 1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	63	70.0	185	5	US-09-991-150-211
2	63	70.0	185	5	US-09-720-533-49
3	63	70.0	185	6	US-10-119-480-148
4	63	70.0	185	6	US-10-119-480-148
5	63	70.0	185	6	US-10-216-159A-148
6	63	70.0	185	6	US-10-216-162-148
7	63	70.0	185	6	US-10-216-163-148
8	63	70.0	185	6	US-10-216-164-148
9	63	70.0	185	6	US-10-216-165-148
10	63	70.0	185	6	US-10-216-166-148
11	63	70.0	185	6	US-10-216-167-148
12	63	70.0	185	6	US-10-216-168-148
13	63	70.0	185	6	US-10-216-160-148
14	63	70.0	185	6	US-10-218-849-148
15	63	70.0	185	6	US-10-218-930-148
16	63	70.0	185	6	US-10-219-003-148
17	63	70.0	185	6	US-10-218-612-148
18	63	70.0	185	6	US-10-218-956-148
19	63	70.0	185	6	US-10-219-010-148
20	63	70.0	185	6	US-10-218-765-148
21	63	70.0	185	6	US-10-218-784-148
22	63	70.0	185	6	US-10-219-061-148
23	63	70.0	185	6	US-10-219-062-148
24	63	70.0	185	6	US-10-219-063-148
25	63	70.0	185	6	US-10-219-064-148
26	63	70.0	185	6	US-10-219-065-148
					Sequence 148, App

27	63	70.0	185	6	US-10-219-070-148	Sequence 148, App
28	63	70.0	185	6	US-10-219-071-148	Sequence 148, App
29	63	70.0	185	6	US-10-219-072-148	Sequence 148, App
30	63	70.0	185	6	US-10-219-073-148	Sequence 148, App
31	63	70.0	185	6	US-10-219-074-148	Sequence 148, App
32	63	70.0	185	6	US-10-219-075-148	Sequence 148, App
33	63	70.0	185	6	US-10-219-077-148	Sequence 148, App
34	63	70.0	185	6	US-10-219-464-148	Sequence 148, App
35	63	70.0	185	6	US-10-219-465-148	Sequence 148, App
36	63	70.0	185	6	US-10-219-466-148	Sequence 148, App
37	63	70.0	185	6	US-10-219-467-148	Sequence 148, App
38	63	70.0	185	6	US-10-219-470-148	Sequence 148, App
39	63	70.0	185	6	US-10-219-471-148	Sequence 148, App
40	63	70.0	185	6	US-10-219-474-148	Sequence 148, App
41	63	70.0	185	6	US-10-219-475-148	Sequence 148, App
42	63	70.0	185	6	US-10-219-476-148	Sequence 148, App
43	63	70.0	185	6	US-10-219-478-148	Sequence 148, App
44	63	70.0	185	6	US-10-219-479-148	Sequence 148, App
45	63	70.0	185	6	US-10-219-480-148	Sequence 148, App

ALIGNMENTS

RESULT 1
US-09-991-150-211
; Sequence 211, Application US/09991150
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC48
; CURRENT APPLICATION NUMBER: US/09/991,150
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 532
; SEQ ID NO 211
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-991-150-211

Query Match 70.0%; Score 63; DB 5; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.3;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXXGKGGXPPPK 19
||| || ||||| |||||

Db 101 VKE-KKLOGKGGG-PPPK 117

Thu Sep 5 11:23:24 2002

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US-09-720-533-49
RESULT 2
; Sequence 49, Application US/09720533
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: LAL, Preeti
; APPLICANT: TANG, Y. Tom
; APPLICANT: GORGONE, Gina A.
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AKERBLOM, Ingrid E.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: YUE, Henry
; APPLICANT: PATTERSON, Chandra
; APPLICANT: REDDY, Roopa
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: BANDMAN, Olga
; TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
; FILE REFERENCE: PF-0541 PCT
; CURRENT APPLICATION NUMBER: US/09/720,533
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/090,762; 60/094,983; 60/102,686; 60/112,129
; PRIOR FILING DATE: 1998-06-26; 1998-07-31; 1998-10-01; 1998-12-11
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PERL Program
; SEQ ID NO 49
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte Clone No: 2593853
US-09-720-533-49

Query Match 70.0%; Score 63; DB 5; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.3;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXXKGKGGXPPPK 19
Db 101 VKE-KKLOGKGGG-PPPK 117

RESULT 3
US-10-119-480-148
; Sequence 148, Application US/10119480
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C1
; CURRENT APPLICATION NUMBER: US/10/119,480
; CURRENT FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 246
; Remaining Prior Application data removed - See File Wrapper or Palm
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-119-480-148

Query Match 70.0%; Score 63; DB 5; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.3;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXXKGKGGXPPPK 19
Db 101 VKE-KKLOGKGGG-PPPK 117

RESULT 4
US-10-216-159A-148
; Sequence 148, Application US/10216159A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C6
; CURRENT APPLICATION NUMBER: US/10/216,159A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-159A-148

Query Match 70.0%; Score 63; DB 6; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.3;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXXKGKGGXPPPK 19
Db 101 VKE-KKLOGKGGG-PPPK 117

RESULT 5
US-10-216-162-148
; Sequence 148, Application US/10216162
; GENERAL INFORMATION:
```

```

; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC2
; CURRENT APPLICATION NUMBER: US/10/216,162
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-162-148

```

```

Query Match          70.0%; Score 63; DB 6; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.3;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

```

```

QY 1 VKEXKXXGKGGGXPXPK 19
   ||| || ||||| ||||
Db 101 VKE-KKLGKGGG-PPPK 117

```

```

RESULT 6
US-10-216-163-148
; Sequence 148, Application US/10216163
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC3
; CURRENT APPLICATION NUMBER: US/10/216,163

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```

; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-163-148

```

```

Query Match          70.0%; Score 63; DB 6; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.3;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

```

```

QY 1 VKEXKXXGKGGGXPXPK 19
   ||| || ||||| ||||
Db 101 VKE-KKLGKGGG-PPPK 117

```

```

RESULT 7
US-10-216-164-148
; Sequence 148, Application US/10216164
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC5
; CURRENT APPLICATION NUMBER: US/10/216,164
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20

```

```

Query Match          70.0%; Score 63; DB 6; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.3;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY      1 VKEXKXXGKGPGGXPPPK 19
      ||| || | ||||| ||||
Db      101 VKE-KKLOGKPGG-PPPK 117

RESULT          9
US-10-216-166-148
; Sequence 148, Application US/102161616
; GENERAL INFORMATION:
; Version 0

```

; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.

```

1 TITLE OF INVENTION: ACIDS AND TRANSFERABLE POLYMER FILMS AND RESINS
2
3 TITLE OF INVENTION: ACIDS ENCODING THE SAME
4
5 FILE REFERENCE: P3530P1C9
6
7 CURRENT APPLICATION NUMBER: US/10/216,166
8
9 CURRENT FILING DATE: 2002-08-09
10
11 PRIOR APPLICATION NUMBER: 10/119,480
12
13 PRIOR FILING DATE: 2002-04-09
14
15 PRIOR APPLICATION NUMBER: 60/059113
16
17 PRIOR FILING DATE: 1997-09-17
18
19 PRIOR APPLICATION NUMBER: 60/062287
20
21 PRIOR FILING DATE: 1997-10-17
22
23 PRIOR APPLICATION NUMBER: 60/063549
24
25 PRIOR FILING DATE: 1997-10-28
26
27 PRIOR APPLICATION NUMBER: 60/064103
28
29 PRIOR FILING DATE: 1997-10-31
30
31 PRIOR APPLICATION NUMBER: 60/069873
32

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```

; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-166-148

Query Match          70.0%; Score 63; DB 6; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.3;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2

Qy      1 VKEXKXKXGKGGXPPK 19
      ||| || ||||| |||||
Db      101 VKE-KKLGKGGG-PPPK 117

RESULT 10
US-10-216-167-148
; Sequence 148, Application US/10216167
; GENERAL INFORMATION:
; Inventor: Patrick Kevin P

```

```

; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C4
; CURRENT APPLICATION NUMBER: US/10/216,167
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-167-148

```

```

Query Match 70.0%; Score 63; DB 6; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.3;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

```

```

QY 1 VKEXKXKXGKGGXPPPK 19
    ||| || ||||| ||||
Db 101 VKE-KKLGKGGG-PPPK 117

```

```

RESULT 11
US-10-216-168-148
; Sequence 148, Application US/10216168
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C10
; CURRENT APPLICATION NUMBER: US/10/216,168
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480

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```

; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-168-148

```

```

Query Match 70.0%; Score 63; DB 6; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.3;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

```

```

QY 1 VKEXKXKXGKGGXPPPK 19
    ||| || ||||| ||||
Db 101 VKE-KKLGKGGG-PPPK 117

```

```

RESULT 12
US-10-216-160-148
; Sequence 148, Application US/10216160
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C8
; CURRENT APPLICATION NUMBER: US/10/216,160
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-160-148

```

```

Query Match 70.0%; Score 63; DB 6; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.3;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

```

```

QY 1 VKEXKXKXGKGGXPPPK 19
    ||| || ||||| ||||
Db 101 VKE-KKLGKGGG-PPPK 117

```

RESULT 13
US-10-218-849-148
; Sequence 148, Application US/10218849
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: US/10/218,849
; Prior Filing Date: 2002-08-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-849-148

Query Match 70.0%; Score 63; DB 6; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.3;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

Qy 1 VKEXKXXGKGPGGPPPK 19
||| || ||||| |||||
Db 101 VKE-KKLGKGGG-PPPK 117
RESULT 14
US-10-218-930-148
; Sequence 148, Application US/10218930
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: US/10/218,930
; Prior Filing Date: 2002-08-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-930-148

Query Match 70.0%; Score 63; DB 6; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.3;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

Qy 1 VKEXKXXGKGPGGPPPK 19
||| || ||||| |||||
Db 101 VKE-KKLGKGGG-PPPK 117
RESULT 15
US-10-219-003-148
; Sequence 148, Application US/10219003
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: US/10/219,003
; Prior Filing Date: 2002-08-12
; Prior Application Number: 10/119,480
; Prior Filing Date: 2002-04-09
; Prior Application Number: 60/059113
; Prior Filing Date: 1997-09-17
; Prior Application Number: 60/062287
; Prior Filing Date: 1997-10-17
; Prior Application Number: 60/063549
; Prior Filing Date: 1997-10-28
; Prior Application Number: 60/064103
; Prior Filing Date: 1997-10-31
; Prior Application Number: 60/069873
; Prior Filing Date: 1997-12-17
; Prior Application Number: 60/078910
; Prior Filing Date: 1998-03-20
; Prior Application Number: 60/079294
; Prior Filing Date: 1998-03-25
; Prior Application Number: 60/079656
; Prior Filing Date: 1998-03-26
; Prior Application Number: 60/079728
; Prior Filing Date: 1998-03-27
; Prior Application Number: 60/081819
; Prior Filing Date: 1998-04-15
; Prior Application Number: 60/081955
; Prior Filing Date: 1998-04-15
; Prior Application Number: 60/082804
; Prior Filing Date: 1998-04-22
; Prior Application Number: 60/084441
; Prior Filing Date: 1998-05-06
; Prior Application Number: 60/085323
; Prior Filing Date: 1998-05-13
; Prior Application Number: 60/085579
; Prior Filing Date: 1998-05-15
; Prior Application Number: 60/086392
; Prior Filing Date: 1998-05-22
; Prior Application Number: 60/089532
; Prior Filing Date: 1998-06-17
; Prior Application Number: 60/089538
; Prior Filing Date: 1998-06-17
; Prior Application Number: 60/089905
; Prior Filing Date: 1998-06-18
; Prior Application Number: 60/090472
; Prior Filing Date: 1998-06-24
; Prior Application Number: 60/090557
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; Prior Application Number: 60/090691
; Prior Filing Date: 1998-06-25
; Prior Application Number: 60/090695
; Prior Filing Date: 1998-06-25

;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/095302
;; PRIOR FILING DATE: 1998-08-04
;; PRIOR APPLICATION NUMBER: 60/095318
;; PRIOR FILING DATE: 1998-08-04
;; PRIOR APPLICATION NUMBER: 60/095916
;; PRIOR FILING DATE: 1998-08-10
;; PRIOR APPLICATION NUMBER: 60/095146
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;; PRIOR APPLICATION NUMBER: 60/096791
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;; PRIOR APPLICATION NUMBER: 60/099598
;; PRIOR FILING DATE: 1998-09-09
;; PRIOR APPLICATION NUMBER: 60/099803
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 60/099811
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 60/099812
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 60/099816
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 60/100038
;; PRIOR FILING DATE: 1998-09-11
;; PRIOR APPLICATION NUMBER: 60/100385
;; PRIOR FILING DATE: 1998-09-15
;; PRIOR APPLICATION NUMBER: 60/100390
;; PRIOR FILING DATE: 1998-09-15
;; PRIOR APPLICATION NUMBER: 60/100627
;; PRIOR FILING DATE: 1998-09-16
;; PRIOR APPLICATION NUMBER: 60/100848
;; PRIOR FILING DATE: 1998-09-18
;; PRIOR APPLICATION NUMBER: 60/100919
;; PRIOR FILING DATE: 1998-09-17
;; PRIOR APPLICATION NUMBER: 60/101477
;; PRIOR FILING DATE: 1998-09-23
;; PRIOR APPLICATION NUMBER: 60/101738
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101741
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101786
;; PRIOR FILING DATE: 1998-09-25
;; PRIOR APPLICATION NUMBER: 60/101916
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;; PRIOR APPLICATION NUMBER: 60/101922
;; PRIOR FILING DATE: 1998-09-24
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;; PRIOR APPLICATION NUMBER: 60/106248
;; PRIOR FILING DATE: 1998-10-29
;; PRIOR APPLICATION NUMBER: 60/106464
;; PRIOR FILING DATE: 1998-10-30
;; PRIOR APPLICATION NUMBER: 60/106905
;; PRIOR FILING DATE: 1998-11-03
;; PRIOR APPLICATION NUMBER: 60/108787
;; PRIOR FILING DATE: 1998-11-17
;; PRIOR APPLICATION NUMBER: 60/108801
;; PRIOR FILING DATE: 1998-11-17
;; PRIOR APPLICATION NUMBER: 60/108849
;; PRIOR FILING DATE: 1998-11-18
;; PRIOR APPLICATION NUMBER: 60/112422
;; PRIOR FILING DATE: 1998-12-15
;; PRIOR APPLICATION NUMBER: 60/113296
;; PRIOR FILING DATE: 1998-12-22
;; PRIOR APPLICATION NUMBER: 60/113605
;; PRIOR FILING DATE: 1998-12-23
;; PRIOR APPLICATION NUMBER: 60/113621

;; PRIOR FILING DATE: 1998-12-23
;; PRIOR APPLICATION NUMBER: 60/115558
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/115565
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/115733
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/119549
;; PRIOR FILING DATE: 1999-02-10
;; PRIOR APPLICATION NUMBER: 60/123618
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;; PRIOR APPLICATION NUMBER: 60/125259
;; PRIOR FILING DATE: 1999-03-19
;; PRIOR APPLICATION NUMBER: 60/125775
;; PRIOR FILING DATE: 1999-03-23
;; PRIOR APPLICATION NUMBER: 60/126773
;; PRIOR FILING DATE: 1999-03-29
;; PRIOR APPLICATION NUMBER: 60/127887
;; PRIOR FILING DATE: 1999-04-05
;; PRIOR APPLICATION NUMBER: 60/130232
;; PRIOR FILING DATE: 1999-04-21
;; PRIOR APPLICATION NUMBER: 60/131022
;; PRIOR FILING DATE: 1999-04-26
;; PRIOR APPLICATION NUMBER: 60/131270
;; PRIOR FILING DATE: 1999-04-27
;; PRIOR APPLICATION NUMBER: 60/131291
;; PRIOR FILING DATE: 1999-04-27
;; PRIOR APPLICATION NUMBER: 60/131445
;; PRIOR FILING DATE: 1999-04-28
;; PRIOR APPLICATION NUMBER: 60/134287
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: 60/140650
;; PRIOR FILING DATE: 1999-06-22
;; PRIOR APPLICATION NUMBER: 60/140723
;; PRIOR FILING DATE: 1999-06-22
;; PRIOR APPLICATION NUMBER: 60/141037
;; PRIOR FILING DATE: 1999-06-23
;; PRIOR APPLICATION NUMBER: 60/144758
;; PRIOR FILING DATE: 1999-07-20
;; PRIOR APPLICATION NUMBER: 60/145698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: 60/146222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: 60/146963
;; PRIOR FILING DATE: 1999-08-03
;; PRIOR APPLICATION NUMBER: 60/149320
;; PRIOR FILING DATE: 1999-08-17
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;; PRIOR FILING DATE: 1999-08-17
;; PRIOR APPLICATION NUMBER: 60/151733
;; PRIOR FILING DATE: 1999-08-31
;; PRIOR APPLICATION NUMBER: 60/164418
;; PRIOR FILING DATE: 1999-11-09
;; PRIOR APPLICATION NUMBER: 60/166361
;; PRIOR FILING DATE: 1999-11-16
;; PRIOR APPLICATION NUMBER: 60/169445
;; PRIOR FILING DATE: 1999-12-07
;; PRIOR APPLICATION NUMBER: 60/169495
;; PRIOR FILING DATE: 1999-12-07
;; PRIOR APPLICATION NUMBER: 60/169835
;; PRIOR FILING DATE: 1999-12-07

Query Match 70.0%; Score 63; DB 6; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.3;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

Oy 1 VKEXKXKXGPGXPPPK 19
 |||||
Db 101 VVE-KKLOGKPGG-PPPK 117

Job time: 1154 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:46:14 ; Search time 34.18 Seconds
(without alignments)
21.523 Million cell updates/sec

Title: US-09-821-726-1
Perfect score: 90
Sequence: 1 VKEXKXKXGKGGXPPK 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	63	70.0	199	1	CL1P_HUMAN
2	56.5	62.8	184	1	CL1P_MOUSE
3	47	52.2	355	1	CLF2_HUMAN
4	47	52.2	687	1	YL18_CAEEL
5	43.5	48.3	721	1	E2BE_HUMAN
6	43.5	48.3	821	1	EP58_MOUSE
7	43	47.8	118	1	MOBC_THIFE
8	43	47.8	379	1	CYRG_BOVIN
9	43	47.8	2339	1	CCAB_RABIT
10	43	47.8	3124	1	CALC_CHICK
11	42.5	47.2	402	1	GUN1_HUMAN
12	42	46.7	161	1	ASFL_HELAN
13	42	46.7	326	1	CC14_CAEEL
14	42	46.7	384	1	VASP_CANFA
15	42	46.7	440	1	FXGA_CHICK
16	42	46.7	648	1	FZD1_HUMAN
17	42	46.7	775	1	PQOF_PSEAE
18	42	46.7	1168	1	MYSC_ACACA
19	41.5	46.1	822	1	EP58_HUMAN
20	41	45.6	109	1	HMB6_APTME
21	41	45.6	142	1	YPUB_KLEPN
22	41	45.6	351	1	KLF2_RAT
23	41	45.6	354	1	KLF2_MOUSE
24	41	45.6	356	1	E2F3_MOUSE
25	41	45.6	523	1	E2BD_HUMAN
26	41	45.6	684	1	SK1L_HUMAN
27	41	45.6	722	1	Z219_HUMAN
28	41	45.6	738	1	PL03_HUMAN
29	41	45.6	929	1	CALC_NOTVI
30	41	45.6	994	1	CLC1_MOUSE
31	41	45.6	994	1	CLC1_RAT
32	41	45.6	1464	1	CAL1_HUMAN
33	41	45.6	1638	1	BRM_DROME

34 40 44.4 198 1 RB16_RAT P35291 rattus norv
35 40 44.4 211 1 CAB4_HUMAN P37796 homo sapien
36 40 44.4 219 1 RB3D_MOUSE Q63942 rattus norv
37 40 44.4 219 1 RB3D_MOUSE Q63942 rattus norv
38 40 44.4 259 1 RNPH_MYCLE P37939 mycobacteri
39 40 44.4 375 1 HXA2_CHICK Q08727 gallus gall
40 40 44.4 375 1 SOX3_MOUSE P53784 mus musculu
41 40 44.4 391 1 EDA_HUMAN Q52838 homo sapien
42 40 44.4 464 1 EDA_MOUSE O54693 mus musculu
43 40 44.4 464 1 S3A2_HUMAN Q15428 homo sapien
44 40 44.4 510 1 PKH_DROME P14734 drosophila
45 40 44.4 656 1 HS7C_DROME P29844 drosophila

ALIGNMENTS

RESULT 1
ID CL1P_HUMAN STANDARD; PRT; 199 AA.
AC Q9NS71;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Call protein.
GN CALL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RX MEDLINE=20296773; PubMed=10835488;
RA Yoshikawa Y., Mukai H., Hino F., Asada K., Kato I.;
RT "Isolation of two novel genes, down-regulated in gastric cancer.";
RL Jpn. J. Cancer Res. 91:459-463(2000).
CC -!- TISSUE SPECIFICITY: Expressed in stomach. No expression is
CC detected in cancer tissue or gastric cancer cell lines.
CC -----
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CC -----
DR EMBL; AB039886; BAA92433.1; -
DR MIM; 606402; -
SQ SEQUENCE 199 AA: 21999 MW; C059B8B9A1338D7A CRC64;

Query Match 70.0%; Score 63; DB 1; Length 199;
Best Local Similarity 78.9%; Pred. No. 0.026;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

Oy 1 VKEXKXKXGKGGXPPK 19
||| || ||||| ||||
Db 115 VKE-KKLOGKGGG-PPPK 131

RESULT 2
ID CL1P_MOUSE STANDARD; PRT; 184 AA.
AC Q9CR36; Q9D7K7; Q9CTZ5;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Call protein homolog.
GN CALL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Thu Sep 5 11:23:25 2002

QC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Stomach, and Tongue;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Asnburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Sakimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustinclach S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -----
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CC -----
DR EMBL; AK008990; BAB26010.1; -
DR EMBL; AK008622; BAB25784.1; -
DR EMBL; AK008641; BAB25801.1; -
DR EMBL; AK008647; BAB25805.1; -
DR EMBL; AK008722; BAB25856.1; -
DR EMBL; AK008745; BAB25872.1; -
DR EMBL; AK008933; BAB25975.1; -
DR EMBL; AK008956; BAB25988.1; -
DR EMBL; AK009145; BAB26103.1; -
DR EMBL; AK019050; BAB31525.1; -
FT CONFLICT 113 113 P -> L (IN REF. 1: BAB26103).
SQ SEQUENCE 184 AA; 20134 MW; 288982F0404FFA8B CRC64;

Query Match 62.8%; Score 56.5; DB 1; Length 184;
Best Local Similarity 70.6%; Pred. No. 0.19;
Matches 12; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

QY 1 VREKXKXGKGGGXP 17
DB 101 VREQK---GKGGGAPP 114

RESULT 3
KLF2_HUMAN
ID KLF2_HUMAN STANDARD; PRT; 355 AA.
AC Q9Y5W3; Q9UKR6; Q9U5S5;
DT 30-MAY-2000 (Rel. 39, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Kruppel-like factor 2 (lung kruppel-like factor).
GN KLF2 OR KLFL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
PP [1]
RP SEQUENCE FROM N.A.

YL18_CAEEL
ID YL18_CAEEL STANDARD; PRT; 687 AA.
AC Q11103;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 76.7 kDa protein C02F12.8 in chromosome X.
GN C02F12.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Miller N.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; U41545; AAK39136.1; -.
DR WormPep; C02F12.8; E03902.
KW Hypothetical protein.
SQ SEQUENCE 687 AA; 76730 MW; C96D04DB4AF1DA18 CRC64;

Query Match 52.2%; Score 47; DB 1; Length 687;
Best Local Similarity 52.9%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
QY 2 KEKKKKXGKGGCGXPPP 18
ID: ||| ||| |||
Db 545 KQKKKKRGRPVSNPPP 561

RESULT 5
E2BE_HUMAN
ID E2BE_HUMAN STANDARD; PRT; 721 AA.
AC Q13144; Q96D04;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Translation initiation factor eIF-2B epsilon subunit (eIF-2B GDP-GTP
DE exchange factor).
GN EIF2B5 OR EIF2BE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung carcinoma;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE OF 81-721 FROM N.A.
RX MEDLINE=96305354; PubMed=8688466;
RA Asuru A.I., Mellor H., Thomas N.S.B., Yu L., Chen J.-J., Crosby J.S.,
RA Hartson S.D., Kimball S.R., Jefferson L.S., Matts R.L.;
RT "Cloning and characterization of cDNAs encoding the epsilon subunit
RT of eukaryotic initiation factor-2B from rabbit and human.";
RL Biochim. Biophys. Acta 1307:309-317(1996).
RN [3]
RP VARIANTS VWM G-73; A-91; F-106; H-113; G-315; H-299; G-315; H-315;
RP P-339; Q-339; W-339; V-386; A-430; R-628 AND K-650, AND VARIANT I-587.
RX MEDLINE=21583742; PubMed=11704758;
RA Leegwater P.A.J., Vermeulen G., Konst A.A.M., Naidu S., Mulders J.,

Visser A., Kersbergen P., Mobach D., Fonds D., van Berkel C.G.M.,
Lemmers R.J.L.F., Frants R.R., Oudejans C.B.M., Schutgens R.B.H.,
Pronk J.C., van der Knaap M.S.;
"Subunits of the translation initiation factor eIF2B are mutant in
leukoencephalopathy with vanishing white matter.";
Nat. Genet. 29:383-388(2001).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF EUKARYOTIC INITIATION FACTOR
CC 2-BOUND GDP FOR GTP.
CC -1- SUBUNIT: COMPLEX OF FIVE DIFFERENT SUBUNITS; ALPHA, BETA, GAMMA,
CC DELTA AND EPSILON.
CC -1- DISEASE: Defects in EIF2B5 are a cause of leukoencephalopathy with
CC vanishing white matter (VWM), a brain disease that occurs mainly
CC in children. The neurological signs of VWM include progressive
CC cerebellar ataxia, spasticity, inconstant optic atrophy and
CC relatively preserved mental abilities. The disease is chronic-
CC progressive with, in most individuals, additional episodes of
CC rapid deterioration following febrile infections or minor head
CC trauma. Head trauma leads only to motor deterioration, whereas
CC infections with fever may end in coma. Death occurs after a
CC variable period of a few years to a few decades, usually following
CC an episode of fever and coma.
CC -1- SIMILARITY: BELONGS TO THE EIF-2B GAMMA/EPSILON SUBUNITS FAMILY.
CC -----
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CC -----
DR EMBL; BC013590; AAH13590.1; -.
DR EMBL; U23028; AAC50646.1; -.
DR MTM; 603945; -.
DR MTM; 603986; -.
DR InterPro; IPR001451; Hexapep_transf.
DR InterPro; IPR003307; eIF5C.
DR Pfam; PF00132; hexapep; 3.
DR Pfam; PF02020; W2; 1.
DR SMART; SM00515; eIF5C; 1.
KW Amino-acid biosynthesis; Translation regulation; Disease mutation;
KW Polymorphism.
FT DOMAIN 505 509 POLY-GLU
FT VARIANT 73 73 V -> G (IN VWM).
FT FTID=VAR_012323.
FT T -> A (IN VWM).
FT FTID=VAR_012291.
FT L -> F (IN VWM).
FT FTID=VAR_012324.
FT R -> H (IN VWM).
FT FTID=VAR_012292.
FT R -> H (IN VWM).
FT FTID=VAR_012325.
FT R -> G (IN VWM).
FT FTID=VAR_012326.
FT R -> H (IN VWM).
FT FTID=VAR_012327.
FT R -> P (IN VWM).
FT FTID=VAR_012328.
FT R -> Q (IN VWM).
FT FTID=VAR_012329.
FT R -> W (IN VWM).
FT FTID=VAR_012330.
FT G -> V (IN VWM).
FT FTID=VAR_012293.
FT V -> A (IN VWM).
FT FTID=VAR_012331.
FT V -> I.
FT FTID=VAR_012332.
FT W -> R (IN VWM).
FT FTID=VAR_012294.
FT E -> K (IN VWM).
FT FTID=VAR_012333.

SQ SEQUENCE 721 AA; 80365 MW; 10109D3A464D336 CRC64;

Query Match 48.3%; Score 43.5; DB 1; Length 721;
Best Local Similarity 34.5%; Pred. No. 48;
Matches 10; Conservative 0; Mismatches 8; Indels 11; Gaps 1;

Qy 1 VKEXKXXKGGPGGX-----PPP 18
| | | | |
Db 13 VSRANKSGAGPGGGGGARGAEPPPP 41

RESULT 6

EP8_MOUSE
ID EP8_MOUSE STANDARD; PRT; 821 AA.
AC Q08509;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Epidermal growth factor receptor kinase substrate EPS8.
GN EPS8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94008987; PubMed=8404850;
RA Fazloli F., Minichiello L., Matoska V., Castagnino P., Miki T.,
Wong W.T., di Fiore P.P.;
RT "Eps8, a substrate for the epidermal growth factor receptor kinase,
enhances EGF-dependent mitogenic signals";
RL EMBO J. 12:3799-3808(1993).

RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 532-591.

RX MEDLINE=97448677; PubMed=9303002;
RA Kishan K.V.R., Scita G., Wong W.T., di Fiore P.P., Newcomer M.E.;
RT "The SH3 domain of Eps8 exists as a novel intertwined dimer.";
RL Nat. Struct. Biol. 4:739-743(1997).
CC -!- FUNCTION: UPON BINDING TO EGF RECEPTOR ENHANCES EGF-DEPENDENT
MITOGENIC SIGNALS. CAN BIND MULTIPLE CELLULAR TARGETS.
CC -!- PTM: PHOSPHORYLATED BY SEVERAL RECEPTOR TYROSINE KINASES.
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN. IT IS SPLIT IN TWO PARTS.
CC
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CC or send an email to license@isb-sib.ch).

CC EMBL; L21671; AAA16358.1; -
CC PDB; LAOJ; 08-JUL-98.
CC MGD; MGI:104684; Eps8.
CC InterPro: IPR000050; PID_domain.
CC Pfam: PF00018; SH3; 1.
CC SMART: SM00462; PTB; 1.
CC SMART: SM00326; SH3; 1.
CC PROSITE: PSS0002; SH3; 1.
KW SH3 domain; Phosphorylation; 3D-structure.
FT DOMAIN 69 129 PH (FIRST PART).
FT DOMAIN 210 213 POLY-PRO.
FT DOMAIN 322 325 POLY-PRO.
FT DOMAIN 381 414 PH (SECOND PART).
FT DOMAIN 421 440 PRO-RICH.
FT DOMAIN 532 591 SH3.
FT DOMAIN 620 650 PRO-RICH.
FT DOMAIN 658 663 POLY-SER.
SQ SEQUENCE 821 AA; 91738 MW; 6B9EB95DD22D910C CRC64;

Query Match 48.3%; Score 43.5; DB 1; Length 821;
Best Local Similarity 41.7%; Pred. No. 54;
Matches 10; Conservative 1; Mismatches 6; Indels 7; Gaps 1;

Qy 2 KEXKXXKGGPG-----GXPPP 18
| | | | |
Db 301 KKSKKSRKKGPGGVTLRAKPPP 324

RESULT 7

MOBC_THIFE
ID MOBC_THIFE STANDARD; PRT; 118 AA.
AC P22899;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE MOBC protein.
GN MOBC.
OS Thiobacillus ferrooxidans.
OC Plasmid pTF-FC2.
OC Bacteria; Proteobacteria; gamma subdivision; Acidithiobacillus.
OX NCBI_TaxID=920;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93015664; PubMed=1400173;
RA Rohrer J., Rawlings D.E.;
RT "Sequence analysis and characterization of the mobilization region of
a broad-host-range plasmid, pTF-FC2, isolated from Thiobacillus
ferrooxidans";
RL J. Bacteriol. 174:6230-6237(1992).
CC
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CC EMBL; M57717; AAA27390.1; -
CC PIR; C43256; C43256.
CC PIR; S27623; S27623.
KW Plasmid

SQ SEQUENCE 118 AA; 12956 MW; 13EAA3B1F1E707DE CRC64;

Query Match 47.8%; Score 43; DB 1; Length 118;
Best Local Similarity 47.1%; Pred. No. 10;
Matches 8; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 2 KEXKXXKGGPGGXPPP 18
| | | | |
Db 78 KPTRKAPVQAPGDTPPP 94

RESULT 8

CYRG_BOVIN
ID CYRG_BOVIN STANDARD; PRT; 379 AA.
AC Q95118;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Cytokine receptor common gamma chain precursor (Gamma-C)
DE (Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64).
GN IL2RG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.

```

RX MEDLINE=96268473; PubMed=8672241;
RA Yoo J., Stone R.T., Solinas-Toldo S., Fries R., Beattie C.W.;
RT "Cloning and chromosomal mapping of bovine interleukin-2 receptor
RL gamma gene.";
CC DNA Cell Biol. 15:453-459(1996).
CC -!- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
CC INTERLEUKINS.
CC -!- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
CC PROBABLY ALSO THE IL-13 RECEPTORS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -----
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CC -----
DR EMBL; U33748; AAB07812.1; .
DR HSP; P31785; 11LN.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN.III.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 379
FT DOMAIN 23 379 CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
FT TRANSMEM 270 290 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 291 379 POTENTIAL.
FT DOMAIN 158 256 CYTOPLASMIC (POTENTIAL).
FT DISULFD 68 78 FIBRONECTIN TYPE-III.
FT DISULFD 109 122 POTENTIAL.
FT CARBOHYD 77 77 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 81 81 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 90 90 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 171 171 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 379 AA; 43037 MW; 33CFAD9C9B032178 CRC64;

```

Query Match 47.8%; Score 43; DB 1; Length 379;
 Best Local Similarity 50.0%; Pred. No. 31;
 Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 VKEXKXKXGPGGXP 16
 | | | | | | | | | |
 Db 345 VSEIPPRGEGPGGP 360

RESULT 9

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ID CCAB_RABIT STANDARD; PRT; 2339 AA.
AC Q05152;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Voltage-dependent N-type calcium channel alpha-1B subunit (Calcium
DE channel, L type, alpha-1 polypeptide isoform 5) (Brain calcium channel
DE III) (BIII).
GN CACNA1B OR CACNL1A5 OR CACHS.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;

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RX MEDLINE=93236885; PubMed=8386525;
RA Fujita Y., Myllyleiff M., Dirksen R.T., Kim M.-S., Nildome T., Nakai J.,
RA Friedrich T., Iwabe N., Miyata T., Furuichi T., Furutama D.,
RA Mikoshiba K., Mori Y., Beam K.G.;
RT "Primary structure and functional expression of the omega-conotoxin-
RT sensitive N-type calcium channel from rabbit brain.";
CC Neuron 10:585-598(1993).
CC -!- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1B
CC GIVES RISE TO N-TYPE CALCIUM CURRENTS. N-TYPE CALCIUM CHANNELS
CC BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED
CC BY OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-GVIA) AND BY OMEGA-AGATOXIN-
CC ILIA (OMEGA-AGA-ILIA). THEY ARE HOWEVER INSENSITIVE TO
CC DIHYDROPYRIDINES (DHP), AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).
CC CALCIUM CHANNELS CONTAINING ALPHA-1B SUBUNIT MAY PLAY A ROLE IN
CC DIRECTED MIGRATION OF IMMATURE NEURONS.
CC -!- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION THROUGHOUT THE BRAIN.
CC -!- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
CC -!- PTM: PHOSPHORYLATED IN VITRO BY CAM-KINASE II, CAPK, PKC AND CGPK
CC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
CC FAMILY.
CC -----
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CC -----
EMBL; D14157; BAA03202.1; .
DR InterPro; IPR002077; Ca.Channel.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR000636; Cation_chan_non_lig.
DR InterPro; IPR001682; Channel_pore_Ca_Na.
DR Pfam; PF00520; Ion_trans; 4.
DR PRINTS; PR00167; CACHANNEL.
DR Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Calcium channel; Glycoprotein; Repeat; Multigene family;
KW Calcium-binding; Phosphorylation; ATP-binding.
FT REPEAT 82 359 I.
FT REPEAT 469 713 II.
FT REPEAT 1142 1424 III.
FT REPEAT 1461 1714 IV.
FT DOMAIN 1 95 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 114 S1 OF REPEAT I (POTENTIAL).
FT DOMAIN 115 132 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 133 152 S2 OF REPEAT I (POTENTIAL).
FT DOMAIN 153 163 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 164 183 S3 OF REPEAT I (POTENTIAL).
FT DOMAIN 184 187 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 188 206 S4 OF REPEAT I (POTENTIAL).
FT DOMAIN 207 225 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 226 245 S5 OF REPEAT I (POTENTIAL).
FT DOMAIN 246 331 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 332 356 S6 OF REPEAT I (POTENTIAL).

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CC -!- PTM: GLYCOSYLATED, CHONDROITIN-SULFATED (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH
 CC INTERRUPTED HELICES (FACIT) FAMILY
 CC -!- SIMILARITY: CONTAINS 4 VWFA DOMAINS.
 CC -!- SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -----
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 CC -----
 DR EMBL; D00824; BAA00701.1; -
 DR EMBL; X61024; CAA43358.1; -
 DR EMBL; M17375; AAA48718.1; -
 DR EMBL; J05137; AAA48635.1; -
 DR EMBL; X67327; CAA47744.1; -
 DR PIR; A28037; A28037.
 DR PIR; A34485; A34485.
 DR HSSP; P17301; IAOX.
 DR InterPro; IPR000087; Collagen.
 DR InterPro; IPR003961; FN.III.
 DR InterPro; IPR003962; FN.III_repeat.
 DR InterPro; IPR003129; TSPN.
 DR Pfam; PF01391; Collagen; 4.
 DR Pfam; PF00041; fn3; 17.
 DR Pfam; PF02210; TSPN; 1.
 DR Pfam; PF00092; vwa; 4.
 DR PRINTS; PR00014; FNTYPEIII.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR SMART; SM00060; FN3; 17.
 DR SMART; SM00210; TSPN; 1.
 DR SMART; SM00327; VWA; 4.
 DR PROSITE; PS0234; VWFA; 4.
 KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
 KW Cell adhesion; Collagen; Signal; Glycoprotein; Alternative splicing.
 FT SIGNAL 1 24
 FT CHAIN 25 3124 COLLAGEN ALPHA 1(XII) CHAIN.
 FT DOMAIN 25 114 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 139 311 VWFA 1.
 FT DOMAIN 332 425 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 439 615 VWFA 2.
 FT DOMAIN 629 720 FIBRONECTIN TYPE-III 3.
 FT DOMAIN 721 811 FIBRONECTIN TYPE-III 4.
 FT DOMAIN 812 904 FIBRONECTIN TYPE-III 5.
 FT DOMAIN 905 998 FIBRONECTIN TYPE-III 6.
 FT DOMAIN 999 1085 FIBRONECTIN TYPE-III 7.
 FT DOMAIN 1086 1178 FIBRONECTIN TYPE-III 8.
 FT DOMAIN 1199 1371 VWFA 3.
 FT DOMAIN 1384 1473 FIBRONECTIN TYPE-III 9.
 FT DOMAIN 1474 1565 FIBRONECTIN TYPE-III 10.
 FT DOMAIN 1566 1654 FIBRONECTIN TYPE-III 11.
 FT DOMAIN 1655 1755 FIBRONECTIN TYPE-III 12.
 FT DOMAIN 1756 1846 FIBRONECTIN TYPE-III 13.
 FT DOMAIN 1847 1936 FIBRONECTIN TYPE-III 14.
 FT DOMAIN 1937 2027 FIBRONECTIN TYPE-III 15.
 FT DOMAIN 2028 2118 FIBRONECTIN TYPE-III 16.
 FT DOMAIN 2119 2206 FIBRONECTIN TYPE-III 17.
 FT DOMAIN 2207 2295 FIBRONECTIN TYPE-III 18.
 FT DOMAIN 2327 2500 VWFA 4.
 FT DOMAIN 2455 2750 NONHELICAL REGION (NC3).
 FT DOMAIN 2751 2902 TRIPLE-HELICAL REGION (COL2)
 FT DOMAIN 2903 2945 WITH 1 IMPERFECTION.
 FT DOMAIN 2946 3048 TRIPLE-HELICAL REGION (COL1)
 FT DOMAIN 3049 3124 WITH 2 IMPERFECTIONS.
 FT DOMAIN 3086 3096 NONHELICAL REGION (NC1).
 FT DOMAIN 3111 3123 ASP/GLU-RICH (ACIDIC).
 FT BINDING 797 ARG/LYS-RICH (BASIC).
 FT TO CHONDROITIN SULFATE (POTENTIAL).
 FT

FT BINDING 890 890 TO CHONDROITIN SULFATE (POTENTIAL).
 FT BINDING 981 981 TO CHONDROITIN SULFATE (POTENTIAL).
 FT SITE 2438 2440 CELL ATTACHMENT SITE (POTENTIAL).
 FT SITE 2899 2901 CELL ATTACHMENT SITE (POTENTIAL).
 FT CARBOHYD 32 32 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1006 1006 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1032 1032 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1044 1044 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1512 1512 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1767 1767 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 2210 2210 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 2273 2273 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 2532 2532 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 2683 2683 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARSPLIC 25 1188 MISSING (IN SHORT ISOFORM).
 FT CONFLICT 1258 1258 T -> S (IN REF. 4).
 FT CONFLICT 1264 1264 D -> E (IN REF. 4).
 FT CONFLICT 2759 2759 P -> A (IN REF. 2).
 FT CONFLICT 2803 2803 L -> F (IN REF. 2).
 FT CONFLICT 2977 2977 V -> F (IN REF. 2).
 FT CONFLICT 3075 3076 QP -> AG (IN REF. 3).
 SQ SEQUENCE 3124 AA: 340578 MW: 094285AFE7F346CF CRC64;
 Query Match 47.8%; Score 43; DB 1; Length 3124;
 Best Local Similarity 77.8%; Pred. No. 2.3e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 10 KGPXGXP 18
 DB 1380 KGPXGXP 1388
 IIII III
 RESULT 11
 GUNI_HUMIN
 ID GUNI_HUMIN STANDARD; PRT; 402 AA.
 AC P56680;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Endoglucanase I (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase).
 GN CEL7B.
 OS Humicola insolens.
 OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
 OX NCBI_TaxID=34413;
 RN [1]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT S37W/P39W.
 RX MEDLINE=97475713; PubMed=935168;
 RA Davies G.J., Ducros V., Lewis R.J., Borchert T.V., Schulein M.;
 RA "Oligosaccharide specificity of a family 7 endoglucanase: insertion
 RT of potential sugar-binding subsites.";
 RL J. Biotechnol. 57:91-100(1997).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND MUTAGENESIS.
 RX MEDLINE=98437137; PubMed=9761741;
 RA Mackenzie L.F., Sulzenbacher G., Dyne C., Jones T.A., Woelldike H.F.,
 RA Schulein M., Withers S.G., Davies G.J.;
 RA "Crystal structure of the family 7 endoglucanase I (Cel7B) from
 RT Humicola insolens at 2.2 A resolution and identification of the
 RT catalytic nucleophile by trapping of the covalent glycosyl-enzyme
 RL intermediate.";
 RL Biochem. J. 335:409-416(1998).
 CC -!- FUNCTION: THE BIOLOGICAL CONVERSION OF CELLULOSE TO GLUCOSE
 CC GENERALLY REQUIRES THREE TYPES OF HYDROLYTIC ENZYMES:
 CC (1) ENDOGLUCANASES WHICH CUT INTERNAL BETA-1,4-GLUCOSIDIC BONDS;
 CC (2) EXOCELLULOHYDROLASES THAT CUT THE DISSACCHARIDE CELLOBIOSE
 CC FROM THE NONREDUCING END OF THE CELLULOSE POLYMER CHAIN;
 CC (3) BETA-1,4-GLUCOSIDASES WHICH HYDROLYZE THE CELLOBIOSE AND OTHER
 CC SHORT CELLO-OLIGOSACCHARIDES TO GLUCOSE.
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 CC linkages in cellulose.
 CC -!- SUBUNIT: MONOMER.
 CC -!- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY C (FAMILY 7 OF GLYCOSYL
CC HYDROLASES).
DR PDB; 1A39; 02-MAR-99.
DR PDB; 2A39; 16-FEB-99.
DR InterPro: IPR001722; Glyco_hydro_7.
DR Pfam: PF00840; Glyco_hydro_7; 1.
DR PRINTS: PR00734; GLHYDRLASE7.
DR ProDom: PD186135; Glyco_hydro_7; 1.
KW Cellulose degradation; Hydrolase; Glycosidase; Glycoprotein;
KW 3D-structure.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 197 197 NUCLEOPHILE.
FT ACT_SITE 202 202 PROTON DONOR.
FT DISULFID 18 24
FT DISULFID 51 73
FT DISULFID 63 69
FT DISULFID 140 365
FT DISULFID 172 195
FT DISULFID 176 194
FT DISULFID 215 234
FT DISULFID 223 228
FT DISULFID 239 315
FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .).
FT CARBOHYD 247 247 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 402 AA; 44577 MW; E0C6D31375D1635F CRC64;

Query Match 47.2%; Score 42.5; DB 1; Length 402;
Best Local Similarity 47.4%; Pred. No. 38;
Matches 9; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

QY 6 KXGKGGG-----GXPPPK 19
DB 42 RAELGPGGCGDGNPPPK 60

RESULT 12
ID ASFL_HELAN
AC P22357; STANDARD; PRT; 161 AA.
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Anther-specific protein SF18 precursor (Fragment).
OS Helianthus annuus (Common sunflower).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
OC Heliantheae; Helianthus.
OX NCBI_TaxID=4232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV_HA401B / CARGILL; TISSUE=Anther;
RX MEDLINE=91338702; PubMed=2102380;
RA Domon C., Evrard J.-L., Herdenberger F., Pillay D.T.N., Steinmetz A.;
RT "Nucleotide sequence of two anther-specific cDNAs from sunflower
(Helianthus annuus L.).";
RL Plant Mol. Biol. 15:643-646(1990).
CC -1- FUNCTION: ANOTHER-SPECIFIC CELL WALL PROTEIN WHICH COULD CONTRIBUTE
CC TO THE CELL WALL ARCHITECTURE OF EPIDERMAL ANOTHER CELLS VIA
CC INTERMOLECULAR DISULFIDE BRIDGES.
CC -1- TISSUE SPECIFICITY: EPIDERMAL ANOTHER CELLS.
CC -1- DEVELOPMENTAL STAGE: LATE DEVELOPMENTAL STAGES.
CC -1- SIMILARITY: BELONGS TO THE GAMMA-PUROTHONIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC

DR EMBL; X53375; CAA37455.1; -.
DR PIR; S12246; S12246.
DR HSSP; P30231; IAYJ.
DR InterPro: IPR002118; Gamma-thionin.
DR InterPro: IPR003614; Knot1.
DR Pfam; PF00304; Gamma-thionin; 1.
DR ProDom; PD002594; Gamma-thionin; 1.
DR SMART; SM00505; Knot1; 1.
DR PROSITE; PS00940; GAMMA_THIONIN; 1.
KW Signal; Cell wall.
FT NON_TER 1 1
FT SIGNAL <1 8
FT CHAIN 9 161 ANOTHER-SPECIFIC PROTEIN SF18.
FT DOMAIN 9 65 GAMMA-THIONIN LIKE DOMAIN.
FT DOMAIN 70 161 PROLINE DOMAIN.
FT DISULFID 18 65 BY SIMILARITY.
FT DISULFID 29 50 BY SIMILARITY.
FT DISULFID 35 59 BY SIMILARITY.
FT DISULFID 39 61 BY SIMILARITY.
SQ SEQUENCE 161 AA; 15363 MW; 27A9CF4633ADA02B CRC64;

Query Match 46.7%; Score 42; DB 1; Length 161;
Best Local Similarity 70.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 GRGPGGXPPP 18
DB 127 GDGGGGAPP 136

RESULT 13
ID CC14_CAEEL
AC P18834; STANDARD; PRT; 326 AA.
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Cuticle collagen 14.
GN COL-14.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=89326131; PubMed=2753356;
RA Cox G.N., Fields C., Kramer J.M., Rosenzweig B., Hirsh D.;
RT "Sequence comparisons of developmentally regulated collagen genes of
Caenorhabditis elegans.";
RL Gene 76:331-344(1989).
CC -1- FUNCTION: NEMATODE CUTICLES ARE COMPOSED LARGELY OF COLLAGEN-LIKE
CC PROTEINS. THE CUTICLE FUNCTIONS BOTH AS AN EXOSKELETON AND AS A
CC BARRIER TO PROTECT THE WORM FROM ITS ENVIRONMENT.
CC -1- SUBUNIT: COLLAGEN POLYPEPTIDE CHAINS ARE COMPLEXED WITHIN THE
CC CUTICLE BY DISULFIDE BONDS AND OTHER TYPES OF COVALENT CROSS-
CC LINKS.
CC -1- SIMILARITY: TO OTHER COLLAGENS. STRONG, TO OTHER CUTICLE
CC COLLAGENS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M25480; AAA27986.1; -.
DR PIR; J50169; J50169.
DR InterPro: IPR002486; Col_cuticle_N.
DR InterPro: IPR000087; Collagen.

FT DOMAIN 321 330 POLY-PRO.
SQ SEQUENCE 440 AA; 44669 MW; 82266C2E1E103A48 CRC64;

Query Match 46.7%; Score 42; DB 1; Length 440;
Best Local Similarity 70.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 GKPGGXPPP 18
| | | | |
Db 92 GDGPGSRPP 101

Search completed: September 4, 2002, 17:05:03
Job time: 1129 sec

US-09-821-726-1

Query Match 91.1%; Score 82; DB 22; Length 19;

Best Local Similarity 100.0%; Pred. No. 0.0009;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VKEXKXKXGKGGGXPXPPK 19

Db 1 VKEXKXKXGKGGGXPXPPK 19

RESULT 2

US-09-821-726-8

; Sequence 8, Application US/09821726

; GENERAL INFORMATION:

; APPLICANT: MARTIN, TERENCE E.

; APPLICANT: TOBACK, F. GARY

; APPLICANT: POWELL, C. THOMAS

; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS

; FILE REFERENCE: 21459/90913

; CURRENT APPLICATION NUMBER: US/09/821,726

; CURRENT FILING DATE: 2001-03-29

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 8

; LENGTH: 21

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-821-726-8

Query Match

Best Local Similarity 70.0%; Score 63; DB 22; Length 21;

Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXKXGKGGGXPXPPK 19

Db 5 VKE-KKLOGKGGG-PPPK 21

RESULT 3

US-09-821-726-10

; Sequence 10, Application US/09821726

; GENERAL INFORMATION:

; APPLICANT: MARTIN, TERENCE E.

; APPLICANT: TOBACK, F. GARY

; APPLICANT: POWELL, C. THOMAS

; APPLICANT: AGARWAL, KAN

; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS

; FILE REFERENCE: 21459/90913

; CURRENT APPLICATION NUMBER: US/09/821,726

; CURRENT FILING DATE: 2001-03-29

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 10

; LENGTH: 25

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-821-726-10

Query Match

Best Local Similarity 70.0%; Score 63; DB 22; Length 25;

Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXKXGKGGGXPXPPK 19

Db 5 VKE-KKLOGKGGG-PPPK 21

RESULT 4

US-09-821-726-6

; Sequence 6, Application US/09821726

; GENERAL INFORMATION:

; APPLICANT: MARTIN, TERENCE E.

; APPLICANT: TOBACK, F. GARY

; APPLICANT: POWELL, C. THOMAS

; APPLICANT: AGARWAL, KAN

; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS

; FILE REFERENCE: 21459/90913

; CURRENT APPLICATION NUMBER: US/09/821,726

; CURRENT FILING DATE: 2001-03-29

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6

; LENGTH: 42

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-821-726-6

Query Match

Best Local Similarity 70.0%; Score 63; DB 22; Length 42;

Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXKXGKGGGXPXPPK 19

Db 24 VKE-KKLOGKGGG-PPPK 40

RESULT 5

US-08-906-708-24

; Sequence 24, Application US/08906708

; GENERAL INFORMATION:

; APPLICANT: Jacobs, Kenneth

; APPLICANT: McCoy, John M.

; APPLICANT: LaVallie, Edward R.

; APPLICANT: Racie, Lisa A.

; APPLICANT: Treacy, Maurice

; APPLICANT: Spaulding, Vikki

; APPLICANT: Agostino, Michael J.

; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES

; TITLE OF INVENTION: ENCODING THEM

; NUMBER OF SEQUENCES: 38

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genetics Institute, Inc.

; STREET: 87 Cambridgepark Drive

; CITY: Cambridge

; STATE: MA

; COUNTRY: U.S.A.

; ZIP: 02140

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/906,708

; FILING DATE:

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Sprunger, Suzanne A.

; REGISTRATION NUMBER: P-41,323

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 498-8284

; TELEFAX: (617) 876-5851

; INFORMATION FOR SEQ ID NO: 24:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 150 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-906-708-24

Query Match 70.0%; Score 63; DB 13; Length 150;
Best Local Similarity 78.9%; Pred. No. 2.3;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXKXGKGGXPPPK 19
||| || ||||| |||||
Db 101 VKE-KKLGKGGG-PPPK 117

RESULT 6
US-09-684-524-212
; Sequence 212, Application US/09684524
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/09/684,524
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 212
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-684-524-212

Query Match 70.0%; Score 63; DB 20; Length 182;
Best Local Similarity 78.9%; Pred. No. 2.8;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXKXGKGGXPPPK 19
||| || ||||| |||||
Db 101 VKE-KKLGKGGG-PPPK 117

RESULT 7
US-10-050-704-212
; Sequence 212, Application US/10050704
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/10/050,704
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 09/684,524
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 212
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-704-212

Query Match 70.0%; Score 63; DB 24; Length 182;
Best Local Similarity 78.9%; Pred. No. 2.8;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXKXGKGGXPPPK 19
||| || ||||| |||||
Db 101 VKE-KKLGKGGG-PPPK 117

RESULT 8
PCT-US98-16318-18
; Sequence 18, Application PC/TUS9816318
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI6051A
; CURRENT APPLICATION NUMBER: PCT/US98/16318
; CURRENT FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US98-16318-18

Query Match 70.0%; Score 63; DB 1; Length 185;
Best Local Similarity 78.9%; Pred. No. 2.8;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXKXGKGGXPPPK 19
||| || ||||| |||||
Db 101 VKE-KKLGKGGG-PPPK 117

RESULT 9
US-09-130-189-18
; Sequence 18, Application US/09130189
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI6051A
; CURRENT APPLICATION NUMBER: US/09/130,189
; CURRENT FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-130-189-18

Query Match 70.0%; Score 63; DB 15; Length 185;
Best Local Similarity 78.9%; Pred. No. 2.8;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

Thu Sep 5 11:23:23 2002

us-09-821-726-1.rapm

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QY 1 VKEXKXXKGGPGGXPPPK 19
    ||| || ||||| |||||
Db 101 VKE-KKLGKGGPGG-PPPK 117

RESULT 10
US-09-684-524-105
; Sequence 105, Application US/09684524
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: p2039p1
; CURRENT APPLICATION NUMBER: US/09/684,524
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-684-524-105

Query Match 70.0%; Score 63; DB 20; Length 185;
Best Local Similarity 78.9%; Pred. No. 2.8;
Matches 15; Conservative 2; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXXKGGPGGXPPPK 19
    ||| || ||||| |||||
Db 101 VKE-KKLGKGGPGG-PPPK 117

RESULT 11
US-09-709-238-211
; Sequence 211, Application US/09709238
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Chen, Jian
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Yuan, Jean
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding the Same
; FILE REFERENCE: P2730R1C1
; CURRENT APPLICATION NUMBER: US/09/709,238
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 60/087,607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: US 60/087,609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: US 60/087,759
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: US 60/087,827
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: US 60/088,021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: US 60/088,025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: US 60/088,028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: US 60/088,029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: US 60/088,030
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;; PRIOR APPLICATION NUMBER: US 60/089,908
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: US 60/089,947
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: US 60/089,948
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: US 60/089,952
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: US 60/090,246
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: US 60/090,252
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: US 60/090,254
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: US 60/090,355
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: US 60/090,429
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: US 60/090,431
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: US 60/090,435
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: US 60/090,349
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: US 60/090,444
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: US 60/090,445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: US 60/090,461
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: US 60/090,472
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: US 60/090,535
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: US 60/090,538
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: US 60/090,540
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: US 60/090,557
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;; PRIOR APPLICATION NUMBER: US 60/090,676
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;; PRIOR APPLICATION NUMBER: US 60/090,690
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;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: US 60/090,694
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: US 60/090,695
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;; PRIOR APPLICATION NUMBER: US 60/090,696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: US 60/090,862
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: US 60/090,863
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: US 60/091,358
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: US 60/091,360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: US 60/091,478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: US 60/091,486
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: US 60/091,519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: US 60/091,544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: US 60/091,626

;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: US 60/091,628
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: US 60/091,633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: US 60/091,646
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: US 60/091,673
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: US 60/091,978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: US 60/091,982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: US 60/092,182
;; PRIOR FILING DATE: 1998-07-09
;; PRIOR APPLICATION NUMBER: US 60/092,472
;; PRIOR FILING DATE: 1998-07-10
;; PRIOR APPLICATION NUMBER: US 60/093,339
;; PRIOR FILING DATE: 1998-07-20
;; PRIOR APPLICATION NUMBER: US 60/094,651
;; PRIOR FILING DATE: 1998-07-30

Query Match 70.0%; Score 63; DB 21; Length 185;
Best Local Similarity 78.9%; Pred No. 2.8;

Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VXEXKXKXGPGGPPPK 19
||| || ||||| ||||
Db 101 VRE-KKLOGKPGG-PPPK 117

RESULT 12

US-09-746-783-146

; Sequence 146, Application US/09746783

; GENERAL INFORMATION:

; APPLICANT: Jacobs, Kenneth

; McCoy, John M.

; LaVallie, Edward R.

; Racie, Lisa A.

; Treacy, Maurice

; Spaulding, Vikki

; Agostino, Michael J.

; Howes, Steven H.

; Rechtel, Kim

; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES

; NUMBER OF SEQUENCES: 231

; CORRESPONDENCE ADDRESS: ENCODING THEM

; ADDRESSEE: Genetics Institute, Inc.

; STREET: 87 Cambridgepark Drive

; CITY: Cambridge

; STATE: MA

; COUNTRY: U.S.A.

; ZIP: 02140

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09746,783

; FILING DATE: 21-Dec-2000

; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Milasincic, Debra J.

; REGISTRATION NUMBER: 46,931

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 742-4214

; INFORMATION FOR SEQ ID NO: 146:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 185 amino acids

; TYPE: amino acid

;
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 146:
US-09-746-783-146

Query Match 70.0%; Score 63; DB 21; Length 185;
Best Local Similarity 78.9%; Pred. No. 2.8;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXXGKGGXPPPK 19
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Db 101 VKE-KKLOGKGGG-PPPK 117

RESULT 13

US-09-821-726-13
; Sequence 13, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-821-726-13

Query Match 70.0%; Score 63; DB 22; Length 185;
Best Local Similarity 78.9%; Pred. No. 2.8;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXXGKGGXPPPK 19
||| || ||||| |||||

Db 101 VKE-KKLOGKGGG-PPPK 117

RESULT 14

US-09-821-726-18
; Sequence 18, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Porcine sp.
US-09-821-726-18

Query Match 70.0%; Score 63; DB 22; Length 185;
Best Local Similarity 78.9%; Pred. No. 2.8;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXXGKGGXPPPK 19
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Db 101 VKE-KKLOGKGGG-PPPK 117

RESULT 15

US-09-941-992-211
; Sequence 211, Application US/09941992
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C1
; CURRENT APPLICATION NUMBER: US/09/941,992
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
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; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
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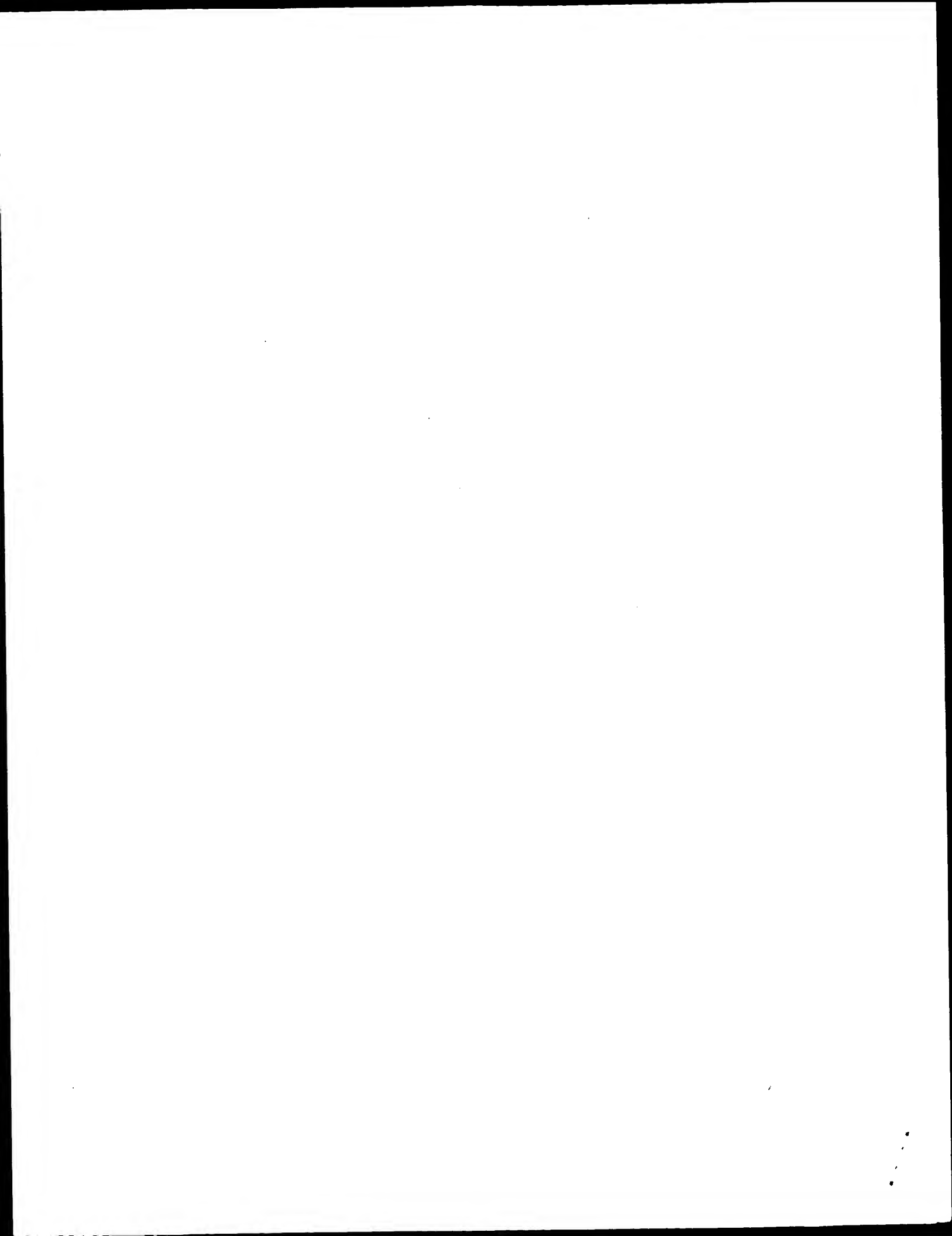
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 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09
 ; PRIOR APPLICATION NUMBER: 60/092472

Query Match 70.0%; Score 63; DB 23; Length 185;
 Best Local Similarity 78.9%; Pred No. 2.8;
 Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VREKXXKXGPGGPPPK 19
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 Db 101 VKE-KKLOGKPGG-PPPK 117

Search completed: September 4, 2002, 16:59:19
 Job time: 1040 sec



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 Date: Sep 4, 2002 5:06 PM
 About: Results were produced by the GenCore software, version 4.5,
 Copyright (c) 1993-2000 CompuGen Ltd.

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Search information block:
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 Query length: 597
 Database: A_Geneseq_032802.*
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 Database length: 111073796
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 DT 16-NOV-1998 (first entry)
 DE Cancer associated protein.
 DE Cancer: PCR: Northern blotting; ribonuclease protection assay;
 DE diagnosis; metastatic cancer.
 OS Synthetic.
 PN W09837187-A1.
 PD 27-AUG-1998.
 PE 18-FEB-1998; 98WO-JP00667.
 PR 21-FEB-1997; 97JP-0052508.
 PA (TAKI) TAKARA SHUZO CO LTD.
 PI Asada K, Hino F, Kato I, Mukai H, Yoshikawa Y;
 WP: 1998-467552/40.
 PT Detection of cancer cells in tissue samples - by changes in mRNA
 expression compared to normal tissue of specific cancer-associated
 gene sequences
 PS Claim 14: Page 64-65; 92pp; Japanese.
 CC The cancer associated proteins AAW69974-W69976 where used in the method
 CC of the invention to detect cancer cells in tissue samples or biological
 CC fluids. They are detected by monitoring the change in mRNA expression
 CC as compared to normal tissue of one or more cancer-associated genes
 CC whose cDNA stringently hybridises to cancer associated gene nucleic acid
 CC fragments. The change in expression may be an increase or a decrease
 CC compared to normal tissue. The mRNA expression may be determined by
 CC PCR, Northern blotting or ribonuclease protection assay, or by
 CC determining the change in the amount of protein encoded by the gene(s) as
 CC compared to normal tissue, for example by using a labelled antibody
 CC recognising the protein. Detection of cancer cells for cancer diagnosis,
 CC including detection of metastatic cancer cells in tissues other than the
 CC primary tumour site.
 XX
 XX
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 Ratio: 4.412 Caps: 0
 Percent Similarity: 93.814 Percent Identity: 74.227
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 1 SerValHisCysPheArgIleuSpluSlyMetLysPheThrIleValPheAl 17

PF 25-JUN-1999; 99WO-US14484.
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 XX 26-JUN-1998; 98US-0090762.
 PR 31-JUL-1998; 98US-0094983.
 PR 01-OCT-1998; 98US-0102686.
 PR 11-DEC-1998; 98US-0112129.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
 PI Akersblom IE, Au-young J, Yue H, Patterson C, Reddy R, Hillman JL;
 PI Bandman O;
 XX
 XX WPI: 2000-160673/14.
 DR N-PSDB; AA298157.
 XX
 PT New human signal peptide-containing proteins useful in treatment,
 PT prevention and diagnosis of e.g. cancer, inflammation and
 PT cardiovascular disease
 XX
 PS Claim 1; Page 193-194; 327pp; English.

AA298109 to AA298242 encode AAY87224 to AAY87357 which represent the human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic, neuroprotective, cardiovascular and antiasthmatic activities, and can be used in gene therapy. HSPs can be used to treat or prevent disorders associated with decreased activity or function of HSP. Antagonists of HSP are used to treat or prevent disorders associated with increased activity or function of HSP. Such diseases include cell proliferation (including cancer), inflammation, cardiovascular, neurological, reproductive or developmental disorders, (e.g. arteriosclerosis, cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia, asthma, Crohn's disease, microbial or other infections, congestive or ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's diseases, schizophrenia, ovulatory defects, muscular dystrophy), HSP nucleic acids can be used for the recombinant production of HSP, for detecting HSP in standard hybridisation and amplification assays (for triplex-forming or ribozyme therapeutics, for detecting related sequences or genetic variations, and for chromosomal mapping). HSP are also used to raise specific antibodies (Ab) and to screen for agonists and antagonists (potential therapeutic agents). Ab are used to diagnose, or monitor, HSP-related diseases (in usual immunoassays), as therapeutic antagonists, in competitive drug screens, and for purification of HSP from natural sources.

SO Sequence 185 AA:

alignment_scores:

Quality:	775.00	Length:	185
Ratio:	4.429	Gaps:	0
Percent Similarity:	94.595	Percent Identity:	75.135

alignment_block:

US-09-821-726-17 x AAY87272

Align seg 1/1 to: AAY87272 from: 1 to: 185

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  190 GTTGACAAATACAAATGATGAGAACTCTGGAATGCCCTCTGGAGCATATAG 239

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ID AAV66686 standard; protein; 185 AA.
AC AAV66686;
XX
XX 05-APR-2000 (first entry)
XX
DE Membrane-bound protein PRO1005.
XX
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmacetical; receptor immunoaderisin; gene mapping.
XX
OS Homo sapiens.
XX
PN MO9963088-A2.
PD
PD 09-DEC-1999.
XX
PF 02-JUN-1999; 99WO-US12252.
XX
XX 02-JUN-1998; 98US-0087607.
XX 02-JUN-1998; 98US-0087609.
XX 02-JUN-1998; 98US-0087759.
XX 03-JUN-1998; 98US-0087827.
XX 04-JUN-1998; 98US-0088021.
XX 04-JUN-1998; 98US-0088025.
XX 04-JUN-1998; 98US-0088028.
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XX 05-JUN-1998; 98US-0088167.
XX 05-JUN-1998; 98US-0088202.
XX 05-JUN-1998; 98US-0088212.
XX 05-JUN-1998; 98US-0088217.
XX 09-JUN-1998; 98US-0088655.

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PR 10-JUN-1998; 98US-0088722.
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 PR 07-JUL-1998; 98US-0091982.
 PR 09-JUL-1998; 98US-0092182.

PR 10-JUL-1998; 98US-0092472.
 PR 20-JUL-1998; 98US-0093339.
 PR 30-JUL-1998; 98US-0094651.
 PR 04-AUG-1998; 98US-0095282.
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 PR 10-AUG-1998; 98US-0096012.
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 PR 18-AUG-1998; 98US-0097022.
 PR 19-AUG-1998; 98US-0097141.
 PR 20-AUG-1998; 98US-0097218.
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 PR 26-AUG-1998; 98US-0097955.
 PR 26-AUG-1998; 98US-0097971.
 PR 26-AUG-1998; 98US-0097974.
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 PR 31-AUG-1998; 98US-0098525.
 PR 16-SEP-1998; 98US-0100634.
 PR 12-JAN-1999; 99US-0115565.

(GETH) GENENTECH INC.
 Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
 Wood WI, Yuan J;
 WPI: 2000-072883/06.
 N-PSDB: AAZ65023.
 Membrane-bound proteins and related nucleotide sequences
 Claim 12; Fig 139; 822pp; English.

The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially


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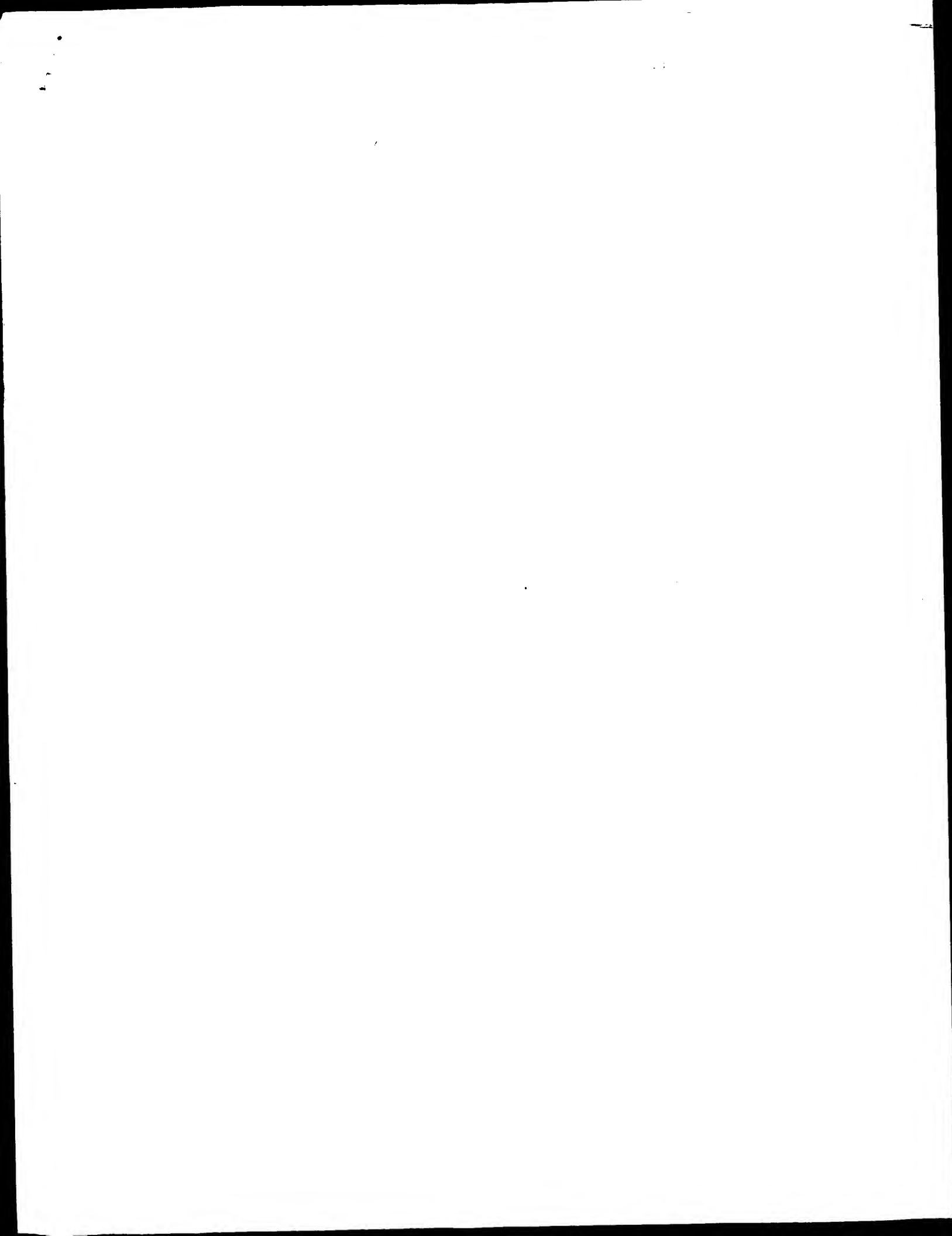
PR      20-MAR-2000: 2000MO-US07377.
XX
XX      (GETH ) GENENTECH INC.
PA
PX
PX      Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DJ,
PI      Ferrara N, Fong S, Gerber H, Gerlstein ME, Goddard A, Godowski PJ,
PI      Grimaldi CJ, Gurey AL, Kijavini IT, Napier MA, Pan J, Paoni NF,
PI      Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
XX      Zhang Z;
XX      WPI: 2001-032160/04.
DR      N-PSDB: AAF44175.
XX
XX      PRO polynucleotides used to produce polypeptides used to target
PI      bioactive molecules such as toxins, radiolabels or antibodies, to
PI      specific cells, to cause targeted cell death -
XX
XX      Claim 12: Fig 149, 935pp: English.
XX
XX      The present invention describes human secreted and transmembrane PRO
CC      proteins. The PRO proteins have cytostatic activity. The PRO proteins
CC      can be used for targeted delivery of bioactive molecules, such as
CC      toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
CC      sequences, and their fragments, can be used as hybridisation probes, in
CC      chromosomal and gene mapping, and in the generation of anti-sense RNA
CC      and DNA. They may also be used to produce transgenic animals which are
CC      used to develop and screen therapeutically useful reagents. The PRO
CC      nucleotide and protein sequence can be used for tissue typing and in
CC      treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
CC      In the isolation of human PRO sequences. AAF44087 to AAF44269 and
CC      AAB65154 to AAB65300 represent human PRO polynucleotide and protein
CC      sequences given in the exemplification of the present invention.
XX
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SQ
XX
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XX      Quality:      201.00      Length:      194
XX      Ratio: 1.703      Gaps: 4
XX      Percent Similarity: 60.825      Percent Identity: 26.804
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XX      90 TGGCCCTTGCTGACTTACTATCATCTGTCAACGACGCGCAACAGTGTG      139
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XX      140 GAAGTGGCAGACGATGATGAGTGTCAACATGACACACATGCGCCAAC      189
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XX      240 AAGTCGCTTGCTGTAAACGACTCTTGCAGAGAAGATCATGTGGC      289
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XX      290 ACAAAATGACAGAAGACGATCCCTCCCTT..... 321
XX      ||||| : : : : : : : : : : : : : : : : : : : :
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 410 ACCCCACAGAGTCGACACCTGACAGATT.....GGAAATCCATC 453
 123 euGluSerLeuIleLysAspValAspTyrPheLeuLeuGlySerProIle 139
 454 GTTGCCATGTCAGAGGGGATTCACATACATGCTGAGAGATTCAAG 503
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 504 AGCAACCTGATTTCTGCTACACGAAAGATGCAACAGTCCCATATACTCT 553
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 ID AAM23556 standard; Protein; 184 AA.
 AC AAM23556;
 DT 12-OCT-2001 (first entry)
 XX Human EST encoded protein SEQ ID NO: 1081.
 DE Human: sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 KW diagnostics; forensic test; gene mapping; genetic disorder;
 KW biodiversity; gene therapy; nutrition.
 OS Homo sapiens.
 XX MO200154477-A2.
 PN 02-AUG-2001.
 PD 25-JAN-2001; 2001WO-US02687.
 PE 25-JAN-2001; 2000US-0491404.
 PR 17-JUL-2000; 2000US-0617746.
 PR 03-AUG-2000; 2000US-0631451.
 PR 15-SEP-2000; 2000US-0663870.
 XX (HYSE-) HYSEQ INC.
 PA Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
 PI Cao Y, Dmanac RA, Zhang J, Werhman T;
 DR WPI: 2001-476164/51.
 DR N-PSDB: AAH98215.
 PT Isolated polypeptide for treatment of diseases, diagnostics, raising
 PT antibodies and research use -
 XX Claim 20; Page 814-815; 1275pp; English.
 XX The present invention provides the protein and coding sequences of novel
 XX proteins from a variety of organisms, including human, dog, cat, horse,
 XX cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 XX urchin and tomato. These were derived from expressed sequence tags (ESTs)
 XX from the organism of interest. They can be used in diagnostics,
 XX forensics, gene mapping, identification of mutations, to assess
 XX biodiversity and for nutritional purposes. The present sequence is a
 XX protein of the invention.

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 17 nSerHisGlyTyrGluValAlaPheAsnIleIleSerProSerAsnGlyG 34
 140 GAAGTGGGAGGAGTCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 189
 34 LysAsnValGlnGlnIleValThrIleAspAsnGluLysAsnThrAlaIle 50
 190 GTTGACAAATACAAATGATGATGATGATGATGATGATGATGATG 239
 51 IleAsnIleHisIleGlySerSerSerSerThrThrIlePheAspTyrIly 67
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 117 P.....ValLysTyrAsnProL 123
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 123 euGluSerLeuIleLysAspValAspTyrPheLeuLeuGlySerProIle 139
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 504 AGCAACCTGATTTCTGCTACAGAAAGTGCATGATCCCATATACTCT 553
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 ID AAE04211 standard; Protein; 184 AA.
 AC AAE04211;
 DT 09-AUG-2001 (first entry)
 XX Human gene 14 encoded secreted protein HNSA27, SEQ ID NO:66.
 DE Human; secreted protein; proliferative disorder; cancer; tumour;
 XX

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; GENERAL INFORMATION:
; APPLICANT: YOSHIKAWA, YOSHIE
; APPLICANT: MUKAI, HIROYUKI
; APPLICANT: ASADA, KIYOZO
; APPLICANT: KATO, IKUNOSHIN
; APPLICANT: KATO, IKUNOSHIN
; TITLE OF INVENTION: CANCER-ASSOCIATED GENES
; FILE REFERENCE: 1422-388P
; CURRENT APPLICATION NUMBER: US/09/377,497
; CURRENT FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 17
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: any n or Xaa = unknown
US-09-377-497-17

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Percent Similarity: 93.814 Percent Identity: 74.227

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; GENERAL INFORMATION:
; APPLICANT: YOSHIKAWA, YOSHIE
; APPLICANT: MUKAI, HIROYUKI
; APPLICANT: ASADA, KIYOZO
; APPLICANT: KATO, IKUNOSHIN
; APPLICANT: KATO, IKUNOSHIN
; TITLE OF INVENTION: CANCER-ASSOCIATED GENES
; FILE REFERENCE: 1422-388P
; CURRENT APPLICATION NUMBER: US/09/377,497
; CURRENT FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 69
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; FEATURE:
; OTHER INFORMATION: any n or Xaa = unknown
US-09-377-497-69

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Ratio: 4.412 Gaps: 0
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113 GTGTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 162
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39 snValAsnAspAspAsnAsnAlaGlySerGlyGlnGlnInsSerValSer 55
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: GENERAL INFORMATION:
: APPLICANT: MARTIN, TERENCE E.
: APPLICANT: TOBACK, F. GARY
: APPLICANT: POWELL, C. THOMAS
: APPLICANT: AGARNAL, KAN
: TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
: FILE REFERENCE: 21459/90913
: CURRENT APPLICATION NUMBER: US/09/821,726
: NUMBER OF SEQ ID NOS: 19
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 13
: LENGTH: 185
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-821-726-13

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alignment_scores:

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Ratio: 4.451          Gaps: 0
Percent Similarity: 94.595      Percent Identity: 75.676

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90 TGCCCTTCTGACTATAGTATGATGTCACAGCAGCAGCAGCAGTGGG 139
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17 calaLeuAlaAsnTyrAsnIleAspValAsnAspAsnAsnAlaG 34

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: Sequence 18, Application PC/TUS9816318
: GENERAL INFORMATION:
: APPLICANT: Jacobs, Kenneth
: APPLICANT: McCoy, John M.
: APPLICANT: Lavallie, Edward R.
: APPLICANT: Racie, Lisa A.
: APPLICANT: Evans, Cheryl
: APPLICANT: Merberg, David
: APPLICANT: Treacy, Maurice
: APPLICANT: Agostino, Michael J.
: APPLICANT: Steininger II, Robert J.
: TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
: FILE REFERENCE: GI6051A
: CURRENT APPLICATION NUMBER: PCT/US98/16318
: NUMBER OF SEQ ID NOS: 30
: SOFTWARE: PatentIn Ver. 2.0
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: ORGANISM: Homo sapiens
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Ratio: 4.429          Gaps: 0
Percent Similarity: 94.595      Percent Identity: 75.135

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Thu Sep 5 11:23:32 2002

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Ratio: 4.429         Gaps: 0
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? APPLICANT: Baker, Kevin P.
? APPLICANT: Botstein, David
? APPLICANT: Desnoyers, Luc
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? APPLICANT: Ferrara, Napoleone
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? APPLICANT: Napier, Mary A.
? APPLICANT: Pan, James
? APPLICANT: Paoni, Nicholas F.

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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
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16 PRIOR FILING DATE: 1998-06-26
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18 PRIOR FILING DATE: 1998-07-01
19 PRIOR APPLICATION NUMBER: 60/091478
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21 PRIOR APPLICATION NUMBER: 60/091544
22 PRIOR FILING DATE: 1998-07-01
23 PRIOR APPLICATION NUMBER: 60/091519
24 PRIOR FILING DATE: 1998-07-02
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27 PRIOR APPLICATION NUMBER: 60/091633
28 PRIOR FILING DATE: 1998-07-02
29 PRIOR APPLICATION NUMBER: 60/091978
30 PRIOR FILING DATE: 1998-07-07
31 PRIOR APPLICATION NUMBER: 60/091982
32 PRIOR FILING DATE: 1998-07-07
33 PRIOR APPLICATION NUMBER: 60/092182
34 PRIOR FILING DATE: 1998-07-09
35 PRIOR APPLICATION NUMBER: 60/092472

Quality:	775.00	Length:	185
Ratio:	4.429	Gaps:	0
Percent Similarity:	94.595	Percent Identity:	75.135

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05-09-821-126-17 X 05-09-989-279-211

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34 LysArgIyGlnGlnSerValSerValaAsnAsnGlnHisAsnValaAlaAsn 50
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51 ValAspAsnAsnAsnGlnTyrPaspSerTTPAsnSerIleTTPAspTyrGI 67
240 AACGTGCTTTGCTGTATACCAAGACTCTTTCGAGAAAGATGCATGCATTGGC 28
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290 ACAAAATGAGACAGGAAGCCATGCGCCCTTCACAGCCCTTGATGGCTG 33
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101 ValLysGluLysLysLeuGlnGlnIlyLysGlyProGlnGlyProProPhe 117

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; sequence 211, Application US/09989293P
; GENERAL INFORMATION;
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APPLICANT: Ashkenazi, Avi J.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Ferrara, Napoli

APPLICANT: Fong, Sherman

APPLICANT: Gelder, Hanspet
; APPLICANT: Gerritsen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul

APPLICANT: Gurney, Austin

APPLICANT: KJ Javlin, Ivar J

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas

APPLICANT: Stewart, Timot

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P M

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Acids

FILE REFERENCE: P2730P1C66

CURRENT FILING DATE: 2001

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PRIOR APPLICATION NUMBER: 1997-06

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67	PRIOR FILING DATE: 1998-07-07

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67 YAsnGlyPheAlaIleAlaTrpArgLeuPheGlnLysLysThrCysIleValH 84
290 ACAAAATGAG 339
84 IsLysMetAsnLysGluValMetProSerIleGlnSerLeuAspAlaLeu 100
340 GTCAAG 389
101 ValLysGluLysLysLeuGlnLysGlyProGlyProProProly 117
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540 TGCCATATATCTGCTGATTCCTTAACATTCCTGCTGAGAGAGATGAG 589
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184 LuAsn 185

seq_name: /cgm2_6/plodata/2/paa/us099_COMB-pep:us-09-989-722-211

seq_documentation_block:
Sequence 211, Application US/09989722
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavir, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC63
CURRENT APPLICATION NUMBER: US/09/989,722
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186

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Percent Similarity: 94.595 Percent Identity: 75.135

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; Sequence 211, Application US/09989723
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fonq, Sherman
; APPLICANT: Gerbot, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Napier, Mary A.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC62
; CURRENT APPLICATION NUMBER: US/09/989,723
; PRIOR FILING DATE: 2001-11-19
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 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09
 PRIOR APPLICATION NUMBER: 60/092472

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 Ratio: 4.429 Gaps: 0
 Percent Similarity: 94.595 Percent Identity: 75.135

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1 MetLysPheThrIleValPheAlaGlyLeuLeuGlyValPheLeuAlaIrr 17
 90 TGCCCTTGCTGACTATATGATATGATGTCACAGCAGCAGGCAACAGTGGTG 139
 17 CAlaLeuAlaAsnIyrAsnIleAsnValAsnAspAsnAsnAsnValAG 34
 140 GAAGTGGGACAGCAGTCACTGAGTGTCAACATGACACAGCAGTGGCCAC 189
 34 IySerGlyGlnGlnSerValSerValAsnAsnGlnIleAsnValAlaAsn 50
 190 GTTGACATATACATGATGATGATGATGATGATGATGATGATGATGATG 239
 51 ValAspAsnAsnAsnGlyIyrAspSerIyrAspSerIyrAspSerIyr 67
 240 AACTGCTTGTGCTGTATACACAGACTCTTCAGAGAGAGAGAGAGAGAG 289
 67 yAsnGlyPheAlaIleThrIyrGlyLeuPheGlnLysIyrThrCysIleValH 84
 290 ACAAAATGAACAGACAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 339
 84 IyLysMetAsnLysGlyValMetProSerIleGlnSerLeuAspAlaLeu 100
 340 GTCAAGAAAGAAAGCTTCAAGGTAAGGCGCCAGGCGGACACCTGCCAA 389
 101 ValLysGlyLysLysLeuGlnGlyLysGlyIyrGlyIyrGlyIyrGly 117
 390 GAGCTGAGTACTGACTGACTGACTGACTGACTGACTGACTGACTGACTG 439
 117 SGIyLeuMetIyrSerValAsnProAsnLysValAspAspLeuSerIyrSP 134
 440 TTGGAATTCATCGTGTCCATGTGCAAGGGGATTCACATACATAGCT 489
 134 heGlyLysAsnIleAlaAsnMetCysArgGlyIleProIleThrMetAla 150
 490 GAAGATTTCAAGGAGCAACCTGATTCGATCTGAGAAAGTGCATCAG 539
 151 GIuGluMetGlnGluAlaSerLeuPhePheIyrSerGlyThrCysIyrTh 167
 540 TGCCATATATCTCTGATTTCTTAACATTTCTTCTGTGAGAGATAGCGG 589
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 590 AGAAC 594
 184 IuAsn 185

LOCATION: (185)

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US-08-997-897-2

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Ratio: 1.492 Gaps: 10
Percent Similarity: 41.447 Percent Identity: 26.316

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Align seg 1/1 to: US-08-997-897-2 from: 1 to: 430

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437 TTGTGCA.....GGTGTGACATCTGTGGGGGT 409
||||| :|||||:
120 YCysPProcysCysSerCysGlnHis**GlyCysArgTyrCys..... 134
408 GACTGAGTACCTCAGGCTCTTGGAGGTGTCCTCCGCGCTTACCGT 359
135 .....ArgTyrPro 137
358 GAAGCTCTTTCTTGTACACGAGCATCAAGGGCTTGA..... 320
||| :|||:
138 GlySerArgTyrProSerSerArgCysProSerLeuArgCysArgArgph 154
319 .....GGGAGGCAATGGCTTCTCTTCATTT. 293
||| :|||:
154 eArgCysProArg**ArgCysGlnArgTyrTyrCysProAsn**ThrG 171
292 .....TGTGCAATGATGATCTTCTCTGAGAGTCTGTTACAGCAA 248
||| :|||:
171 LysArgCysArgCysProSerSerArg..... 181
247 AGCCAGTTCTATAGTCCAGAGGCAATCCAGAGTTCC.....ATCA 204
||| :|||:
182 **GlnTyr**SerProAlaGlyCysArgArgThrAlaArgCysArgCys 198

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203 TTGTATTTGTACAGCTTGCCACGT.....TGTGTCATTTGTTGAC 163
||| :|||:
198 scCysCysArgCysTyrArgThrArgCysCysCysArgCysArgCys 215
162 ACTGACATG.....ACTGTCGCCACTTCCACCACTGTTGCCGT 125
215 InsertLeuGly**SerArgProArgSerArgSerArgArgCysSerArg 231
124 CGTCT 119
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232 ArgArg 233

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seq_name: /cgn2_6/plodata/2/1aa/6B-COMB.pep:US-09-156-836B-2

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seq_documentation_block:
Sequence 2, Application US/09156836B
Patent No. 6242585
GENERAL INFORMATION:
APPLICANT: Srivastava, Ranjana
APPLICANT: Kumar, Deepak
APPLICANT: Srivastava, Brahm Shanker
TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS SPECIFIC DNA FRAGMENT
FILE REFERENCE: U 011876-4
CURRENT APPLICATION NUMBER: US/09/156,836B
PRIOR FILING DATE: 1996-09-18
PRIOR APPLICATION NUMBER: 08/997,897
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 430
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
FEATURE:
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LOCATION: (4)
OTHER INFORMATION: amino acid has not been identified
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LOCATION: (159)
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 803 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; INDIVIDUAL ISOLATE: PS63B
; IMMEDIATE SOURCE:
; CLONE: E. coli NM522(pMVC1642) NRRL B-18961
US-08-158-232-10

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  Ratio: 0.931       Gaps: 10
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142 AGTGGCAGCAGTCACTGACGCTCAACAAATGACACACACGCGCCAAAC 189
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431 ProAlaProMetSerVal...ValAsnAlaGlnThrGlnThrAlaGlnTyr 446
   ::::::::::::::::::::
190 GTTGACAAATACAAATGATGACGACACCTGCGATGCCCTCTGG...GACT 235
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446 rThAsnGlyGlnAsnLleTrpThrAsnLysAsnLysAsnLysAsnLys 463
   ::::::::::::::::::::
236 ATGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 285
   ::::::::::::::::::::
463 hIleuAlaGlyTyrCysThrThrAsnLysAsnLysAsnLysAsnLys 479
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286 GTGCAC.....AAATGACGACGACGACGACGACGACGACGACGACG 315
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480 AsnAsnSerThrGlyTyrGlyGlnSerCysAsnGlnSerLeuProGlyG 496
   ::::::::::::::::::::
316 TCCTTCACAGCCCTTGATCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 364
   ::::::::::::::::::::
496 nLysIleHisAlaLeuTyrProPheTrpGlnThrAsnValLeuGlyGln 513
   ::::::::::::::::::::
365 AGGCGCCAGGCGGACCACTCCCAAGACCTGAGTACTGACGACGACG 414
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513 erGlyLysLeuGlyLeuLeuAlaSerHisIleProTyrAsnLysSerPro 529
   ::::::::::::::::::::
415 AACGAGA...GTGACACACCTGACGACAAATTTGGAATCCATCGTGGCAT 461
   ::::::::::::::::::::
530 AsnAsnThrIleGlyAsnLysAsnLysAsnLysAsnLysAsnLysAsn 545
   ::::::::::::::::::::
462 GTGCAAGGAGGATCCACAA..... 480
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546 ...LysGlyIleProValGlnLysGlyTyrAlaSerSerGlyGlnLysV 561
   ::::::::::::::::::::
481 .....TACATGCTGACGATTCACAGACGACGACGACGACGACGACG 525
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561 aLgIuIleIleArgGlnTrpIleAsnGlyAlaAsnValIleGlnLysSer 577
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seq_documentation_block:
; Sequence 10, Application US/08304626
; Patent No. 5616495
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; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel M.
; APPLICANT: Kennedy, M. Keith
; APPLICANT: Randall, John Brooks
; APPLICANT: Meier, Henry
; APPLICANT: Wick, Heidi Jane
; APPLICANT: Forcetrada, Luis
; APPLICANT: Schaeff, Harry E.
; APPLICANT: Schwab, George E.
; TITLE OF INVENTION: No. 5616495e1 Bacillus thuringiensis Isolates
; TITLE OF INVENTION: Active Against Hymenopteran Pests and Genes Encoding
; TITLE OF INVENTION: Hymenopteran-Active Toxins
; NUMBER OF SEQUENCES: 39
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/304,626
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/887,980
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/SCJ 104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
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; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 803 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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; ANTI-SENSE: NO
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; INDIVIDUAL ISOLATE: PS63B
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US-08-304-626-10

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101 ACTATAGTATCATGTGACGACGACGCAACAGTGTGTA..... 141
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431 ProAlaProMetSerVal...ValAsnAlaGlnThrGlnThrAlaGlnTy 446
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446 rThraspDlYGLuAsnLleTrpThrAspTrpThrGlyArgSerTrpLeuc 463
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; Patent No. 5753492
; GENERAL INFORMATION:
; APPLICANT: Schnepf, Harry E.
; APPLICANT: Schwab, George E.
; APPLICANT: Payne, Jewel M.
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Poncetrada, Luis
; TITLE OF INVENTION: No. 5753492e1 Nematode-Active Toxins and Genes
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; APPLICATION NUMBER: US/08/316,301A
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/871,510
; FILING DATE: 23-APR-1992

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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/693,018
; FILING DATE: 03-MAY-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/565,544
; FILING DATE: 10-AUG-1990
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/084,653
; FILING DATE: 12-AUG-1987
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/830,050
; FILING DATE: 31-JAN-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lloyd, Jeff
; REGISTRATION NUMBER: 35,589
; REFERENCE/DOCKET NUMBER: MA20CCD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 803 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; INDIVIDUAL ISOLATE: PS63B
; IMMEDIATE SOURCE:
; CLONE: E. coli NM522(pMYC 1642) NRRL B-18961
; US-08-316-301A-12

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seq_documentation_block:
; Sequence 10, Application US/08611928
; Patent No. 5824792
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Kennedy, M. Keith
; APPLICANT: Randall, John Brooks
; APPLICANT: Meier, Henry
; APPLICANT: Ulck, Heidi Jane
; APPLICANT: Foncerrada, Luis
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Schwab, George E.
; APPLICANT: Fu, Jenny
; TITLE OF INVENTION: No. 5824792el Bacillus thuringiensis Toxins Active
; TITLE OF INVENTION: Against Hymenopteran Pests
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/611, 928
; FILING DATE: 06-MAR-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158, 232
; FILING DATE: 24-NOV-1993
; APPLICATION NUMBER: US 07/887, 980
; FILING DATE: 22-MAY-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/797, 645
; FILING DATE: 25-NOV-1991
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/703, 977
; FILING DATE: 22-MAY-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794

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; REFERENCE/DOCKET NUMBER: M/SC104.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 803 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; INDIVIDUAL ISOLATE: PS63B
; IMMEDIATE SOURCE:
; CLONE: E. coli NM522(pMTC1642) MRRL B-18961
; US-08-611-928-10

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Ratio: 0.931 Gaps: 10
Percent Similarity: 54.891 Percent Identity: 25.543

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: Sequence 10, Application US/09173891
: Patent No. 6077937
: GENERAL INFORMATION:
: APPLICANT: Payne, Jewel
: APPLICANT: Kennedy, M. Keith
: APPLICANT: Randall, John Brooks
: APPLICANT: Meier, Henry
: APPLICANT: Uick, Heidi Jane
: APPLICANT: Foncerada, Luis
: APPLICANT: Schnepf, H. Ernest
: APPLICANT: Schwab, George E.
: APPLICANT: Fu, Jenny
: TITLE OF INVENTION: No. 6077937el Bacillus thuringiensis Toxins Active
: TITLE OF INVENTION: Against Hymenopteran Pests
: NUMBER OF SEQUENCES: 51
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: David R. Salivanchik
: STREET: 2421 N.W. 41st Street, Suite A-1
: CITY: Gainesville
: STATE: FL
: COUNTRY: USA
: ZIP: 32606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/173,891
: FILING DATE:
: CLASSIFICATION:
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 08/158,232
: FILING DATE:
: APPLICATION NUMBER: US 07/887,980
: FILING DATE: 22-MAY-1992
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 07/797,645
: FILING DATE: 25-NOV-1991
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 07/703,977
: FILING DATE: 22-MAY-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Salivanchik, David R.
: REGISTRATION NUMBER: 31,794
: REFERENCE/DOCKET NUMBER: M/SCJ104.C1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 904-375-8100
: TELEFAX: 904-372-5800
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 803 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHEICAL: YES
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Bacillus thuringiensis
: INDIVIDUAL ISOLATE: PS63B
: IMMEDIATE SOURCE:
: CLONE: E. coli NM522(pMTC1642) NRRL B-18961
: US-09-173-891-10

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 Quality: 94.00

Ratio: 0.931 Gaps: 10
 Percent Similarity: 54.891 Percent Identity: 25.543

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seq_documentation_block:

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: Sequence 12, Application US/09076137B
: Patent No. 6166195
: GENERAL INFORMATION:
: APPLICANT: Schnepf, Harry E.
: APPLICANT: Schwab, George E.
: APPLICANT: Payne, Jewel M.
: APPLICANT: Naraya, Kenneth E.
: APPLICANT: Foncerada, Luis
: TITLE OF INVENTION: No. 6166195el Nematode-Active Toxins and Genes which Code
: TITLE OF INVENTION: therefor
: FILE REFERENCE: MA-200CCD2
: CURRENT APPLICATION NUMBER: US/09/076,137B
: CURRENT FILING DATE: 1998-05-12
: EARLIER APPLICATION NUMBER: 08/316,301
: EARLIER FILING DATE: 1994-09-30
: NUMBER OF SEQ ID NOS: 42
: SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 12

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seq_documentation_block:
; Sequence 10, Application PC/TUS9303164
; GENERAL INFORMATION:
; APPLICANT: Jessell, Thomas M
; APPLICANT: Klar, Avihu
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
; TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/03164
; FILING DATE: 19930402
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 40028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP 01
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 807 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-03164-10

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seq_documentation_block:
; Sequence 4, Application US/08930996A
; Patent No. 6100449
; GENERAL INFORMATION:
; APPLICANT: Fluhr, Robert
; APPLICANT: Eshed, Yuval
; APPLICANT: ORI, Naomi
; APPLICANT: PARAN, Ilan
; APPLICANT: ZAMIR, Daniel
; TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE
; LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND

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Page 12

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? Sequence 2, Application US/08896449A
? Patent No. 6040143
? GENERAL INFORMATION:
? APPLICANT: Venta, Patrick J
? APPLICANT: Yuzbaslyan-Gurkhan, Vilma
? APPLICANT: Schall, William D
? APPLICANT: Brewer, George J
? TITLE OF INVENTION: DNA ENCODING CANINE VON WILLEBRAND
? TITLE OF INVENTION: FACTOR AND METHODS OF USE
? NUMBER OF SEQUENCES: 11
? CORRESPONDENCE ADDRESSES:
? ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
? STREET: 5445 Corporate Drive
? CITY: Troy
? STATE: Michigan
? COUNTRY: USA
? ZIP: 48098
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/896,449A
? FILING DATE: 18-JUL-1997
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Smith, Deann F.
? REFERENCE/DOCKET NUMBER: 2115-001226
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 248-641-1600
? TELEFAX: 248-641-0270
? TELEX: 287637
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 2813 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-896-449A-2

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? Quality: 76.50 Length: 195
? Ratio: 0.922 Gaps: 11
? Percent Similarity: 42.564 Percent Identity: 23.590

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2309 aAlaArgLeuValArgGlnAsnAlaValGlnCysCysProGluTyrlucys 2325
143 .....CTTCACCACTGTTCCCGTCGCGTT 118
2326 ValCysAspLeuValSerCysAspLeuProProValProPro..... 2339
117 GACACTGATACTATATGTCAGCAGGCGCAGGTGAGAGACACCAAGAA 68
2340 .....CysGluAspGlyLeuGlnMetThrLeuThra 2350
67 GTCCAGCAAAAGGCAATTGTGAACCTTCATCTTGCT 33
2350 snProGlyGluCysArgProAsnPhenThrCysAla 2361
```




```

|||||
117 ylysglyproglyglyprobrofrolsglyleumettyrserValasp 134
413 CCACAGAGCTCGACAACTGGACAACTTGGAAAAATCCATCGTGGCAG 462
134 romslnlyValaspaspleuserlyspheglylysasnillealasnMet 150
463 TGCAGGGGATTCCACATATCATGCTGGAAGATTCAAGAGCAAACT 512
151 CysArgGlyIleprothrlyrmetalaGlumetGlnGluAlaSerle 167
513 GATTGCTACTCGAAAAAGTCATCGCAATATCTCTGATTCTTA 562
167 uphpehTySerGlyThrCysTyThrThrSerValleuTripleVala 184
563 ACATTCTCTCTGTGGAGGAATGACGAGAGAC 594
184 spliserphecysglyaspthrValGluasn 194

```

seq_name: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-991-150-211

seq_documentation_block:

```

: Sequence 211, Application US/09991150
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gutney, Austin L.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2730P1C48
: CURRENT APPLICATION NUMBER: US/09/991,150
: CURRENT FILING DATE: 2001-11-16
: Prior Application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 532
: SEQ ID NO 211
: LENGTH: 185
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-991-150-211

```

alignment_scores:

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Quality: 775.00 Length: 185
Ratio: 4.429 Gaps: 0
Percent Similarity: 94.595 Percent Identity: 75.135

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alignment_block:

US-09-821-726-17 x US-09-991-150-211

Align seg 1/1 to: US-09-991-150-211 from: 1 to: 185

40 ATGAAGTTCACAATTCCTTTCGTGACATTCCTTGCTTCCTGACAC 89

```

|||||
1 MetlyspheThrIleValPheAlaGlyLeuencIlyalPheleuAlaPr 17
90 TGCCCTTCTGACTATATCTAGTGTCAACAGACAGGCAACAGTGTG 139
17 CalaleuAlasnTyraSnIleasnValasnPasPasnAsnAsnLaG 34
140 GAAGTGGCAGCAGTCAAGTGTCAACATGAAACATGAGTGGCCAA 189
34 lyserGlyGlnGlnSerValSerValasnAsnGlnHIsarValAlaSn 50
190 GTTGCAATTAACAATGATGAGTCACTCGAATGCCCTGGGACTATAG 239
51 ValaspasnaAsnGlyTyPaspserTyPasnserIleTyPaspTyG 67
240 AAGTGGCTTCTGCTCAACCCAGCTCTGCGAACAACATCATGCTTGC 289
67 yasnGlyPheAlaIatThrArgLeupheGlnTyLysThrCysIleValH 84
290 ACAAAATGAAGAGAGAGCCATGCCCTCCCTTCAAGCCCTTGATGCG 339
84 IslysmetasnlysgluValMetProSerIleGlnSerleuAspAlaLeu 100
340 GTCAAGGAAAAGAACTTCAGGGTAAGGCCCGAGGGGACCACTCCAA 389
101 ValysGlnTyLysLeuGlnGlyProGlyProGlyPropoly 117
390 GAGCCTGAGTACTGCTCAACCCAGCTCAAGGAGTCAACATGAGT 439
117 sGlyLeuMetTySerValasnProasnTyLysValaspaspleuserlysp 134
440 TTGGAATTCATCGTTCGATGTCAAGGAGTTCACATCATCATGCT 489
134 heglyLysasnIleAlaasnMetCysArglyIleprothrTyMetAla 150
490 GAAGAGATTCAAGAGCAACCTGATTTCTACTCAGAAAAGTCATCAG 539
151 GluGlnMetGlnGluAlaSerleuphepheTySerGlyThrCysTyThr 167
540 TGCCAAATTAATCTGATTCATTCATTCATTCCTTGGGAGGAATACCG 589
167 rThSerValleuTripleValaspIleSerphecysglyAspThrValG 184
590 AGAAC 594
184 luasn 185

```

seq_name: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-720-533-49

seq_documentation_block:

```

: Sequence 49, Application US/09720533
: GENERAL INFORMATION:
: APPLICANT: INCYTE PHARMACEUTICALS, INC.
: APPLICANT: LAL, Preeti
: APPLICANT: TANG, Y. Tom
: APPLICANT: GORGONE, Gina A.
: APPLICANT: CORLEY, Neil C.
: APPLICANT: GUEGLER, Karl J.
: APPLICANT: BAUGHN, Mariah R.
: APPLICANT: AKERLOW, Ingrid E.
: APPLICANT: AU-YOUNG, Janice
: APPLICANT: YUE, Henry
: APPLICANT: PATTERSON, Chandra
: APPLICANT: REDDY, Roopa
: APPLICANT: HILLMAN, Jennifer L.
: APPLICANT: BANDMAN, Olga
: TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
: FILE REFERENCE: PF-0541 PCT
: CURRENT APPLICATION NUMBER: US/09/720,533
: CURRENT FILING DATE: 2002-08-26
: PRIOR APPLICATION NUMBER: 60/090,762; 60/094,983; 60/102,686; 60/112,129
: PRIOR FILING DATE: 1998-06-26; 1998-07-31; 1998-10-01; 1998-12-11
: NUMBER OF SEQ ID NOS: 268

```

```

; SOFTWARE: PERL Program
; SEQ ID NO 49
; LENGTH: 185
; TYPE: prt
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte Clone No: 2593853
US-09-720-533-49

```

```

alignment_scores:
  Quality: 775.00      Length: 185
  Ratio: 4.429         Gaps: 0
  Percent Similarity: 94.595  Percent Identity: 75.135

```

```

alignment_block:
US-09-821-726-17 x US-09-720-533-49  ..

```

```

Align seg 1/1 to: US-09-720-533-49 from: 1 to: 185

```

```

40 ATGAAGTTCAACAATTCCTTCTGCTGAGCTTCTGTCTCTCTGACTCC 89
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MetLysPheThrIleValAlaPheAlaGlyLeuLeuGlyValPheLeuAlaPr 17
90 TGGCCTTGCTGACTATAGTATGACTGTCAAGACGACGCGACAGTGTG 139
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 cAlaLeuAlaAsnTyraSnIleAsnValAlaSnAspAsnAsnAlaG 34
140 GAAGTGGCGCAGCAGTCACTGAGTGTCAACATCAACACAACTGGCCAA 189
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 LySerGIyGlnGlnSerValSerValAsnAsnGlnHisAsnValAlaAsn 50
190 GTTGACAATPACAAATGATGATGAACTCTGGAATGCCCTCGAGCATATG 239
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51 ValAspAsnAsnAsnGlyTrpAspSerTrpAsnSerIleTrpAspTyrGl 67
240 AACTGCTTTGCTGTAAACGAGACTCTTCGAGAAGAAGTCATGCAATTGC 289
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67 yAsnGlyPheAlaAlaThrArgLeuPheGlnLysLysThrCysIleValH 84
290 ACAAAATGAAGAAGAACCATGCTCCCTCTTAAGCCCTTGATGCGCTG 339
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84 IStyMetLysnLysGluValMetProSerIleGlnSerLeuAspAlaLeu 100
340 GTCAAGAAAGAAAGCTTCAAGGTAAGGCGCCAGGGGACCACTGCCAA 389
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101 ValLysGlnLysLysLeuGlnGlyLysGlyProGlyGlyProProProl 117
390 GAGCTGAGTACTGACTCAACCCCAACAGAGTGCACAACTGGACAAGT 439
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
117 sGlyLeuMetTyrSerValAsnProAsnLysValAspAspLeuSerLysP 134
440 TTGGAATTCATCGATGTCATGTGCAAGGGATTCACACATACATGCGCT 489
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
134 heGlyLysAsnIleAlaAsnMetCysArgGlyIleProThrTyrMetAla 150
490 GAAGAGATTCAGAGCAAACTGATTTGTACTTCAGAAAAGTGCATCGAG 539
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
151 GluGlnMetGlnGlnLaseSerLeuPhePheTyrSerClyThrCysTyrTh 167
540 TGGCAATATATCTGTGATTTCTTAACATTTCTCTTGAGAGCAATAGCG 589
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
167 rThrSerValLeuTrpIleValAlaSplLeSerPheCysGlyAspThrValG 184
590 AGAAC 594
|||||
184 LuAsn 185

```

```

seq_name: /cgn2_6/ptodata/2/paa/US10_NBW_COMB.pep:US-10-119-480-148

```

```

seq_documentation_block:
; Sequence 148, Application US/10119480

```

```

; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C1
; CURRENT APPLICATION NUMBER: US/10/119,480
; CURRENT FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 246
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 148
; LENGTH: 185
; TYPE: prt
; ORGANISM: Homo Sapien
US-10-119-480-148

```

```

alignment_scores:
  Quality: 775.00      Length: 185
  Ratio: 4.429         Gaps: 0
  Percent Similarity: 94.595  Percent Identity: 75.135

```

```

alignment_block:
US-09-821-726-17 x US-10-119-480-148  ..

```

```

Align seg 1/1 to: US-10-119-480-148 from: 1 to: 185

```

```

40 ATGAAGTTCAACAATTCCTTCTGCTGAGCTTCTGTCTCTCTGACTCC 89
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 MetLysPheThrIleValAlaPheAlaGlyLeuLeuGlyValPheLeuAlaPr 17
90 TGGCCTTGCTGACTATAGTATGACTGTCAAGACGACGCGACAGTGTG 139
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 cAlaLeuAlaAsnTyraSnIleAsnValAlaSnAspAsnAsnAlaG 34
140 GAAGTGGCGCAGCAGTCACTGAGTGTCAACATCAACACAACTGGCCAA 189
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 LySerGIyGlnGlnSerValSerValAsnAsnGlnHisAsnValAlaAsn 50
190 GTTGACAATPACAAATGATGATGAACTCTGGAATGCCCTCGAGCATATG 239
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51 ValAspAsnAsnAsnGlyTrpAspSerTrpAsnSerIleTrpAspTyrGl 67
240 AACTGCTTTGCTGTAAACGAGACTCTTCGAGAAGAAGTCATGCAATTGC 289
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67 yAsnGlyPheAlaAlaThrArgLeuPheGlnLysLysThrCysIleValH 84
290 ACAAAATGAAGAAGAACCATGCTCCCTCTTAAGCCCTTGATGCGCTG 339
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84 IStyMetLysnLysGluValMetProSerIleGlnSerLeuAspAlaLeu 100
340 GTCAAGAAAGAAAGCTTCAAGGTAAGGCGCCAGGGGACCACTGCCAA 389
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101 ValLysGlnLysLysLeuGlnGlyLysGlyProGlyGlyProProProl 117
390 GAGCTGAGTACTGACTCAACCCCAACAGAGTGCACAACTGGACAAGT 439
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
117 sGlyLeuMetTyrSerValAsnProAsnLysValAspAspLeuSerLysP 134
440 TTGGAATTCATCGATGTCATGTGCAAGGGATTCACACATACATGCGCT 489
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
134 heGlyLysAsnIleAlaAsnMetCysArgGlyIleProThrTyrMetAla 150
490 GAAGAGATTCAGAGCAAACTGATTTGTACTTCAGAAAAGTGCATCGAG 539
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```



```

; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-162-148
```

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alignment_scores:
  Quality: 775.00      Length: 185
  Ratio: 4.429         Gaps: 0
  Percent Similarity: 94.595  Percent Identity: 75.135
```

alignment_block:
US-09-821-726-17 x US-10-216-162-148 ..

Align seg 1/1 to: US-10-216-162-148 from: 1 to: 185

```

40 ATGAAGTTACAAATGGCTTGGTGGACTTCTGGTCTTCCTGACTCC 89
  |||||||.....:|||||.....:|||||.....:|||||
  1 MetLysPheThrIleValIlePheAlaGlyLeuGlyValIlePheLeuAlaIpr 17
90 TGCCCTTGCTGACTATAGTATCAGTGTCAACGACGACGACGACAGTGTG 139
  |||||||.....:|||||.....:|||||.....:|||||
  17 oAlaIleuAlaAsnTyrAsnIleAsnValIAsnAspAsnAsnAlaIag 34
140 GAAGTGGGACGACGACGACGACGACGACGACGACGACGACGACGACG 189
  |||||||.....:|||||.....:|||||.....:|||||
  34 LysSerIyGlnGlnSerValIserValIAsnAsnGlnIHisnValAlaIAsn 50
190 GTTGCAATAAACAATGATGATGAACCTCCGGAATGCCCTGGGACTATAG 239
  |||||||.....:|||||.....:|||||.....:|||||
  51 ValAspAsnAsnAsnGlyTyrPaspSerTyrPaspSerIleTyrPaspTyrG 67
240 AACTGGCTTGGTGTAAACGACGACGACGACGACGACGACGACGACGAC 289
  |||||||.....:|||||.....:|||||.....:|||||
  67 yAsnGlyPheAlaIleAlaThrArgIleuPheGlnIlysIleuAlaIAsn 84
290 ACAAAATGAAGAAGAGGACGACGACGACGACGACGACGACGACGACG 339
  |||||||.....:|||||.....:|||||.....:|||||
  84 lLysMetAsnLysGlnValIleMetProSerIleGlnSerIleuAspAlaIeu 100
340 GTCAAGGAAGAAGAGCTTCAGGGTAAAGGGGACGACGACGACGACGAC 389
  |||||||.....:|||||.....:|||||.....:|||||
  101 ValLysGlnLysLysLeuGlnIleGlyGlyProGlyGlyProProIy 117
390 GAGCGTGAAGTACTAGTCACCCACGACGACGACGACGACGACGACGAC 439
  |||||||.....:|||||.....:|||||.....:|||||
  117 sGlyLeuMetTyrIserValIAsnProAsnLysValIAspAspLeuSerLysP 134
440 TTGGAATAATCCATCGTTGCCATGTGCAAGGGGATTCACCAATACATG 489
  |||||||.....:|||||.....:|||||.....:|||||
  134 heGlyLysAsnIleAlaAsnMetCysArgGlyIleProThrTyrIleAla 150
490 GAAGATTCAGAGGACAACTGATTCGACGACGACGACGACGACGACGAC 539
  |||||||.....:|||||.....:|||||.....:|||||
  151 GluGlnMetClnGlnIleAlaSerIleuPheIleTyrSerGlyThrCysTyrTh 167
540 TGCCAATATACCTCTGATTCCTTACATTCCTTCTGTGGAGGAATAGGG 589
```

```

;.....:|||||.....:|||||.....:|||||.....:|||||
167 rThSerValIleuThrIleValIAspIleSerPheCysGlyAspThrValG 184
590 AGAAC 594
  ||||||
184 lAsn 185
```

seq_name: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:US-10-216-163-148

seq_documentation_block:

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; Sequence 148, Application US/10216163
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C3
```

```

; CURRENT APPLICATION NUMBER: US/10/216,163
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-163-148
```

```
alignment_scores:
  Quality: 775.00      Length: 185
  Ratio: 4.429         Gaps: 0
  Percent Similarity: 94.595  Percent Identity: 75.135
```

alignment_block:
US-09-821-726-17 x US-10-216-163-148 ..

Align seg 1/1 to: US-10-216-163-148 from: 1 to: 185

```

40 ATGAAGTTACAAATGGCTTGGTGGACTTCTGGTCTTCCTGACTCC 89
  |||||||.....:|||||.....:|||||.....:|||||
  1 MetLysPheThrIleValIlePheAlaGlyLeuGlyValIlePheLeuAlaIpr 17
90 TGCCCTTGCTGACTATAGTATCAGTGTCAACGACGACGACGACGACGAC 139
  |||||||.....:|||||.....:|||||.....:|||||
```

```

17  oAlaLeuAlaAsnTyrAsnIleAsnValAsnAspAsnAsnAlaG 34
140 GAAGTGGGACAGTCAAGTCAAGTCAACATGAACACAGTGGCCAA 189
134 lYserGIyngInserValSerValAsnSngIuhIsaValAlaAsn 50
190 GTTGACATAAACAATGAGTGAACCTCTGGAATGCCCTGGAGCTAATG 239
51 ValAspAsnAsnAsnGlyTTPAspSerTTPAsnSerIleTTPAspTyrGI 67
240 AACGCGCTTGCTGTACACAGACTCTCGAGAGAGAACTCATGTGCTGC 289
67 yAsnGIyPheAlaIaThrArgLeuPheGlnLysLysThrCysIleValH 84
290 ACAAAATGAAGAAGAGCCATGCCCTCCCTCAAGCCCTTGATGCGCTG 339
84 iLysMetAsnLysGlnValMetProSerIleGlnSerIleuAspAlaLeu 100
340 GTCAAGAAAAAGAGCTTCAAGGGTAAAGGCCCAAGGGGACCCTCCAA 389
101 ValLysGlnLysLysLeuGlnGlyLysGlyProGlyGlyProProGly 117
390 GAGCTGAGTCACTCAACCCCAACAGAGTGCAGAACCTGACACAGT 439
117 sGIyLeuMetTyrSerValAsnProAsnLysValAspAspLeuSerLysP 134
440 TTGGAATATCCATGCTGCATGTGCAAGGGATTCACATACATAGCT 489
134 heGlyLysAsnIleAlaAsnMetCysArgLylleProThrIlyrMetAla 150
490 GAAGAGATTCAAGAGCAAACTGATTCGTACTCAGAAAAGTGCATCAG 539
151 GluLysMetGlnGlnLysLeuPhePheTyrSerGIyThrCysTyrTh 167
540 TGCCATATATCTGTGATTCCTTACATTCCTCTGTGAGAGATACCG 589
167 rThSerValleuTripleValAspIleSerPheCysGIyAspThrValG 184
590 AGAAC 594
184 LuAsn 185

```

```

seq_name: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:US-10-216-164-148
seq_documentation_block:
; Sequence 148, Application US/10216164
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Geritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C5
; CURRENT APPLICATION NUMBER: US/10/216,164
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31

```

```

; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-164-148

```

```

alignment_scores:
Quality: 775.00 Length: 185
Ratio: 4.429 Gaps: 0
Percent Similarity: 94.595 Percent Identity: 75.135

```

```
alignment_block:
US-09-821-726-17 x US-10-216-164-148 ..

```

```
Align seg 1/1 to: US-10-216-164-148 from: 1 to: 185

```

```

40 ATGAAGTTACAAATTCCTTCTGCTGACTTCTGTGCTTCTCTGACTGCC 89
1 MetLysPheThrIleValAlaPheAlaGlyLeuGlnGlyValAlaPheLeuAlaPr 17
90 TGCCCTTGCTGACTATAGTATGATGATGTCACAGCAGCAGGCAACAGTGGTG 139
17 oAlaLeuAlaAsnTyrAsnIleAsnValAsnSrpAsnSngIuhIsaValAlaAsn 34
140 GAAGTGGGACAGAGTCAAGTCAAGTCAACATGAACACAGCTGGCCAA 189
34 lYserGIyngInserValSerValAsnSngIuhIsaValAlaAsn 50
190 GTTGACATAAACAATGAGTGAACCTCTGGAATGCCCTTGAGACTATAG 239
51 ValAspAsnAsnAsnGlyTTPAspSerTTPAsnSerIleTTPAspTyrGI 67
240 AACTGCGCTTGCTGTACACAGACTCTCGAGAGAGTGCATGATGCTGC 289
67 yAsnGIyPheAlaIaThrArgLeuPheGlnLysLysThrCysIleValH 84
290 ACAAAATGAAGAAGAGCCATGCCCTCCCTCAAGCCCTTGATGCGCTG 339
84 iLysMetAsnLysGlnValMetProSerIleGlnSerIleuAspAlaLeu 100
340 GTCAAGAAAAAGAGCTTCAAGGGTAAAGGCCCAAGGGGACCCTCCCA 389
101 ValLysGlnLysLysLeuGlnGlyLysGlyProGlyGlyProProGly 117
390 GAGCTGAGTCACTCAACCCCAACAGAGTGCAGAACCTGACACAGT 439
117 sGIyLeuMetTyrSerValAsnProAsnLysValAspAspLeuSerLysP 134
440 TTGGAATATCCATGCTTGCATGTGCAAGGGATTCACATACATAGCT 489
134 heGlyLysAsnIleAlaAsnMetCysArgLylleProThrIlyrMetAla 150
490 GAAGAGATTCAAGAGCAAACTGATTCGTACTCAGAAAAGTGCATCAG 539
151 GluLysMetGlnGlnLysLeuPhePheTyrSerGIyThrCysTyrTh 167
540 TGCCATATATCTGTGATTCCTTACATTCCTCTGTGAGAGATACCG 589
167 rThSerValleuTripleValAspIleSerPheCysGIyAspThrValG 184

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590 AGAAC 594
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184 Luasn 185

seq_name: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:US-10-216-165-148

seq_documentation_block:
: Sequence 148, Application US/10216165
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Desnoyers, Luc
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Smith, Victoria
: APPLICANT: Stephan, Jean-Philippe F.
: APPLICANT: Watanabe, Colin L.
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3530P1C7
: CURRENT FILING DATE: 2002-08-09
: PRIOR FILING DATE: 2002-04-09
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/062287
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/063549
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/064103
: PRIOR FILING DATE: 1997-10-31
: PRIOR APPLICATION NUMBER: 60/069873
: PRIOR FILING DATE: 1997-12-17
: PRIOR APPLICATION NUMBER: 60/078910
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/079294
: PRIOR FILING DATE: 1998-03-25
: PRIOR APPLICATION NUMBER: 60/079656
: PRIOR FILING DATE: 1998-03-26
: PRIOR APPLICATION NUMBER: 60/079728
: PRIOR FILING DATE: 1998-03-27
: Remaining prior Application data removed - See file Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 246
: SEQ ID NO 148
: LENGTH: 185
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-216-165-148

alignment_scores:
Quality: 775.00 Length: 185
Ratio: 4.429 Gaps: 0
Percent Similarity: 94.595 Percent Identity: 75.135

alignment_block:
US-09-821-726-17 x US-10-216-165-148 ..
Align seg 1/1 to: US-10-216-165-148 from: 1 to: 185

40 ATGAAGTTCACAAATGGCTTTGGCTGCTTGGTCTCTTCTGACTCC 89
|||||
1 MetlyspherthriLevalphealaglyLeuleuclyvalpheleualapr 17

90 TGCCTTGCTGATATAGTATCAGTGCACAGCAGCAGCAACAGTGTG 139
|||||
17 CAlaleuAlaAsnTytrAsnIleAsnValAsnAspAsnAsnAlaag 34

140 GAAGTGGCAGCAGTCAAGTGTCTCAACAATGAAACAACAGTGGCCAC 189
```

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|||||
34 lYserGlyngInserValSerValAsnAsnGluHIsAsnValAlaAsn 50
|||||
190 GTTGACCAATAACAATGATGCAGTCCCTCGAATGCCCTCGGACTATAG 239
|||||
51 ValAspAsnAsnAsnGlyTrpAspSerTrpAsnSerIleTrpAspTrpG 67
240 AACTGAGCTTGGCTGTACCAAGCTCTTCGACAGAGATGCATGATGGC 289
|||||
67 yAsnGlyPheAlaAlaThrArgLeuPheGlnIleSylsThrCysIleValH 84
290 ACAAATGAAAGAGAGAGAGCCATGCCCTTCATCAAGCCCTTGATCCGCTG 339
|||||
84 lSylsMetAsnIlysgLuValMetProSerIleGlnSerIleAsnAlaLeu 100
340 GTCAAGGAAAAGACCTTCAGGGTAAAGGCCAGGGGACCACTCCCAA 389
|||||
101 ValIlysgLuIlysgLeuGlnIlysgIlyProGlyIlyProProIly 117
390 GAGCCTGAGTACTGACGTCAACCCCAAGAGTGCACAGCTGACAGT 439
|||||
117 sGlyLeuMetIlySerValAsnProAsnIlyValAspAsnIlySerIly 134
440 TTGAAATATCATCGTTGCCATGTCAAGGGGATTCACATATATGCT 489
|||||
134 heGlyIlyAsnIleAlaAsnMetCysArgGlyIleProThrIlyMetAla 150
490 GAAGATTTCAAGAGCAACCTGATTCGTACTAGAAAAGTGCATGAG 539
|||||
151 GluGluMetGlnGluAlaSerIleuPhePheTythrCysTytrH 167
540 TGCCAAATATACTCTGATCTTACATTTCTCTGTGAGGAATAAGCGG 589
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167 rHrIserValLeuTrpIleValAlaSpIleSerPheCysIlyspHrValG 184

590 AGAAC 594
|||||
184 Luasn 185

seq_name: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:US-10-216-166-148

seq_documentation_block:
: Sequence 148, Application US/10216166
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Desnoyers, Luc
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Smith, Victoria
: APPLICANT: Stephan, Jean-Philippe F.
: APPLICANT: Watanabe, Colin L.
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3530P1C9
: CURRENT FILING DATE: 2002-08-09
: PRIOR FILING DATE: 2002-04-09
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/062287
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/063549
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/064103
: PRIOR FILING DATE: 1997-10-31
: PRIOR APPLICATION NUMBER: 60/069873
: PRIOR FILING DATE: 1997-12-17
: PRIOR APPLICATION NUMBER: 60/078910
```

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;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/079294
;; PRIOR FILING DATE: 1998-03-25
;; PRIOR APPLICATION NUMBER: 60/079656
;; PRIOR FILING DATE: 1998-03-26
;; PRIOR APPLICATION NUMBER: 60/079728
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 246
;; SEQ ID NO 148
;; LENGTH: 185
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-216-166-148
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alignment_scores:
    Quality: 775.00      Length: 185
    Ratio: 4.429        Gaps: 0
    Percent Similarity: 94.595    Percent Identity: 75.135
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alignment_block:

US-09-821-726-17 x US-10-216-166-148

Align seg 1/1 to: US-10-216-166-148 from: 1 to: 185

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|||||.....|.....|.....|.....|.....|.....|
1 MetLysPheThrIleValPheAlaGlyLeuLeuGlyValPheLeuAlaPr 17
|||||.....|.....|.....|.....|.....|.....|
90 TGGCCCTTGCTGACTATAGTATGCTGACAGCAGCAGCGCAAGTGGTG 139
|||||.....|.....|.....|.....|.....|.....|
17 CAlaLeuAlaAsnTyraIleAsnValAsnAspAsnAsnAlaG 34
|||||.....|.....|.....|.....|.....|.....|
140 GAAGTGGCAGCAGTCACTGAGTGCACAAATGACACACAGCTGGCCAA 189
|||||.....|.....|.....|.....|.....|.....|
34 LysSerGlyGlnGlnSerValSerValAsnAsnGlnHisValAlaAsn 50
|||||.....|.....|.....|.....|.....|.....|
190 GTTGACAAATACAAATGATGATGAACTCTGGAATGCCCTGGAGATATAG 239
|||||.....|.....|.....|.....|.....|.....|
51 ValAspAsnAsnAsnGlyTyrPaspSerTyrPaspSerIleTyrPaspTyrG 67
|||||.....|.....|.....|.....|.....|.....|
240 AACTGGCTTGGTGTAAACCACTCTTGAGAGAAGAAGTATGATGGC 289
|||||.....|.....|.....|.....|.....|.....|
67 yAsnGlyPheAlaAlaTyrArgLeuPheGlnLysLysThrCysIleValH 84
|||||.....|.....|.....|.....|.....|.....|
290 ACAAATGAAGAGAGAGAGCCATGCCCTCCCTTCAAGCCCTTGATGGCTG 339
|||||.....|.....|.....|.....|.....|.....|
84 IsLysMetAsnLysGlnValMetProSerIleGlnSerLeuAspAlaLeu 100
|||||.....|.....|.....|.....|.....|.....|
340 GTCAAGAAAAGAGCTTCAGGGTAAGGGCCAGGGGAGCCACCTCCCA 389
|||||.....|.....|.....|.....|.....|.....|
101 ValLysGlyLysLysLeuGlnGlyLysGlyProGlyGlyProProTyr 117
|||||.....|.....|.....|.....|.....|.....|
390 GAGCGTGAAGTACGTCACCAACCCCAAGAGTGCACAACTGCAGCAAGT 439
|||||.....|.....|.....|.....|.....|.....|
117 SGlyLeuMetCysSerValAsnProAsnLysValAspAspLeuSerLysP 134
|||||.....|.....|.....|.....|.....|.....|
440 TTGGAATTCATCGTTCATGTCAGAGGAGGATTCACAAATACATGAGCT 489
|||||.....|.....|.....|.....|.....|.....|
134 heGlyLysAsnIleAlaAsnMetCysArgGlyIleProThrTyrMetAla 150
|||||.....|.....|.....|.....|.....|.....|
490 GAAAGGATTCAGAGCAACCGATTTGCTACTCAGAAAAGTGCATCAG 539
|||||.....|.....|.....|.....|.....|.....|
151 GlnGlnMetGlnGlnValAsnSerLeuPhePheThrCysTyrTyr 167
|||||.....|.....|.....|.....|.....|.....|
540 TGGCAATTAATCTGATTTTAAATTTCTTCTGCTGGAGAAATAGCGG 589
|||||.....|.....|.....|.....|.....|.....|
167 rThSerValLeuTyrPheValAspIleSerPheCysGlyAspThrValG 184
|||||.....|.....|.....|.....|.....|.....|
590 AGAAG 594
|||||
184 LuAsn 185
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seq_name: /cgn2_6/plodata/2/paa/us10_NEW_COMP.pep:US-10-216-167-148

seq_documentation_block:

Sequence 148 Application US/10216167

GENERAL INFORMATION:

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;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Gerritsen, Mary
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Smith, Victoria
;; APPLICANT: Stephan, Jean-Philippe F.
;; APPLICANT: Watanabe, Colin I.
;; APPLICANT: Wood, William I.
```

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3530P1C4

CURRENT FILING DATE: 2002-08-09

PRIOR APPLICATION NUMBER: 10/119,480

PRIOR FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/062287

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/063549

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/064103

PRIOR FILING DATE: 1997-10-31

PRIOR APPLICATION NUMBER: 60/069873

PRIOR FILING DATE: 1997-12-17

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/079294

PRIOR FILING DATE: 1998-03-25

PRIOR APPLICATION NUMBER: 60/079656

PRIOR FILING DATE: 1998-03-26

PRIOR APPLICATION NUMBER: 60/079728

PRIOR FILING DATE: 1998-03-27

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 246

SEQ ID NO 148

LENGTH: 185

TYPE: PRT

ORGANISM: Homo Sapien

US-10-216-167-148

alignment_scores:

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Quality: 775.00      Length: 185
Ratio: 4.429        Gaps: 0
Percent Similarity: 94.595    Percent Identity: 75.135
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alignment_block:

US-09-821-726-17 x US-10-216-167-148

Align seg 1/1 to: US-10-216-167-148 from: 1 to: 185

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40 ATGAAGTTCAAAATTCCTTGGTGGACTTCTTGGTGTCTTCTGACTCC 89
|||||.....|.....|.....|.....|.....|.....|
1 MetLysPheThrIleValPheAlaGlyLeuLeuGlyValPheLeuAlaPr 17
|||||.....|.....|.....|.....|.....|.....|
90 TGGCCCTTGCTGACTATAGTATGCTGACAGCAGCAGCGCAAGTGGTG 139
|||||.....|.....|.....|.....|.....|.....|
17 CAlaLeuAlaAsnTyraIleAsnValAsnAspAsnAsnAlaG 34
|||||.....|.....|.....|.....|.....|.....|
140 GAAGTGGCAGCAGTCACTGAGTGCACAAATGACACACAGCTGGCCAA 189
|||||.....|.....|.....|.....|.....|.....|
34 LysSerGlyGlnGlnSerValSerValAsnAsnGlnHisValAlaAsn 50
|||||.....|.....|.....|.....|.....|.....|
```



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190 GTTGCAATTAACAATGATGGAAGTCTGGAATGCCCTGGAGCTATAG 239
|||||
51 ValAspAsnAsnAsnglyTTrpAspSerTrpAsnSerIleTrpAspTyrGI 67
240 AAGCGCTTGTCTGTAACCGACACTCTTCGAGAAAGTCAAGCTTGTGC 289
|||||
67 yAsnglyPheAlaIatThrArgLeuPheGlnLysLysThrCysIleValH 84
290 ACAAATGAAGAGAGAGAGCCATGCCCTCCCTTCAAGCCCTGATGCCCTG 339
|||||
84 IsLysMetAsnLysGluValMetProSerIleGlnSerLeuAspAlaLeu 100
340 GTCAAGGAGAGAGAGCTTCAAGGTTAAGGCCCAAGGGAGCCACCTCCAA 389
|||||
101 ValLysGluLysLysLeuGlnGlyLysGlyProGlyGlyPropropoly 117
390 GAGCCTGAGTACTGAGTCAACCCCAAGACAGTGCAGAACCTGAGCAAGT 439
|||||
117 sGlyLeuMetLysSerValAsnProAsnLysValAspAspLeuSerLysP 134
440 TTGGAAATCCATCGTTCATGTCGTCAGAGGAGATTCACATACATAGCT 489
|||||
134 heGlyLysAsnIleAlaAsnMetCysArgGlyIleProThrTyrMetAla 150
490 GAAGAGATTCAAGAGCAACCTGATTGCTACTCAGAGAAAGTGCATCAG 539
|||||
151 GluGluMetGlnGluAlaSerLeuPhePheTyrSerGlyThrCysTyrTh 167
540 TGCCAATATATCTGATTCCTTAACATTCTCTCTGAGAGGAATAGCGG 589
|||||
167 rThSerValLeuThrIleValAspIleSerPheCysGlyAspThrValG 184
590 AGAAC 594
|||||
184 LuAsn 185

seq_name: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:US-10-216-168-148

seq_documentation_block:
; Sequence 148, Application US/10216168
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gertlisen, Maty
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowskl, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Collin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C10
; CURRENT APPLICATION NUMBER: US/10/216.168
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25

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; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-168-148

alignment_scores:
Quality: 775.00 Length: 185
Ratio: 4.429 Gaps: 0
Percent Similarity: 94.595 Percent Identity: 75.135

alignment_block:
US-09-821-726-17 x US-10-216-168-148 ..

Align seg 1/1 to: US-10-216-168-148 from: 1 to: 185

40 ATGAACTGCAAAATGCTTGTCTGAGCTTCTGCTGCTGCTGCTGCTGCTC 89
|||||
1 MetLysPheThrIleValAlaPheAlaGlyLeuGlyValAlaPheAlaIaPr 17
90 TGCCCTGCTGCTATAGTATGATGATGATGATGATGATGATGATGATG 139
|||||
17 oAlaLeuAlaAsnTyrAsnIleAsnValAsnAspAsnAsnAlaAsn 34
140 GAAGTGGCAGCAGTCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGT 189
|||||
34 LysSerGlyGlnGlnSerValSerValAsnAsnGlnHisAsnValAlaAsn 50
190 GTTGACATTAACAATGATGATGATGATGATGATGATGATGATGATGAT 239
|||||
51 ValAspAsnAsnAsnglyTTrpAspSerTrpAsnSerIleTrpAspTyrGI 67
240 AACTGCTTGTGCTGTAACAGACTCTTGAGAGAAAGTCAATGATGATGC 289
|||||
67 yAsnglyPheAlaIatThrArgLeuPheGlnLysLysThrCysIleValH 84
290 ACAAATGAAGAGAGAGCCATGCCCTCCCTTCAAGCCCTGATGCCCTG 339
|||||
84 IsLysMetAsnLysGluValMetProSerIleGlnSerLeuAspAlaLeu 100
340 GTCAAGGAGAGAGCTTCAAGGTTAAGGCCCAAGGGAGCCACCTCCAA 389
|||||
101 ValLysGluLysLysLeuGlnGlyLysGlyProGlyGlyPropropoly 117
390 GAGCCTGAGTACTGAGTCAACCCCAAGACAGTGCAGAACCTGAGCAAGT 439
|||||
117 sGlyLeuMetLysSerValAsnProAsnLysValAspAspLeuSerLysP 134
440 TTGGAAATCCATCGTTCATGTCGTCAGAGGAGATTCACATACATAGCT 489
|||||
134 heGlyLysAsnIleAlaAsnMetCysArgGlyIleProThrTyrMetAla 150
490 GAAGAGATTCAAGAGCAACCTGATTGCTACTCAGAGAAAGTGCATCAG 539
|||||
151 GluGluMetGlnGluAlaSerLeuPhePheTyrSerGlyThrCysTyrTh 167
540 TGCCAATATATCTGATTCCTTAACATTCTCTCTGAGAGGAATAGCGG 589
|||||
167 rThSerValLeuThrIleValAspIleSerPheCysGlyAspThrValG 184
590 AGAAC 594
|||||
184 LuAsn 185

seq_name: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:US-10-216-160-148

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290 ACAAATGACAGAGAGACCATGCCCTCCCTTCAAGCCCTTGATGCGCTG 339
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84 lslYmeTAsnIlysgIuValmeTProSerIleGInSerLeuAspAlaLeu 100
340 GTCAAGGAAAGAACCTTCAGGTTAAGGCCCGGAGGACCACTCCCAA 389
|||||.....:|||||.....:|||||.....:
101 ValYsgIuLyLysLeuGInGlyLysGlyProGlyProProProLy 117
390 GAGCCTGAGTACTGACTGCAACCCCAACAGAGTGCACACCTGGCAAGT 439
|||||.....:|||||.....:|||||.....:
117 sGlyeuMeTylSerValAsnProAsnLySValAspAspLeuSerLysP 134
440 TTGGAAATCCATCGCTTCCCATGTGCAAGGGGATTCCAAATACATGCT 489
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134 heGlyLysAsnIleAlAsnMeTcysArgIyleProThrTyMeTala 150
490 GAAGGATTCAAGAGCAACCTGATTTCGACTCAGAAAAGTCATCAG 539
|||||.....:|||||.....:|||||.....:
151 GluGluMeTcGInGluAlaSerLeuPhePheYrSerGlyThrcysTryth 167
540 TGCCAAATATCTGTGATTTCTTAACATTTCTTGTGAGGAATAGCGG 589
|||||.....:|||||.....:|||||.....:
167 rThSerValleuTrpIleValAspIleSerPheCysGlyAspThrValG 184
590 AGAAC 594
|||||
184 IuAsn 185

```

seq_name: /cgn2_6/plodata/2/paa/US10_NEW_COMB.pep:US-10-218-930-148

seq_documentation_block:

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: Sequence 148, Application US/10218930
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Desnoyers, Luc
: APPLICANT: Geritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Smith, Victoria
: APPLICANT: Stephan, Jean-Philippe F.
: APPLICANT: Watanabe, Colin L.
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3530P1C13
: CURRENT APPLICATION NUMBER: US/10/218,930
: CURRENT FILING DATE: 2002-08-12
: Prior Application removed - See file wrapper or Palm
: NUMBER OF SEQ ID NOS: 246
: SEQ ID NO 148
: LENGTH: 185
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-218-930-148

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alignment_scores:

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Quality: 775.00 Length: 185
Ratio: 4.429 Gaps: 0
Percent Similarity: 94.595 Percent Identity: 75.135

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alignment_block:

US-09-821-726-17 x US-10-218-930-148 ..

Align seg 1/1 to: US-10-218-930-148 from: 1 to: 185

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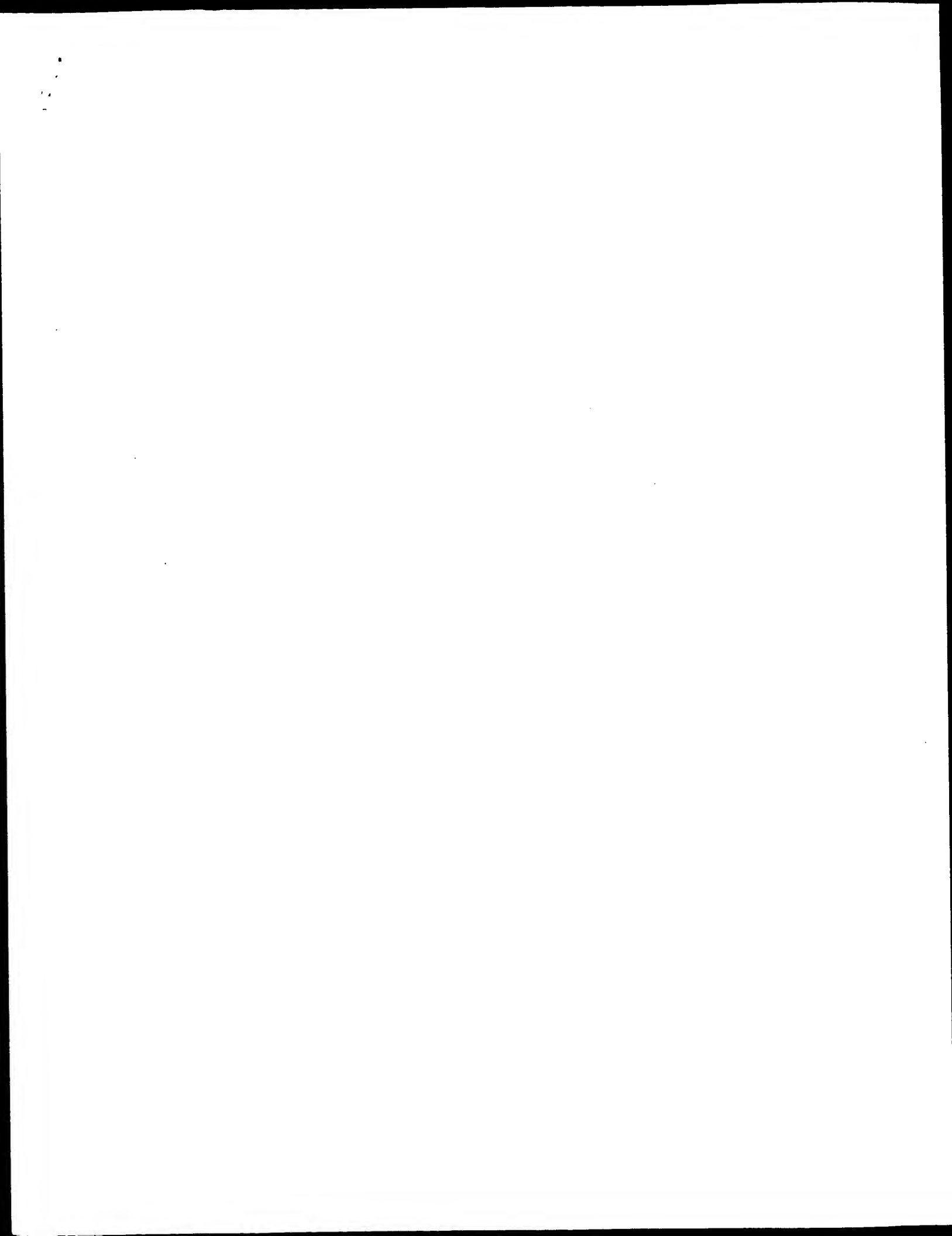
40 ATGAAGTTCACATTCGCTTGTGAGCTTCTTGCTGCTCTCTCTCTCTCC 89
|||||.....:|||||.....:|||||.....:
1 MetLysPheThrIleValIlePheAlaGlyLeuLeuGlyValIleLeuAlaPr 17
90 TGCCCTTGCTGACTATAGTATCATGTGTCAAGCAGCAGCAACAGTGTG 139

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|||||.....:|||||.....:|||||.....:
17 oAlaLeuAlaAsnTyRAsnIleAsnValAsnAspAspAsnAsnIaG 34
140 GAAGTGGCCACGACGACTGAGTGTCAACATGTAACACACAGTGGCCAC 189
|||||.....:|||||.....:|||||.....:
34 lYSerGlyGInGInSerValSerValAsnAsnGluHisAsnValAlaAsn 50
190 GTTGCAATTAACATGTGATGGAACTCCTGGAAATGCCCTTGGGACTAT 239
|||||.....:|||||.....:|||||.....:
51 ValAspAsnAsnAsnGlyTrpAspSerTrpAsnSerIleTrpAspTrygl 67
240 AACTGCGTTTGCTGTAAACCACTCTTCGAAACAATACTCATGTGCTGC 289
|||||.....:|||||.....:|||||.....:
67 yAsnIlyPheAlaAlaThrAlaGluPheGInLyLysThrcysIleValH 84
290 ACAAATGACAGAGAGAGCCATGCCCTCCCTTCAAGCCCTTGATGCGCTG 339
|||||.....:|||||.....:|||||.....:
84 lslYmeTAsnIlysgIuValmeTProSerIleGInSerLeuAspAlaLeu 100
340 GTCAAGGAAAGAACCTTCAGGTTAAGGCCCGGAGGACCACTCCCAA 389
|||||.....:|||||.....:|||||.....:
101 ValYsgIuLyLysLeuGInGlyLysGlyProGlyProProProLy 117
390 GAGCCTGAGTACTGACTGCAACCCCAACAGAGTGCACACCTGGCAAGT 439
|||||.....:|||||.....:|||||.....:
117 sGlyeuMeTylSerValAsnProAsnLySValAspAspLeuSerLysP 134
440 TTGGAAATATCTGTGATTTCTTAACATTTCTTGTGAGGAATAGCGG 489
|||||.....:|||||.....:|||||.....:
134 heGlyLysAsnIleAlAsnMeTcysArgIyleProThrTyMeTala 150
490 GAAGGATTCAAGAGCAACCTGATTTCGACTCAGAAAAGTCATCAG 539
|||||.....:|||||.....:|||||.....:
151 GluGluMeTcGInGluAlaSerLeuPhePheYrSerGlyThrcysTryth 167
540 TGCCAAATATCTGTGATTTCTTAACATTTCTTGTGAGGAATAGCGG 589
|||||.....:|||||.....:|||||.....:
167 rThSerValleuTrpIleValAspIleSerPheCysGlyAspThrValG 184
590 AGAAC 594
|||||
184 IuAsn 185

```



574 SGLYSERASMEPRHEARGALAGLYASPTIRPYSCYSSERTINCYST 591
 284 TTGTGCACAAATGAAGAAGAACCATG.....CCC 315
 591 hrtYrHISAspHEALALysAsnValALcysLeuArgCysGLyGLyPro 607
 316 TCCCTTCAGCCCTTGATGGCTGCTGCAAGGAAAGACGCTTCAGGGTAA 365
 608 LysSerTILeRGlySPALASerGIuThrAsnHISrTylLeAspSerSe 624
 366 G.....GGCCGAGGGGACCACTCCCAAGACCTGAGTACTCATGCA 409
 624 rThrPheGLyProLAserArgThrProSerAsnAsnLISerValA 641
 410 ACCCCAC.....AGAGTCACACCTGCACAAAGTTT 441
 641 snThrAsnGLyGLySerAsnALAGLYArgThrAspGLyAsnAspAsnLys 657
 442 GGAAATCCATCGTGCATG 462
 658 GLYArgAspLISerLeuMet 664

seq_name: p1r2:JC7210

seq_documentation_block:

mollusc shell matrix protein N66 - Pinctada maxima
 C:Species: Pinctada maxima
 C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
 C:Accession: JC7210
 R:Kono, M.; Hayashi, N.; Samata, T.
 Biochem. Biophys. Res. Commun. 269, 213-218, 2000
 A:Title: Molecular mechanism of the nacreous layer formation in Pinctada maxima.
 A:Reference number: JC7210; MUID:20160475
 A:Accession: JC7210
 A:Molecule type: mRNA
 A:Residues: 1-568 <KON>
 A:Cross-references: DDBJ:AB032612
 C:Comment: This protein is rich in asparagine and glycine residues, it serves as a product layer. It is also important in calcification.
 C:Keywords: matrix protein

alignment_scores:
 Quality: 89.50 Length: 177
 Ratio: 1.053 Gaps: 8
 Percent Similarity: 48.023 Percent Identity: 23.164

alignment_block:
 US-09-821-726-17 x JC7210 ..

Align seg 1/1 to: JC7210 from: 1 to: 568

124 GACGGCAACAGTGTGGAATGGGACACACTGACGTGCTCAACATGA 173
 392 AsnGLyAsnAsnGLyGLyAsnGLy.....AsnAsnGL 402
 174 ACACAGCTGGCCACCTGACATATACATGATGACACTCTGATG 223
 402 YAsnAsnGLyAspAsnGLyAsnGLyAspAsnGLyTyrAsnGLyAspAsnG 419
 224 CC.....CTCTGGACCTATAGACTGGCTTGGCT 252
 419 LysAsnSerAspGLyArgLeuArgArgTrpAspLeuAlaAsn..... 432
 253 GTAACCGAGCTCTTCGAGAGAG.....TCATGCATGT 267
 433 ValArgArgMetHISALAGLArgTyrHisPheSerGLyGLyCysTLeuA 449
 288 GCACAAATGAGAAGAGCCATGCCCTTCACAGCCCTTGATGCGC 337
 449 LysLysAlaLysArgLeuSer.....ArgILeLeuGLyCysA 462
 338 TGTCAAGGAAAGAGACTTCAG.....GGTAAGGGCCCA 372

462 LaTYArgHISLysLysValArgLISrPheLysArgAsnGLyGLyLys 478
 373 GGGGG.ACCACCTCCCAAGACCTGAGTACTGATCAACCCCAAGAG 421
 479 GLYLeuAspValAspLISrPheProGLuMetValLeuProPheMetLysTyr 495
 422 TCGA.....CMAC 429
 495 rArgHISrTyrThrTyrGLyGLySerLeuThrThrProProCysAsnG 512
 430 CTGCACAAAGTTTGAATAATCATGCTGTCATGTGCAAGGGAT..... 473
 512 LuThrValLeuThrValValGLyLysCysHISValGLyValSerArgArg 528
 474TCCACATACAGCGCTGAGAGAGATTCACAGAGCAA 508
 529 ValLeuAspAlaLeuArgAsnValGLyGLyTyrGLyAspGLyTrpThrLe 545
 509 ACCTGATTTCGACTCAGAAAGTGACATCAG 539
 545 uSerLysTyrGLyThrArgArgProThrGln 555

seq_name: p1r2:T35096

seq_documentation_block:

hypothetical protein SCAG6.36 - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 15-Sep-2000
 C:Accession: T35096
 R:Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.
 submitted to the EMBL Data Library, July 1999
 A:Reference number: Z21567
 A:Accession: T35096
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-266 <SEE>
 A:Cross-references: EMBL:AL096884, PIDN:CA851459.1; GSPDB:GN00070; SCOEDB:SC4G6.36
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCOEDB:SC4G6.36
 C:Superfamily: Streptomyces coelicolor probable secreted protein SCC22.22c

alignment_scores:
 Quality: 89.00 Length: 173
 Ratio: 1.085 Gaps: 8
 Percent Similarity: 47.399 Percent Identity: 26.012

alignment_block:
 US-09-821-726-17 x T35096 ..

Align seg 1/1 to: T35096 from: 1 to: 266

28 GGTGAGCAACAGATGAGTTCACAAATTCCTTGTGAGCTTCTTGNGT 77
 123 GLYAspTyrLysLeuSerPheThrVal.....GLYTh 135
 78 CTTCGCGACTCCTGCCCTTGCTGACTATAGTACATGCTCAACGACGAGC 127
 135 rPheLeu.....AspG 139
 128 GCACAGTGTGGAAGTGGCGACAGCTAGT.....AGTGTCAACAT 171
 139 LysAsnLeuGLyGLyLysSerLysAsnAlaLeuSerAlaLeuLysAla 155
 172 GAACACAGCTGGCCACAGCTTCACATATACATGATGGAATCCTCGAA 221
 156 AlaLeuAsnVal.....SerProG 162
 222 TGCCCTCTGGAGCTATAGAACTGGCTTGTGCTGAACGAGACTCTTCGAGA 271
 162 uAlaPheValAspTyrTyrThrAlaLeuTyrSerThrLysTyrHisProG 179

seq_documentation_block:
hypothetical protein B-120 - human
C:Species: Homo sapiens (man)
C:Date: 17-Dec-1982 #sequence_revision 17-Aug-1995 #text_change 13-Aug-1999
C:Accession: A04523
R:Watson, R.; Oskarsen, M.; Vande Woude, G.F.
Proc. Natl. Acad. Sci. U.S.A. 79, 4078-4082, 1982
A:Title: Human DNA sequence homologous to the transforming gene (mos) of Moloney murine

seq_documentation_block:
 disease_resistance_protein_homolog_11 - potato (fragment)
 C:Species: Solanum tuberosum (potato)
 C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 03-Nov-2000
 C:Accession: T07755
 R:Leister, D.; Ballvora, A.; Salamini, F.; Gebhardt, C.
 Nature genet. 14, 421-429, 1996
 A:Title: A PCR based approach for isolating pathogen resistance genes from potato
 A:Reference number: Z16117; MUID:97099453
 A:Accession: T07755
 A:Status: translated from GH/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-227 <LEI>
 A:Cross-references: EMBL:060069; NID:01708709; PTD:ARC49588.1; PTD:01708710


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263 TCTTGAGAGAGATCATGATTCATGTCACAAATGAGAGAGAGCCATG 312
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
89 eupheglinlysthrCysIleValIhIstysMetAlaSLySLuValMet 105
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
313 CCCCTCCCTCAAGCCCTTGATGCGCTGCTCAAGAGAAAGAGCTTCAGG 362
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
106 ProserIleGlnSerLeuAspAlaIleValIySLySLySLySLySLy 122
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
363 TAAGGCGCCAGGGGAGCAGCCTCCAGAGAGCTGAGTACTGATCAAC 412
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
122 lysylglyProGlyGlyProIleProIleGlyLeuMetIleSerVala 139
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
413 CCAAGAGAGTGGACAGCAGTGGAGATGGAAATCCATGCTGCTCCATG 462
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
139 rosllyslValaspAspLeuSerIleGlyLysAsnIleAlaSLyMet 155
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
463 TGCAGAGGGGATTCACATATCATGCTGAGAGAGATTCAGAGCAACCT 512
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
156 CysArgGlyIleProIleThrIleMetAlaGluGluMetGluAlaSer 172
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
513 GATTTCGTACTCAGAAAGTGCATGCTGATCTGATCTGATCTTA 562
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
172 uphepethySerGlyThrCysIleThrIleSerValIleuIleVala 189
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
563 ACATTCCTTCTGTGGAGATAGCGAGAGAC 594
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
189 splIleSerPheCysGlyAspThrValGluAsn 199
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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seq_name: swissprot.40:cllp_mouse

seq_documentation_block:

ID CLIP_MOUSE STANDARD: PRT; 184 AA.

AC O9CR36, Q9D7K7, Q9C7Z5:

DT 01-MAR-2002 (Rel. 41, Created)

DT 01-MAR-2002 (Rel. 41, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Call protein homolog.

GN

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Stomach, and Tongue;

RA MEDLINE=21085660; Pubmed=11217851;

RA Kawai J., Shitagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,

RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Offield D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima T., Mazzarelli J., Momberts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmung L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

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CC or send an email to license@isb.ch.
CC -----
DR EMBL: AK008990: BAB2610.1: -
DR EMBL: AK008622: BAB25784.1: -
DR EMBL: AK008641: BAB25801.1: -
DR EMBL: AK008647: BAB25805.1: -
DR EMBL: AK008722: BAB25856.1: -
DR EMBL: AK008745: BAB25872.1: -
DR EMBL: AK008933: BAB25975.1: -
DR EMBL: AK008956: BAB25988.1: -
DR EMBL: AK009145: BAB26103.1: -
DR EMBL: AK019050: BAB31525.1: -
FT CONFLICT 113 113
FT SEQUENCE 184 AA; 20134 MW; 288982FE0404FFAB8 CRC64;

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alignment_scores:
Quality: 627.00 Length: 185
Ratio: 3.870 Gaps: 3
Percent Similarity: 87.568 Percent Identity: 63.243

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alignment_block:

US-09-821-726-17 x CLIP_MOUSE

Align seg 1/1 to: CLIP_MOUSE from: 1 to: 184

```

40 ATGAAGTTACACATTCGCTTGTGTCAGTCTTGTGTCCTTCTGACTCC 89
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MetIleuThrMetPheValIleGlyLeuLeuGlyLeuLeuAlaIlePrt 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
90 TGCCCTTGCTGCTATATGATCATGTCACAC...GAGCAGGCGCACAGCTG 136
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17 oglyPheAla...TyrThrValaSLySLySLySLySLySLySLySLySLy 33
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
137 GTGAGAGGGGCGACGACGATGAGTGGTCAACATGCAACAGCTGGCC 186
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
33 spgIySerGlyGlnIleSerValSerIleAsnGlyValIhIAsnValaIa 49
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
187 AACGTTGACATTAACATGATGATGAGTCTGGAATGCCCTTGAGACTA 236
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
50 AsnIleAspAsnAsnAsnGlyTrpAspSerTrpAsnSerIleuTrpAspTy 66
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
237 TAGAAGCTGCTTGTGTAACACAGCTCTTGAGAGAGATCATGACTG 286
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
66 rGlusnSerPheAlaIleThrArgLeuPheSerIleSLySerIleVal 83
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
287 TGCACAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 336
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
83 AlhIAsrMetAlaSLySLySLySLySLySLySLySLySLySLySLy 99
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
337 CTGTGCAAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 386
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
100 MetValIySLySLySLySLySLySLySLySLySLySLySLySLySLy 114
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
387 CAAGAGCGCTGAGGTCTGATGCAACCCACAGAGAGAGAGAGAGAG 436
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
114 OlyAspSLyMetIleSerValaSLySLySLySLySLySLySLySLy 131
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
437 AGTTTGAAGAAATCCATGCTGATGATGATGATGATGATGATGATG 486
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
131 hrPheGlyProIySLySLySLySLySLySLySLySLySLySLySLy 147
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
487 GCTGAAGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 536
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
148 AlaGluGluIleProGlyProAsnGlnProIleuTrpSLySLySLy 164
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
537 CAGTGCATATATCTGATGATGATGATGATGATGATGATGATGATG 586
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
164 rThrAlaAspIleuTrpIleuArgMetSerPheCysGlyThrSerV 181
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
587 CGGAG 591
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
181 alGlu 182
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

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DR SMART; SM00049; DEP; 1.
 DR SMART; SM00228; PDZ; 1.
 DR PROSITE; PS50186; DEP; 1.
 DR PROSITE; PS50106; PDZ; 1.
 DR Developmental protein.
 FT DOMAIN 251 323 PDZ.
 FT DOMAIN 425 499 DEP.
 FT DOMAIN 390 393 POLY-SER.
 FT CONFLICT 122 125 MISSING (IN REF. 2).
 FT CONFLICT 211 211 T -> N (IN REF. 2).
 SQ SEQUENCE 695 AA; 75350 MW; A9FA449F95CF75P2 CRC64;

alignment_scores:
 Quality: 87.00 Length: 112
 Ratio: 1.359 Gaps: 5
 Percent Similarity: 57.143 Percent Identity: 26.786

alignment_block:
 US-09-821-726-17 x DVL_MOUSE ..

Align seg 1/1 to: DVL_MOUSE from: 1 to: 695

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133 AGCGTGAAGTGGCGACGATGTCAGATGTCACATGACACACGCT 182
    :::::::::::::::::::::
596 Alaglyglyserglysergluser.....Asphisthrva 607
183 GGCACAGCTTGACATATGATGATGAACTCTGGAATGCCCTGGG 232
    | :::::::::::::::::::::
607 lProserglyserglyserThrglytrp.....Trrg 618
233 ACTATGAACTGGCTTGTCTGTAACAGACTCTTGAGAGAAGTCATGC 282
    :::::::::::::::::::::
618 lAtrg.....ProvalsergluserfarglyserSer... 629
283 ATTGTGCACAAATGAGAGAGGACGCTCCCTTCAGCCCTTA 332
    :::::::::::::::::::::
630 ...ProtrgsergluserAlaSerAlaValAlaProglglyleupProleuH 645
333 TGCCTGTGTCAGGAAAGAGAGGTTTCAGGGTAAAGGCCCGGACAC 382
    :::::::::::::::::::::
645 sProleuthrlysalatryAlaValAlaGlyglyProglglylProP 662
383 CTGCCAAGAGCCTGAGTACTGACTGATCAACCCCAACAGAGTCGACA 432
    | :::::::::::::::::::::
662 rovalAtrggluleuAla...AlaValProProglglyleuthrlyserArg 677
433 GACAGTTTGGAAATCCATCCTTGCGCATGTCACAG 468
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678 GluserPheglInlysalamegllyAsnProCysglu 689

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seq_name: SwissProt_40:DVL_RAT

seq_documentation_block:

ID DVL_RAT STANDARD: PRT: 695 AA.
 AC Q9WVB9; Q9WVB9;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Segment polarity protein disvelled homolog DVL-1 (Disvelled-1)
 DE (DSH homolog 1) (Fragments).
 GN DVL1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NX NCB1_TaxID=10116;
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=WISTAR K170T;
 RC de Lange R.P.J., Burr K., Clark J.S., Negri C.D., Brosnan M.J.,
 RA St Clair D.M., Shaw D.J., Dominiczak A.F.;
 RT "Does Disvelled-1 determine sensitivity to cerebral ischaemic insult
 in a rat model of stroke?";

RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MAY PLAY A ROLE IN THE SIGNAL TRANSDUCTION PATHWAY
 CC MEDIATED BY MULTIPLE WNT GENES.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- SIMILARITY: BELONGS TO THE DSH FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 DEP DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
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DR EMBL; AF143548; AAD41492.2; -.
DR EMBL; AF143547; AAD41492.2; JOINED.
DR EMBL; AF143550; AAD41493.1; -.
DR EMBL; AF143549; AAD41493.1; JOINED.
DR InterPro: IPR000591; DEP.
DR InterPro: IPR001158; DIX.
DR InterPro: IPR001478; PDZ.
DR Pfam; PF00778; DIX; 1.
DR Pfam; PF00610; DEP; 1.
DR ProDom; PD003639; DIX; 1.
DR SMART; SM00021; DAX; 1.
DR SMART; SM00049; DEP; 1.
DR PROSITE; PS50186; DEP; 1.
DR PROSITE; PS50106; PDZ; PARTIAL.
KW Developmental protein.
FT DOMAIN 251 323 PDZ.
FT DOMAIN 425 499 DEP.
SQ SEQUENCE 695 AA; 75684 MW; BDEA252BA1E87601 CRC64;

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alignment_scores:
 Quality: 87.00 Length: 112
 Ratio: 1.359 Gaps: 5
 Percent Similarity: 57.143 Percent Identity: 26.786

alignment_block:

US-09-821-726-17 x DVL_RAT ..

Align seg 1/1 to: DVL_RAT from: 1 to: 695

```

133 AGTGTGAAGTGGCGACGATGTCAGATGTCACATGACACACGCT 182
    :::::::::::::::::::::
596 Alaglyglyserglysergluser.....Asphisthrva 607
183 GGCACAGCTTGACATATGATGATGAACTCTGGAATGCCCTGGG 232
    | :::::::::::::::::::::
607 lProserglyserglyserThrglytrp.....Trrg 618
233 ACTATGAACTGGCTTGTCTGTAACAGACTCTTGAGAGAAGTCATGC 282
    :::::::::::::::::::::
618 lAtrg.....ProvalsergluserfarglyserSer... 629
283 ATTGTGCACAAATGAGAGAGGTTTCAGGGTAAAGGCCCGGACAC 332
    :::::::::::::::::::::
630 ...ProtrgsergluserAlaSerAlaValAlaProglglyleupProleuH 645
333 TGCCTGTGTCAGGAAAGAGAGGTTTCAGGGTAAAGGCCCGGACAC 382
    :::::::::::::::::::::
645 sProleuthrlysalatryAlaValAlaGlyglyProglglylProP 662
383 CTGCCAAGAGCCTGAGTACTGACTGATCAACCCCAACAGAGTCGACA 432
    | :::::::::::::::::::::
662 rovalAtrggluleuAla...AlaValProProglglyleuthrlyserArg 677
433 GACAGTTTGGAAATCCATCCTTGCGCATGTCACAG 468
    :::::::::::::::::::::
678 GluserPheglInlysalamegllyAsnProCysglu 689

```

seq_name: SwissProt_40:CTNB_URECA

```

seq_documentation_block:
ID CTNB_URECA STANDARD; PRT; 818 AA.
AC P35224;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Beta-catenin.
OS Urechis caupo (limpkeeper worm) (Spoonworm).
OC Eukaryota; Metazoa; Echinura; Xenopneusta; Urechidae; Urechis.
OX NCBI_TaxID=6431;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93305730; PubMed=8318544;
RA Rosenthal E.T.;
RT "Identification of homologues to beta-catenin/plakoglobin/armadillo
in two invertebrates, Urechis caupo and Trilipneustes gratilla."
RL Blochm. Biophys. Acta 1173:337-341(1993).
CC -1- FUNCTION: BINDS TO THE CYTOSOLIC DOMAIN OF THE CELL-CELL
ADHESION MOLECULE E-CADHERIN, AND PERHAPS TO OTHER (MEMBRANE)
PROTEINS. THE ASSOCIATION OF CATENINS TO CADHERINS PRODUCES A
COMPLEX WHICH IS LINKED TO THE ACTIN FILAMENT NETWORK, AND WHICH
SEEMS TO BE OF PRIMARY IMPORTANCE FOR CADHERINS CELL-ADHESION
PROPERTIES.
CC -1- SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
CC -1- SIMILARITY: CONTAINS 7 ARM REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch.)
CC -----
DR EMBL: L10355; AAA30330.1; -
DR HSSP: Q02248; 2BCT.
DR InterPro: IPR000225; Armadillo.
DR Pfam: PF00514; Armadillo_seg; 12.
DR SMART: SM00185; ARM; 11.
DR PROSITE: PS50176; ARM_REPEAT; 9.
KW Cell adhesion; Cytoskeleton; structural protein; Repeat.
FT REPEAT 164 203 ARM 1.
FT REPEAT 248 287 ARM 2.
FT REPEAT 412 451 ARM 3.
FT REPEAT 454 495 ARM 4.
FT REPEAT 501 541 ARM 5.
FT REPEAT 543 582 ARM 6.
FT REPEAT 648 687 ARM 7.
SQ SEQUENCE 818 AA; 89070 MW; 1DF174BEF745CID CRC64;

```

alignment_scores:

Quality: 83.50 Length: 123
 Ratio: 1.128 Gaps: 7
 Percent Similarity: 60.163 Percent Identity: 26.829

alignment_block:

US-09-821-726-17 x CTNB_URECA ..

Align seg 1/1 to: CTNB_URECA from: 1 to: 818

```

115 GTCAAGAGAGAGGCGC..AACAGTGTGGAGAGGAGGAGCAGCAGTGTAG 161
      ::::|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
47 MetGlyAspSerIleYtIleGlnSerGlyAlaThrThGlnAlaProProse 63
162 TGTCAACAATGAACACACAGCTGGCCACAGCTGACATTAACAATGATGTA 211
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
63 ValSerSerIleYtIleGlnSerGlyAlaThrThGlnAlaProProse 80
212 ACTCTGGAATGCCCTGTGGAGCTATAGAACTGGCTTTGCTGTACACAGA 261

```

seq_name: SwissProt_40:DPSD_CLOPA

```

seq_documentation_block:
ID DPSD_CLOPA STANDARD; PRT; 296 AA.
AC Q46192;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative phosphatidylserine decarboxylase (EC 4.1.1.65).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 6013;
RA Meyer J.;
RT Submitted (NOV-1993) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: phosphatidyl-L-serine =
phosphatidylethanolamine + CO(2).
CC -1- COFACTOR: Pyruvoyl group (by similarity).
CC -1- PATHWAY: AMINOPHOSPHOLIPID BIOSYNTHESIS.
CC -1- SIMILARITY: TO THE C-TERMINAL OF YEAST PSD2.
CC -----
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch.)
CC -----
DR EMBL: Z28353; CAA82212.1; -
DR InterPro: IPR003817; PS_Dcarboxylase.
DR Pfam: PF02666; PS_Dcarboxylase; 1.
KW Phospholipid biosynthesis; Lyase; Decarboxylase; Pyruvate; Zymogen.
FT SITE 255 256 CLEAVAGE (NONHYDROLYTIC)
FT MOD_RES 256 256 (BY SIMILARITY).
FT MOD_RES 256 256 CONVERTED TO A PYRUVOL GROUP
SQ SEQUENCE 296 AA; 34243 MW; A131FA6D2FB0472A CRC64;

```

alignment_scores:

Quality: 83.00 Length: 132
 Ratio: 1.297 Gaps: 6
 Percent Similarity: 48.485 Percent Identity: 27.273

alignment_block:

US-09-821-726-17 x DPSD_CLOPA ..

```

554 LeuAlaLeuAlaIleGlnGlyArgSpleLysLeuSerAsnAspLys 570
511 .....CTGATTTCGACTCAGAAAGGATCGACGCAATATAC 550
570 sLeuLeuGlnValArgAsnPherThrAsnLysIleTyrAsnAlaLysAsn 587
551 TCTGATTCTTACATTTC 570
587 yLeuLeuAsnGlnLys 593

```

seq_name: SwissProt_40:CH12_COCIM

seq_documentation_block:

```

ID CH12_COCIM STANDARD; PRT; 860 AA.
AC P54197;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Endochitinase 2 precursor (EC 3.2.1.14).
GN CTS2.
OS Coccidioides immitis.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Orygenales; Mitosporic Orygenales; Coccidioides.
OX NCBI_TaxID=5501;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C735;
RX MEDLINE=96144270; PubMed=8566773;
RA Pishko E.J., Kirkland T.N., Cole G.T.;
RT "Isolation and characterization of two chitinase-encoding genes
RT (cts1, cts2) from the fungus Coccidioides immitis.";
RL Gene 167:173-177(1995).
CC -!- FUNCTION: MAY BE ASSOCIATED WITH ENDOSPORULATION.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-
CC acetyl-D-glucosamine polymers of chitin.
CC SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
CC HYDROLASES).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: LA1662; AAA92642.1; -.
DR HSSP: P23472; 2HW.
DR InterPro: IPR001579; Chitinase_2.
DR Pfam: PF00192; chitinase_2; 1.
DR PROSITE: PS01095; CHITINASE_18; 1.
KW Hydrolyase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
KW Glycoprotein.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 860 ENDOCHITINASE 2.
FT CARBOHYD 90 90 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 860 AA; 91395 MW; 5E34B54FAA663F3C CRC64;

```

alignment_scores:

```

Quality: 78.50 Length: 149
Ratio: 1.006 Gaps: 7
Percent Similarity: 52.349 Percent Identity: 30.872

```

alignment_block:

US-09-821-726-17 x CH12_COCIM

Align seg 1/1 to: CH12_COCIM from: 1 to: 860

```

116 TCACAGCAGCAGCAGCAGTGTGTAAGTGGCAGCAGTCACTAGTGC 165
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
347 SerThrValThrSerThrThrSerAlaSerThrSerThrGln...ThrSe 362

```

```

166 AACATGAAACACAAAGTGCCACGCTTGACATTAACATGCATGCAATC 215
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
362 rSerGlnSerThrThrMetGluThrLysThrLeuSerAlaSerThr 379
216 CTGGAATGCCCTCTGGACTATAGAACCTGGCTTGCTGTATACCACTCT 265
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
379 rOserSerProSer...ThrValSerProSerSerThrMetGlnThrThr 394
266 TCGAAGAAGAAGTCAATGATGTCACCAAAATGAAAGAACCCATGCC 315
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
395 SerThrGlySerThrSerIleGluThrValThrThrArgSerGlnGluPr 411
316 TCCCTTCAAGCCCTTGATGCCGTGTCAAGAAAGAACCTTACGGCTAA 365
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
411 oProSerThrThrIle.....SerThrArgSerAlaSerThrGlu 424
366 GGGCCAGGGGAGCACCCTCCAGACGCTGA.....GGTAC 402
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
424 Lu.ProValThrThrArgSerGlnGluProProSerThrThrIleSerTh 440
403 TCAGTCAACCCCAACAGAGTGCACACCTGGACAAAGTTGGAAATTCAT 452
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
440 rArgSerAlaSerThrGluThrValThrThrArgSerGlnGluProPro 457
453 CGTGCATWGTCAAGGGGATTCACATACATAGCGCTGAAGATTCAG 502
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
457 eThrThrThrIleSer.....ThrThrSerAlaSerThrGlu 468
503 GAGCAACCTGATTTCGTACTCAGAAAGATGCATGACGTCATTA 547
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
469 ThrSerThr.....SerSerGlnAspSerProSerThrThrIle 481

```

seq_name: SwissProt_40:VWF_CANFA

seq_documentation_block:

```

ID VWF_CANFA STANDARD; PRT; 2813 AA.
AC Q28295; Q28311; Q9T814;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Von Willebrand factor precursor (VWF).
GN F8VWF OR VWF.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Stoy S.J., Shibuya H., Nonneman D.J., Holzhauser J., Mohammed I.H.,
RA Johnson G.S.;
RA Submitted (Aug-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Montgomery R.R., Fahs S., Montgomery M.W.;
RA Submitted (Aug-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Venta P.J., Li J., Yuzbasiyan-Gurkan V., Brewer G.J., Schall W.D.;
RA "Complete sequence of the structural gene for canine von Willebrand
RA factor and identification of a mutation causing Scottish terrier von
RA Willebrand's disease.";
RA Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1234-1669 FROM N.A.
RA TISSUE=Blood;
RA Mancuso D.J., Christopherson P.A., Kroner P.A., Montgomery R.R.;
RA "The canine von Willebrand factor gene: sequence and expression of
RA a region encoding the glycoprotein Ib/IX binding domain.";
RA Submitted (Jan-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: IMPORTANT IN THE MAINTENANCE OF HOMEOSTASIS, IT
CC PARTICIPATES IN PLATELET-VESSEL WALL INTERACTIONS BY FORMING A
CC NONCOVALENT COMPLEX WITH COAGULATION FACTOR VIII AT THE SITE OF

```



```

seq_documentation_block:
ID          SYV_CAMJF          STANDARD:          PRT:          870 AA.
AC          Q9PEP4:
DT          16-OCT-2001 (Rel. 40) Created)
DT          16-OCT-2001 (Rel. 40) Last sequence update)
DT          16-OCT-2001 (Rel. 40) Last annotation update)
DE          Vallyl-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA ligase) (ValRS).
GN          VALS OR C10725
OS          Campylobacter jejuni.
OC          Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC          Campylobacter.
OX          NCBI_TaxID=197;
RN          [1]
RP          SEQUENCE FROM N.A.
RC          STRAIN=NCCTC 11168;
RX          MEDLINE=20150912; Pubmed=10688204;
RA          Parkhill J., Wren B.W., Mungall K., Kelley J.M., Churcher C.,
RA          Basham D., Chillingworth T., Davies R.M., Feltham T., Holtroyd S.,
RA          Jagers K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA          Quail M.A., Rastread M.A., Rutherford K.M., van Vliet A.H.M.,
RA          Whitehead S., Barrall B.G.;
RT          "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT          reveals hypervariable sequences."
RL          Nature 403:665-668(2000).
CC          -I- CATALYTIC ACTIVITY: ATP + L-Valine + tRNA(Val) = AMP + diphosphate
CC          + L-Valyl-tRNA(Val).
CC          -I- SUBUNIT: MONOMER (BY SIMILARITY).
CC          -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC          -I- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-tRNA SYNTHETASE FAMILY.
CC          -----
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CC          use by non-profit institutions as long as its content is in no way
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112 AGTGTCAACGACGACGCG.....CAACAGTGG 13
430 yscysglnserGlnasnphelysglnaspluasvalleuasprhtrp 444
138 TGGAAG.....TGGCGACAGCTAGTACGTCTCAACANTGAACCA 17
447 PheSerSerIleuTrpAla.MetSerThrIeu..... 45
179 ACGTGGCCAACTGTGCATAATAACAATGATGAGCACTCTCGAAT..... 22
458GCTCTGGGACTATAGA.....GlytrpGlyasnGluAsntrpGly 46
223GCCCTGGGACTATAGA..... 24
466 LysAspIlyIleTrpSerGluIulysAspleuLysAspPheIyrProasne 48
241ACTGGCTTGGT.....GIACCAGACTCT 26
482 rleuLeuIlehrhIlyPheasplleleuPhehrtrpAlaIalargmetm 49
266 TCGAAGAAGATCATGCTATTGTGCACAAATGAGAAGAAGACCATCC 31
499 etPheGlnserThrAsnValleuIleuIleGlnleuProPheIysAsple... 51
316 TCCTTCAAGCCCTGATGGCGTGGTCAAGAAAGAAGACCTTCAGGGTAA 36
515TyrIleuHISAlaLeuValLysAspIuGln..... 52
366 GGGCCCAAGGGGGACCACTCCCAAGAGCCCTAGGTACTCAGTCAACCCCA 41
525GlyArgIlyMetSerIysSerIeuGlyAsnValIleasproa 53
416 ACAGAGTCGACCAACCTGAGCAAGATTGTGGAAATTCATCGTCCATGTGC 46
539 sn.....GlnserIleIyGlnIutrySerIalAspIleleuArgPheThr 55
466 AAGGGATTCCAACATTCATGAGCTGGAAGAAGATTCGAAGACCAAC..... 51

CC	VASCULAR INJURY (BY SIMILARITY).	
CC	-1- SUBUNIT: MULTIMERIC (BY SIMILARITY).	
CC	-1- TISSUE SPECIFICITY: BLOOD.	
CC	-1- PTM: ALL CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN OR	
CC	INTERCHAIN DISULFIDE BONDS (BY SIMILARITY).	
CC	-1- SIMILARITY: CONTAINS 3 WMFA DOMAINS.	
CC	-1- SIMILARITY: CONTAINS 3 WMFC DOMAINS.	
CC	-1- SIMILARITY: CONTAINS 4 WMFD DOMAINS.	
CC	-1- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).	
CC	-1- SIMILARITY: SOME, TO SILKFORM HEMOCYTIN.	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation	
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CC	use by non-profit institutions as long as its content is in no way	
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CC	entities requires a license agreement (See http://www.isb.ch/announce/	
CC	or send an email to license@isb-sib.ch).	
CC	-----	
DR	EMBL: I76227; AAB0549.1; -.	
DR	EMBL: I16903; AAA30903.1; -.	
DR	EMBL: AF099154; AAD04919.1; -.	
DR	EMBL: U66246; AAB93766.1; -.	
DR	HSSP: P04275; IAU0.	
DR	InterPro: IPR000359; Cys_knot.	
DR	InterPro: IPR000004; SADB.	
DR	InterPro: IPR002919; TIL.	
DR	InterPro: IPR001007; WMFC.	
DR	InterPro: IPR001846; WVD.	
DR	InterPro: IPR002035; WMFA.	
DR	Pfam: PF00007; Cys_Knot; 1.	
DR	Pfam: PF01826; TIL; 4.	
DR	Pfam: PF00092; Wva; 3.	
DR	Pfam: PF00093; Wvc; 3.	
DR	Pfam: PF00094; Wvd; 4.	
DR	PRINTS: PR00453; WMFADOMAIN.	
DR	SMART: SM00041; CT; 1.	
DR	SMART: SM00327; WVA; 3.	
DR	SMART: SM00214; WVC; 5.	
DR	SMART: SM00216; WVD; 4.	
DR	PROSITE: PS01185; CTCK_1; 1.	
DR	PROSITE: PS01225; CTCK_2; 1.	
DR	PROSITE: PS01234; WMFA; 3.	
DR	PROSITE: PS01208; WMFC; 3.	
KW	Blood coagulation; Platelet; Glycoprotein; Extracellular matrix;	
KW	Plasma; Hemostasis; Repeat; Cell adhesion; Signal.	
KW	SIGNAL	1 22
FT	PROPEP	23 763
FT	CHAIN	764 2813
FT	DOMAIN	35 179
FT	DOMAIN	388 541
FT	DOMAIN	764 787
FT	DOMAIN	788 833
FT	DOMAIN	826 853
FT	DOMAIN	867 1013
FT	DOMAIN	1277 1453
FT	DOMAIN	1498 1665
FT	DOMAIN	1691 1871
FT	DOMAIN	1950 2102
FT	DOMAIN	2216 2261
FT	DOMAIN	2255 2326
FT	DOMAIN	2429 2495
FT	DOMAIN	2580 2650
FT	DOMAIN	2724 2812
FT	SITE	531 533
FT	SITE	698 700
FT	SITE	2507 2509
FT	DISULFID	767 808
FT	DISULFID	776 804
FT	DISULFID	810 821
FT	DISULFID	867 996
FT	DISULFID	889 1031
FT	DISULFID	898 993

FT	DISULEFID	914	921	BY SIMILARITY.
FT	DISULEFID	1060	1084	BY SIMILARITY.
FT	DISULEFID	1071	1111	BY SIMILARITY.
FT	DISULEFID	1089	1091	BY SIMILARITY.
FT	DISULEFID	1153	1165	BY SIMILARITY.
FT	DISULEFID	1149	1169	BY SIMILARITY.
FT	DISULEFID	1126	1130	BY SIMILARITY.
FT	DISULEFID	1196	1199	BY SIMILARITY.
FT	DISULEFID	1234	1237	BY SIMILARITY.
FT	DISULEFID	1272	1458	BY SIMILARITY.
FT	DISULEFID	1669	1670	BY SIMILARITY.
FT	DISULEFID	1686	1872	BY SIMILARITY.
FT	DISULEFID	1879	1904	BY SIMILARITY.
FT	DISULEFID	1899	1940	OR 1942 (BY SIMILARITY).
FT	DISULEFID	1972	2123	BY SIMILARITY.
FT	DISULEFID	1950	2085	BY SIMILARITY.
FT	DISULEFID	1927	2088	BY SIMILARITY.
FT	DISULEFID	1993	2001	BY SIMILARITY.
FT	DISULEFID	2774	2774	BY SIMILARITY.
FT	DISULEFID	2739	2788	BY SIMILARITY.
FT	DISULEFID	2750	2804	BY SIMILARITY.
FT	DISULEFID	2754	2806	BY SIMILARITY.
FT	DISULEFID	?	2811	BY SIMILARITY.
FT	CARBOHYD	99	99	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	156	156	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	211	211	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	666	666	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	857	857	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	1231	1231	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	1515	1515	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	1574	1574	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	2223	2223	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	2290	2290	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	2357	2357	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	2400	2400	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	2546	2546	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	2585	2585	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	2790	2790	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CONFLICT	70	70	G -> E (IN REF. 2).
FT	CONFLICT	55	55	V -> I (IN REF. 3).
FT	CONFLICT	266	266	A -> G (IN REF. 2).
FT	CONFLICT	280	280	I -> V (IN REF. 2).
FT	CONFLICT	409	411	VCH -> ICG (IN REF. 2).
FT	CONFLICT	994	994	G -> A (IN REF. 1).
FT	CONFLICT	1021	1021	F -> L (IN REF. 2).
FT	CONFLICT	2381	2381	L -> P (IN REF. 2).
FT	CONFLICT	2406	2406	P -> L (IN REF. 2).
SO	SEQUENCE	2813	AA: 309716 MW: 50F93E15E72F80C CRC64;	

alignment_scores:		
Quality:	78.50	Length: 195
Ratio:	0.957	Gaps: 11
Percent Similarity:	42.051	Percent Identity: 24.103

```
alignment_block:
```

US-09-821-726-17/rev x VWF_CANFA .

Align seg 1/1 to: VWF_CANFA from: 1 to: 2813

```

484 TGTATGTTGGAATCCCCCTGGACA...TGGCAACGATGATTTTC... 443
||| ::::: |||::: |||::: |||
2184 CysAqGThrlvSGlWVA]CvsVa]AsnTlraVraVra]aAenbocvva] 3300

```

```

742 .CGGGGAGGCA.....GGTGT. 425
      :::::|||||      |||||
2200 ametSerCysProProSerLeuValTyrAsnHisCysGluHisGlyCysP 2217

```

424 ..CGACTCTGTTGGGGTTGACTGAGTACCTCAGGCTCTTGGGAGGTGTC 377
 ||||| ||| |||:: |||::
 2217 TGTATGTCGAGG|G|VASTTbTbSArSArCueG|uVAcG|bTb 3331

376 CCGCTGGGCCCTTACCGCTGAAGCTTCTTTCCCTTGACCAAGCGCATCAAG 327

[illegible]

RA Borkova D., Blocker H., Sharfe M., Grimm M., Loehnert T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fairman B., Granderath R., Dauner D., Herzl A.,
RA Meunier O., Argitrou A., Vitale D., Liguori R., Piravandi E.,
RA Massenet O., Ougley F., Clabaud G., Muendlein A., Felber K.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chetoui F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Bagues M., Terol J., Torres A.,
RA Perez-Perez J., Purnelle R., Bent E., Johnson S., Racou D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Frances P., Bielke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj L., Schütz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Shest P., Cordes M., Abut-Friedel J.,
RA Stomering T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Krimer J., Platten L., Mardis E., Dante M., Pezin K., Hillier L.,
RA Nelson J., Speith J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
RA Antonolu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Granaat S., Shodja N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Marra M., Martienssen R., McCombie W.R.,
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana".
RT Nature 402:769-777(1999).
RN [2]
RN SEQUENCE OF 83-112, AND SUBCELLULAR LOCATION.
RP STRAIN-CV. COLUMBIA.
RC MEDLINE:20487156; PubMed:11034343;
RX Kieselbach T., Bystedt M., Hynds P., Robinson C., Schroeder W.P.,
RT "A peroxidase homologue and novel plastocyanin located by proteomics
RT to the Arabidopsis chloroplast thylakoid lumen."
RL FEBS Lett. 480:271-276(2000).
CC -I- FUNCTION: PLAYS A KEY ROLE IN HYDROGEN PEROXIDE REMOVAL IN
CC THE CHLOROPLASTS AND CYTOSOL OF HIGHER PLANTS.
CC -I- CATALYTIC ACTIVITY: L-ascorbate + H(2)O(2) -> dehydroascorbate + 2
CC H(2)O.
CC -I- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
CC -I- SIMILARITY: TO ASCORBATE PEROXIDASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AL161513; CAB78025.1; -
DR InterPro: IPR002016; Peroxidase.
DR PRINTS: PR00456; PEROXIDASE.
KW Oxidoreductase; Peroxidase; Hydrogen peroxide; Chloroplast;
KW Transit peptide; Thylakoid.
FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
FT TRANSIT 2 82 THYLAKOID.
FT CHAIN 83 349 POTATIVE L-ASCORBATE PEROXIDASE.
SQ SEQUENCE 349 AA: 37934 MW: AB0439188BDA861 CRC64;

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alignment_scores:      114  
    quality:          78.00  
    ratio:            1.345  
Percent Similarity:   50.877  
Percent Identity:     27.193
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alignment_block:
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Align seg 1/1 to: TL29_ARATH from: 1 to: 349

292 AAAATGAGAGGAGGAGCCATGCCCTCCCTTCAAGCCCTT...GA 332

5


```

107 LysalalysProgluLeuValProSerLeuLeuLysLeuAlaLeuAsnAs 123
333 TGCCCTGTCAGCAAGAAAGACTTCAGGGTAAAGGCCAGGGGACCAC 362
123 palamethrThrTyrAspLysAlaThrLysSerGlyGlyAlaAsnGly 138
383 CTCCCAAGACCTGAGTACTCACTCAACCCCAACAGAGTCGCAAC 429
139 SerIleArgPheSerSerLeuLeuSerArgAlaGluAsnGlu 152
430 CTGCACACTTTGGAAATTCATCGT 455
153 GlyLeuSerAspGlyLeuSerLeuIleGluValLysLysGluLeuAs 169
456 TGCCATGTCGACAGGAGGATTCACATCATGCTGCAAGAGATCA 501
169 pSerIleSerLysGlyLysProLysSerTyrAlaAspIleLeuLeu 186
502 GGAGCAACCTGATTCCTCACTCAAGAAAGTCATCATGCAATATA 549
186 IacGlyGlnSerAlaValLysPheThrTyrLeuAlaSerAla 199
550 CTCTGCAATTCCTTAACTTCCTCTGCGAGCAATACCGGAG 591
200 IleArgLysCysGlyGlyAsnGluGlu 208
seq_name: SwissProt_40:XYNA_RUMFL

```

```

seq_documentation_block:
ID XYNA_RUMFL STANDARD: PRT: 954 AA.
AC P29126:
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Bifunctional endo-1,4-beta-xylanase XYLA precursor (EC 3.2.1.8).
GN XYNA.
OS Ruminooccus flavefaciens.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Ruminooccus.
OX NCBI_TaxID=1265;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17.
RA MEDLINE=92261318; PubMed=1584021;
RA Zhang J.-X., Flint H.J.;
RA "A bifunctional xylanase encoded by the xyna gene of the rumen
RA cellulolytic bacterium Ruminooccus flavefaciens 17 comprises two
RA dissimilar domains linked by an asparagine/glutamine-rich sequence."
RA Mol. Microbiol. 6:1013-1023(1992).
CC -1- FUNCTION: XYLANASE DOMAIN 1 RELEASES MORE XYLO-OLIGOSACCHARIDES
CC AND DOMAIN 2 MORE XYLOSE.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xyans.
CC -1- PATHWAY: XYLAN DEGRADATION.
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO CELLULASE FAMILY
CC G (FAMILY 11 OF GLYCOSYL HYDROLASES).
CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO CELLULASE FAMILY
CC F (FAMILY 10 OF GLYCOSYL HYDROLASES).
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Z11127; CA77476.1; -
DR PIR: S18043; S18043.
DR PIR: S20907; S20907.
DR HSSP: P48793; 1XND.
DR InterPro: IPR001000; Glyco_hydro_10.

```

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DR InterPro: IPR001137; Glyco_hydro_11.
DR Pfam: PF00331; Glyco_hydro_10; 1.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00134; GLHYDRLASE11.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00591; GLYCOSYL_HYDROL_F10; 1.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F12; 1.
DR Xylan degradation; Hydrolyase; Multifunctional enzyme;
KW Repeat; Signal.
FT SIGNAL 1 27 OR 28, OR 29 (POTENTIAL).
FT CHAIN 28 954 BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYLA.
FT DOMAIN 28 244 XYLANASE DOMAIN 1.
FT DOMAIN 245 622 ASN/GLN/TRP-RICH (LINKER).
FT DOMAIN 623 954 XYLANASE DOMAIN 2.
FT ACT_SITE 122 122 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 223 223 PROTON DONOR (BY SIMILARITY).
FT ACT_SITE 774 774 PROTON DONOR (BY SIMILARITY).
FT ACT_SITE 884 884 NUCLEOPHILE (BY SIMILARITY).
SO SEQUENCE 954 AA; 111362 MW; 1033567D4526BBD CRC64;

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alignment_scores:
Quality: 77.00 Length: 46
Ratio: 2.406 Gaps: 2
Percent Similarity: 69.565 Percent Identity: 39.130

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alignment_block:
US-09-821-726-17 x XYNA_RUMFL
Align seg 1/1 to: XYNA_RUMFL from: 1 to: 954

```

```

106 AGTATCATGTCTCAACAGTACGACGACGACGCTGTGAGTGGCAGCAGT 155
235 SerValSerValThrGlnGlyLysSerSerAspAsnGlyGlnGlnGln 251
156 AGTCACTGTCAACATGACACACAGTGGCCAGTGTGACATTAACATG 205
251 nAsnAsnSprTrpAsnGlnGlnAsn...AsnAsnGlnGlnGlnAsnAsn 267
206 GATGCACTCTGTG.....AATGCCCTCTGGGAC 234
267 sPTrpAsnAsnTrpGlyGlnGlnAsnAsnAspTrpAsn 279

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seq_name: SwissProt_40:Z335_HUMAN
seq_documentation_block:
ID Z335_HUMAN STANDARD: PRT: 1342 AA.
AC Q9H422; Q9H684;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Zinc finger protein 335.
GN ZNF335.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagdley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
RA Coulson A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Ellington A.G., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

```

RA Levaslaho M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McElay K., McMurtry A.A.,
 RA Milne S., Misty D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 [2]
 RP SEQUENCE OF 455-1342 FROM N.A.
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Oktani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
 RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
 RT "NDO human cDNA sequencing project.";
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MAY FUNCTION AS A TRANSCRIPTION FACTOR.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC
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 CC
 DR EMBL; AL162458; CAC10457.1; -
 DR EMBL; AK026157; BAB15379.1; A1T-INT1.
 DR InterPro; IPR000822; Znf-C2H2.
 DR Pfam; PF00096; Zf-C2H2; 13.
 DR SMART; SM00355; Znf-C2H2; 13.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 6.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 13.
 DR Transcription regulation; Zinc-finger; Metal-binding; Nuclear protein;
 KW DNA-binding; Repeat.
 FT FT 245 268 C2H2-TYPE.
 FT ZN_FING 465 487 C2H2-TYPE.
 FT ZN_FING 495 517 C2H2-TYPE.
 FT ZN_FING 523 545 C2H2-TYPE.
 FT ZN_FING 562 584 C2H2-TYPE.
 FT ZN_FING 590 612 C2H2-TYPE.
 FT ZN_FING 621 643 C2H2-TYPE.
 FT ZN_FING 649 672 C2H2-TYPE.
 FT ZN_FING 678 701 C2H2-TYPE.
 FT ZN_FING 1019 1041 C2H2-TYPE.
 FT ZN_FING 1047 1069 C2H2-TYPE.
 FT ZN_FING 1075 1097 C2H2-TYPE.
 FT ZN_FING 1103 1126 C2H2-TYPE.
 FT DOMAIN 1178 1330 GLN-RICH.
 SQ SEQUENCE 1342 AA; 144892 MW; 6D230DE0B3AE70 CRC64;

alignment_scores: Quality: 77.00 Length: 43
 Ratio: 2.750 Gaps: 1
 Percent Similarity: 65.116 Percent Identity: 44.186

alignment_block:
 US-09-821-726-17 x 2335_HUMAN ..
 Align seg 1/1 to: 2335_HUMAN from: 1 to: 1342

340 GTCAGAGAAAGAGTTGAGGTAAGCCGAGGGGAGCCACCTCCCA 389
 ::::||||| ||| ||| :::: ||||| |||||
 729 TlglulduleuysglnghlnhsseAlaAlaProglyproproprose 745
 390 GAGCTGAGGTACTCACTCAACCCCAACAGAGTGCACACCTTGACAAGT 439

seq_name: SwissProt_40:MTSL_RHIME
 seq_documentation_block:
 ID MTSL_RHIME STANDARD: PRT: 376 AA.
 AC 030569;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Modification methylase SmeIP (EC 2.1.1.72) (Adenine-specific
 DE methyltransferase SmeIP) (M.SmeIP) (M.CcmII).
 GN SmeIM OR CCRM OR R00926 OR SMC00021.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=97440139; PubMed=9294447;
 RA Wright R., Stephens C., Shapiro L.;
 RT "The CCRM DNA methyltransferase is widespread in the alpha subdivision
 RT of proteobacteria, and its essential functions are conserved in
 RT Rhizobium meliloti and Caulobacter crescentus.";
 RL J. Bacteriol. 179:5869-5877(1997).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21396507; PubMed=11481430;
 RA Capella D., Barclay-Hubler F., Gonzy J., Bothe G., Ampe F., Patut J.,
 RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
 RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
 RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
 RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;
 RT "Analysis of the chromosome sequence of the legume symbiont
 RT Sinorhizobium meliloti strain 1021.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
 CC -1- FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDED SEQUENCE
 CC GATTC AND CAUSES SPECIFIC METHYLATION ON A-2 ON BOTH STRANDS.
 CC CCRM-MEDIATED METHYLATION HAS IMPORTANT CELLULAR FUNCTIONS.
 CC APPEARS TO CONTRIBUTE TO THE ACCURATE CELL-CYCLE CONTROL OF DNA
 CC REPLICATION AND CELLULAR MORPHOLOGY.
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA adenine = S-
 CC adenosyl-L-homocysteine + DNA 6-methylaminopurine.
 CC
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 CC
 DR EMBL; AF011894; AAB71350.1; -
 DR EMBL; AL591785; CAC45498.1; -
 DR REBASE; 3264; M.SmeIP.
 DR InterPro; IPR002295; D21N6_mtfase.
 DR InterPro; IPR001091; N4_Mtase.
 DR InterPro; IPR002052; N6_Mtase.
 DR InterPro; IPR002941; N6_N4_Mtase.
 DR InterPro; IPR000051; SAM_bind.
 DR Pfam; PF01555; N6_N4_Mtase; 1.
 DR PRINTS; PR00506; D21N6MTRASE.
 DR PRINTS; PR00508; S21N4MTRASE.
 DR PROSITE; PS00092; N6_MTASE; 1.
 KW Transferase; Methyltransferase; DNA replication; Complete proteome.
 FT CONFLICT 135 141 NPMENK -> GPDAELQ (IN REF. 1).

FT CONFLICT 157 157 P -> A (IN REF. 1).
SQ SEQUENCE 376 AA: 41442 MW: 790DE7FE3D22900A CRC64;

alignment_scores:

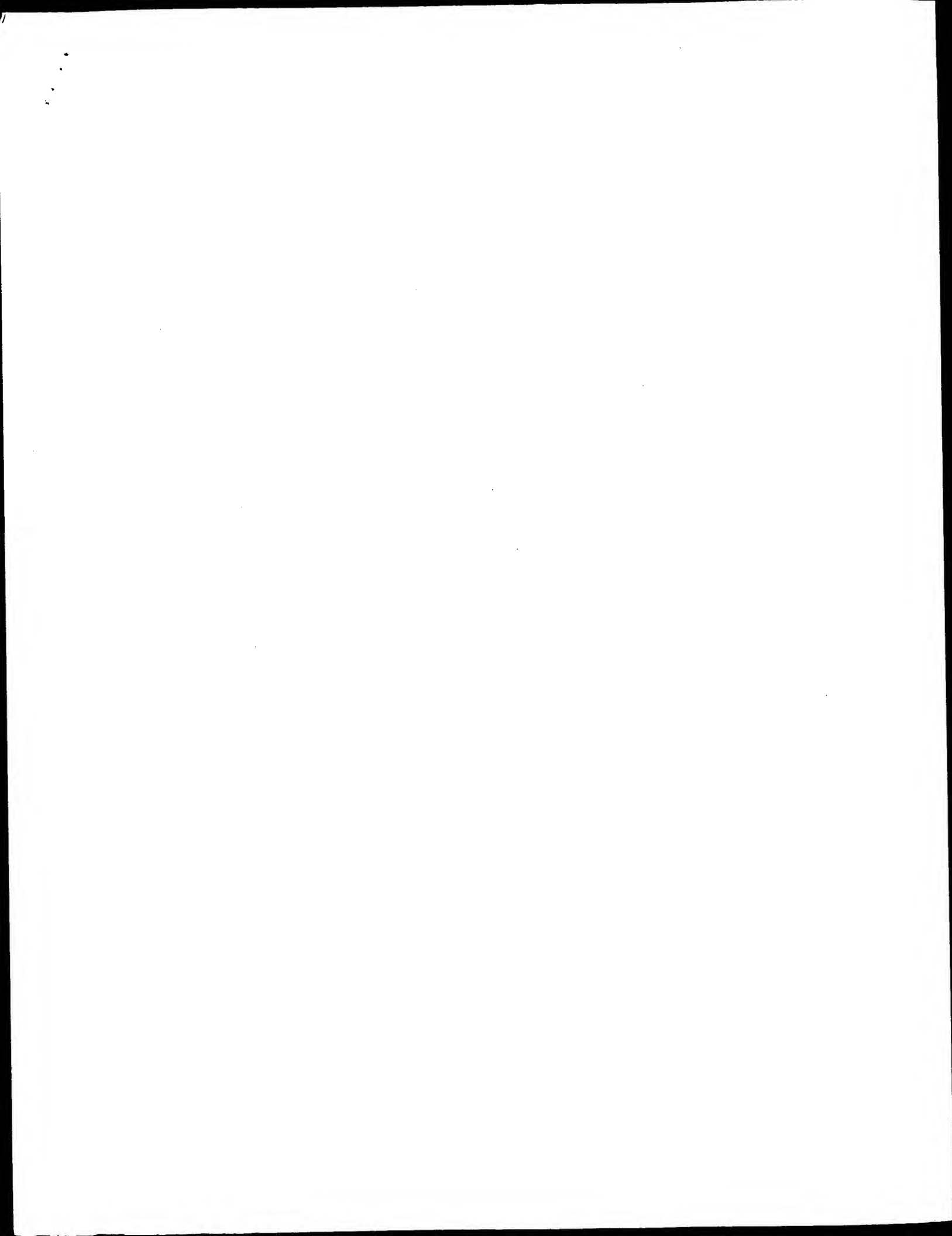
Quality: 76.50 Length: 94
Ratio: 1.417 Gaps: 3
Percent Similarity: 57.447 Percent Identity: 27.660

alignment_block:

US-09-821-726-17 x MTS1_RHIME

Align seg 1/1 to: MTS1_RHIME from: 1 to: 376

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31 GAAGCCAGATGAAGTTC...ACAATTGCCCTTGCTGCACTTCTT..... 72
   ||| : : : : ||| ||| : : : : : : : : : : : : : : : : : :
285 GLUPROArgValAlaIapheasnThrLeuValGIuserGIyleuIleIysPr 301
   ||| : : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
73 .GGTGTCTTCTGACTCTGCCCTTCTGCTACTATAGTATCACTGTCACG 121
   ||| : : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
301 ogIytrIhValIleuthrAspAlaIySarGArGtYrSerAlaIleValArgA 318
   ||| : : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
122 ACGACGGCAACAGTGGTGGAGCTGGCGACAGCTCAGTGAAGTGTCAACAAT 171
   ||| : : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
318 laSpGIyThrIleuAlaSerGIyGIuAlaGIySerIleHisArGIleu 334
   ||| : : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
172 GAACACACAGCTGGCCACAGCTTGACATAACAATGATGGAATCCTCGGA 221
   ||| : : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
335 GIyAlaIySValGIInclYleuAspAlaCySaSnGIyTrP..... 347
   ||| : : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
222 TCCCTCTGTGGACTATAGAACTGGCTTGCTGTATACCACTCTTCGAGA 271
   ||| : : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
348 .ThretrIphIsPheGIuGIuGIySerValIleuIysProIleAspGIuL 364
   ||| : : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
272 AGAAGTCATGCAATTGTGCACAAATGAAGAAG 303
   ||| : : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
364 euArgSerValIleArgAsnAspLeuAlaIyS 374
```



OM of: US-09-821-726-17 to: SPTREMBL_19:* out_format: pfs

Date: Sep 4, 2002 5:15 PM

About: Results were produced by the Gencore software, version 4.5,
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Command line parameters:

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-MODEL=frame+np_model -DEV=xlp
-O=/c9n2_1/USPRO.spool/US09821726/runat_04092002_163855_17608/app_query.fasta_1.664
-DB=SPTREMBL_19 -OFMT=fasta -SUFFIX=tspe -GAPOP=12.000
-GAPEXT=4.000 -MISMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-OGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-RGAPOP=6.000 -RGAPEXT=7.000 -YGAPO=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -STAR=1 -MATRIX=blsnum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTPR=plis
-NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09821726_@CGN1_1_265 -NGPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPHY -WAIT -THREADS=1
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Search information block:

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Query: US-09-821-726-17
Query length: 597
Database: SPTREMBL_19:*
Database sequences: 562222
Database length: 172994929
Search time (sec): 82.480000
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Score list:

Sequence	Strd Orig	ZScore	Escore	Len	Documentation
SP_rodent:Q9D077	+	252.50	476.77	176-18	191 Q9D077 mus musculus (mouse). 11
SP_rodent:Q9C056	+	217.00	408.26	126-14	184 Q9C056 mus musculus (mouse). 18
SP_rodent:Q9M078	+	97.50	165.16	0.1303	574 Q9M078 candida albicans (yeast)
SP_mammal:Q9XSV8	+	90.50	141.22	0.9847	1637 Q9XSV8 bos taurus (bovine). 57
SP_invertebrate:Q76810	+	90.00	155.87	0.7506	373 Q76810 anopheles gambiae (afr)
SP_invertebrate:Q9NL38	+	89.50	149.74	0.9514	568 Q9NL38 pinctada maxima. n66 m
SP_bacteria:Q9S253	+	89.00	156.27	0.8794	266 Q9S253 streptomyces coelicolor
SP_invertebrate:Q9VSD9	+	87.50	143.79	1.65	700 Q9VSD9 drosophila melanogaster
SP_organelle:Q9TJ56	+	87.00	149.73	1.55	348 Q9TJ56 leptotrichia munitus. nad
SP_bacteria:Q9R4U7	+	87.00	149.15	1.58	369 Q9R4U7 streptomyces coelicolor
SP_rodent:Q9U0G5	+	87.00	142.81	1.87	695 Q9U0G5 rattus norvegicus (rat)
SP_invertebrate:Q94477	+	86.00	149.76	1.89	285 Q94477 dictyostelium discoide
SP_bacteria:Q669974	+	84.50	143.28	3.02	1297 Q669974 streptomyces coelicolor
SP_invertebrate:Q952B0	+	84.50	131.88	4.12	1328 Q952B0 leishmania major. pos
SP_invertebrate:Q9N654	+	84.50	124.32	5.05	2786 Q9N654 leishmania major. pos
SP_bacteria:Q92R58	+	83.50	149.13	3.14	186 Q92R58 caenorhabditis elegans
SP_invertebrate:Q17169	+	83.00	135.92	4.96	642 Q17169 caenorhabditis elegans
SP_invertebrate:Q09519	+	83.00	130.00	5.82	1168 Q09519 caenorhabditis elegans
SP_bacteria:Q9J712	+	82.50	131.75	6.12	410 Q9J712 neisseria meningitidis
SP_invertebrate:Q9W1W2	+	81.50	137.44	6.38	425 Q9W1W2 drosophila melanogaster
SP_bacteria:Q9LAD3	+	81.50	137.08	6.44	441 Q9LAD3 clostridium cellulosum
SP_plant:Q02056	+	81.50	136.72	6.51	707 Q02056 hordeum vulgare (barley)
SP_plant:Q04054	+	81.50	132.05	7.39	989 Q04054 hordeum vulgare (barley)
SP_rodent:Q9W1W9	+	81.50	128.74	8.08	2304 Q9W1W9 mus musculus (mouse). ar
SP_invertebrate:Q9M548	+	81.50	120.38	10.13	2422 Q9M548 drosophila melanogaster
SP_invertebrate:Q46083	+	81.50	119.88	10.27	227 Q46083 drosophila melanogaster
SP_plant:Q93572	+	81.00	142.31	6.17	280 Q93572 solanum tuberosum (potat)
SP_plant:Q94G55	+	81.00	140.24	6.53	326 Q94G55 oryza sativa (rice). hyf
SP_plant:Q9SXY8	+	81.00	138.44	6.85	336 Q9SXY8 oryza sativa (rice). bet
SP_plant:Q9SXY7	+	81.00	138.38	6.86	810 Q9SXY7 oryza sativa (rice). bet
SP_fungi:Q03388	+	81.00	129.74	8.67	1338 Q03388 saccharomyces cerevisiae
SP_invertebrate:Q23927	+	81.00	124.78	9.92	263 Q23927 dictyostelium discoide
SP_plant:Q48991	+	80.50	139.89	7.27	1107 Q48991 oryza sativa (rice). nos
SP_human:Q9H4D6	+	80.50	125.68	10.68	405 Q9H4D6 homo sapiens (human). m
SP_bacteria:Q56451	+	80.00	134.65	9.24	807 Q56451 xanthomonas sp. mercury
SP_mammal:Q9GLX9	+	80.00	127.84	11.11	3570 Q9GLX9 bos taurus (bovine). vsg
SP_human:Q99552	+	80.00	113.14	16.55	241 Q99552 homo sapiens (human). m
SP_bacteria:Q33798	+	79.50	138.81	9.11	241 Q33798 salmonella typhimurium.

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seq_name: SP_rodent:Q9D077
seq_documentation_block:
ID Q9D077 PRELIMINARY: PRT: 191 AA.
AC Q9D077
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 1190003M12R1K. PROTEIN.
GN 1190003M12R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nakato I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okada T., Furuno M., Aono H., Balderelli R., Bash G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Kombeets P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez L., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Hayashizaki Y., Yoshida K., Hasegawa Y., Kawai H., Kohlski S.,
RA Hayashizaki Y.
RA *Functional annotation of a full-length mouse cDNA collection.*;
RL Nature 409:685-690(2001).
DR EMBL: AK004474; BAB23320.1;
DR MGI: 1916138; 1190003M12R1K.
SO SEQUENCE 191 AA: 20772 MW: 7607DB4796A8B4D CRC64;

alignment_scores:
Quality: 252.50 Length: 204
Ratio: 1.913 Gaps: 7
Percent Similarity: 64.706 Percent Identity: 31.863

alignment_block:
US-09-821-726-17 x Q9D077
Align seg 1/1 to: Q9D077 from: 1 to: 191

1 ATGCGTACCTTCTGACCTTCATTCGATTCGTGAAGCCAGATGAAGTTCAC 50
||||| ||||| : : : : :
1 MetPro.....LeuHisSerLeuGluAlaGAspAsnMetAlaGlyLe 14
51 AATGCGCTTGGTGGACTTGGTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTG 100
||||| : : : : : ||||| : : : : :
14 uUaIaIProSeIleuValThraValPheLeuValIProAlaLeuAla. 30
101 ACTATAGTATCAGTTCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGT 144
: : : : : : : : : : : : : : : : : : : : : : : : : : :
31 .....LeuThrAsnThrSerAspSerTyrProLeuAspIleVal 44
145 GCGAGCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGT 194
||| ||||| : : : : : : : : : : : : : : : : : : : : :

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45 GYTHrGlnThrIleHsValaAspAlaLeuArgGlyValValSerIleAr 61
195 CAATTAACATGATGATGAACTCTGGAATGCGCTCTGGAGTATAGAACTG 244
61 gaSpAsnSerValGlnSerIleUtrPaspGlyValMeAspTyrLysAsnA 78
245 GCTTTGCTGTAACGACGACTTTCGAGAAAGTCATGATTCGTCACAAA 294
78 spleuLeuAlaAlaValLeuPheSerLysMetAlaCysValLeuAlaLys 94
295 ATGAAGAAGAAAGCCATGCCCTCCCT.....CAAGCCCTTGA 332
95 MetAspProAlaAlaPheProSerLeuAspAspIleThrGlnAlaLeu.. 110
333 TGCCCTGGTCAAGAAAGAGCTTCAGGGTAAAGGCCGAGGGA.... 378
111 .....GlyLysGlnAlaSerGlyHisT 118
379 ..CCACCTCCCAAGAGCCTGAGTACTCAGTCAACCCCAACAGAGTGCAC 426
118 yrProPThrArgGlyLeuThrTyrThrValLeuProSerArgIleLys 134
427 AACCGGACAGTTTGGAAATCCATGCTGCCATGTGCAAGGGGATTCC 476
135 AsnLeuAlaGlnTyrGlyValProIleLysAspLeuLysArgAlaValPr 151
477 AACATACATGCT...GAAGAGATTCAAGAGCAACCTGATTCGTA 523
151 oThrTyrPheAlaArgGlnGlnLysGlnGlyThrAlaLeuThrMetAsp 168
524 CAGAAATGATCATGCTGCAATATCTGATTCGATTCATTCATTCCTTC 573
168 roAspSerCysSerGlnLeuGlnLeuSerPheMetGlyLeuSerIle 184
574 TCTGGAGGAATA 585
185 CysGlyGlnIle 188
seq_name: sp_rodent:Q9CQ56
seq_documentation_block:
ID Q9CQ56 PRELIMINARY; PRT: 184 AA.
AC Q9CQ56;
DT 01-JUN-2001 (TREMblrel, 17, Created)
DT 01-JUN-2001 (TREMblrel, 17, Last sequence update)
DE 01-JUN-2001 (TREMblrel, 17, Last annotation update)
DE 1810036H07RIK PROTEIN.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=STOMACH, AND PANCREAS;
RX MEDLINE=21085660; Pubmed=11217851;
RA Arkawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda Y.,
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa K., Itawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
RA Saito T., Okazaki Y., Gojodori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Botelli D., Boujunga N., Carninci P., de Bonaudo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofman M., Hume D.A., Kamita M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Winking L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa T., Kawaji H., Kohlsuki S.,

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RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK008986; BAB26008.1; -.
DR EMBL; AK007451; BAB25046.1; -.
DR EMBL; AK007705; BAB25201.1; -.
DR MGD; MGI:1913534; 1810036H07RIK.
SQ SEQUENCE 184 AA; 20469 MW; 612A18FABE652230 CRC64;

alignment_scores:
Quality: 217.00 Length: 184
Ratio: 1.750 Gaps: 3
Percent Similarity: 67.391 Percent Identity: 28.261

alignment_block:
US-09-821-726-17 x Q9CQ56 ..

Align seg 1/1 to: Q9CQ56 from: 1 to: 184

40 ATGAAGTTCACAATGCTTTGCTGACTTTCGTGCTTCGTA 89
||||| .....|
1 MetLysProLeuValAlaPheLeuValAlaLeuSerIlePheGlyIleG1 17
90 TGCCCTTGTGACTATGATATCATGTCATACAGACAGGCAACAGTGTG 139
::: |||||: .....|
17 nserGlnAlaGlnGlnIlePheAsnIlePheValProSerLysAsnGlyG 34
140 GAAGTGGGACGACGTCAGTGCAGTGCACATGACATGACACACAGTGGCCAC 189
||||| .....|
34 LysnIleGlnGlnIleThrValThrIleAspAsnGlnIleAsnThrAlaThr 50
190 GTTGACAAATGACATGATGATGAACTCTGGAATGCGCTTGGACTGACT 239
||||| .....|
51 IleAsnIleHisSerGlySerSerSerThrThrIlePheAspTyrIly 67
240 AACTGCTTTCGCTTAACCGACTCTTCGAGAAAGATCATGATGATGTCG 289
: |||||: .....|
67 shISGlyTyrIleAlaSerArgValLeuSerArgArgAlaCysTyrValI 84
290 ACAAAATGAAGAAGAACCCATGCCCTCCCTTCAGCCCTGATGGCTG 339
||||| .....|
84 IeLysMetAspHisLysAlaIleProAlaLeuAspLysLeuGlnArgPhe 100
340 GTCAAGGAAGAAAGCTTCAGGCTAAGGCTAAGGCGCCAGGGGACCACTCCCA 389
::: |||||: .....|
101 LeuTyrGlnLysGlnThrMet...AsnAlaIleAspSerProGlnTyrTh 116
390 GAGCCTGAGTACTCATCAACCCCAACAGAGTCGACAACTGTGAC.... 435
||||| .....|
116 rTTPValArgTyrAsnProLeuLysSerLeuIleThrLysValAspTyrP 133
150 GIuGlyGlnValAlaThrLysProLysGlnValSer...ThrGlyAlaC 165
484 ATGCTGAAGAGATTCAAGAGCAAACTGATTCGTACACAGAAAGT 533
||||| .....|
534 CATGATGTCCAATATCTGCTGATTCATTCATTCCTTGTGTGAGAA 583
||||| .....|
165 sAlaLysValGlyLeuLeuGlnGlyIleLeuGlnValSerIleCysGlyI 182
584 TA 585
||
182 le 182

seq_name: sp_organelle:Q9MJF8
seq_documentation_block:
ID Q9MJF8 PRELIMINARY; PRT: 574 AA.
AC Q9MJF8;

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[illegible]

233 16C4111FC16AG1A
111...

535 TGCACITTTTCTGAGTACGAATCAGGTTGCTTCCTGAATCTCTTCAGCC 486
|||::: ::::: ||| ::::: |||||

```

620 CysAsnAsnCysThrCysArgAlaGlycInLeuSerCysThrAlaGlnPr 636
485 ATGATGTTGGAAATCCCTTCCACATGGCAACGATGATTTTCCAAACT 436
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
636 cCysProProAlaHisCysAlaTrpSerArgTrpSerAlaTrpSer. 652
435 GTCCAGGTTGCGACTCTGTGGGT.....TGA 407
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
653 ..ProCysSerArgSerCysGlyProAlaGlyGlnInSerArgPheArg 668
406 CTGAGTACTCAGGCTCTTGG.....GAGGTGGTCCC 375
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
669 SerSerThrSerGlySerTrpAlaProGluCysArgGlnGlnInserG 685
374 CCTGGGCTTACCTGTAAGCTTTCTTCTTGGACACGCGCATCAAGGC 325
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
685 nSerGlnProCysProGlnSerProCysProLeuGlnGlnGlnGlnG 702
324 TTGAA.....GGAGAGGCGAGCTTCTTCTTCTTCTTCTTCTTCT 287
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
702 hArgProArgSerLeuGlnYaspSerTrpLeuGlnaspGly..CysG 717
286 CAATGC 281
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
718 GlnCys 719
seq_name: sp_invertebrate:076810

```

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seq_documentation_block:
ID 076810 PRELIMINARY; PRT; 373 AA.
AC 076810;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ICHT PROTEIN.
GN ICHT.
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
OC Anophelinae.
NCBI_TaxID=7165;
RX MEDLINE=99016033; PubMed=9799221;
RA STRAIN=SUAKOKO; TISSUE=MAINLY MIDGUT;
RX MEDLINE=99016033; PubMed=9799221;
RA Diopoulous G., Seeley D., Wolf A., Kafatos F.C.;
RT "Malaria infection of the mosquito Anopheles gambiae activates immune-
RT responsive genes during critical transition stages of the parasite
RT life cycle."
RL EMBO J. 17:6115-6123(1998).
DR EMBL: AJ010903; CAA09389.1; -.
DR InterPro: IPR002557; Chitin binding.
DR Pfam: PF01607; Chitin_bind_2; 2.
DR SMART: SM00494; ChitBD2; 2.
SQ SEQUENCE 373 AA; 40647 MW; CFAE3811FC224161 CRC64;

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alignment_scores:
Quality: 90.00 Length: 127
Ratio: 1.698 Gaps: 4
Percent Similarity: 41.732 Percent Identity: 28.346
alignment_block:
US-09-821-726-17 x 076810 ..
Align seg 1/1 to: 076810 from: 1 to: 373

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92 CCCTTGCTAGTATAGTATGATGTCACGACGACGCA.....ACAGT 135
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
133 ProThrThrThrThrSerAlaProThrProSerGlnTrpThrAs 149
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
136 GGTGGAAGTGGGACGAGTCAAGTGAATGAACACACAGCTGG. 184
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

149 ProThrIleThrThrThrProValTrpThrAspProThrTrpTrpS 166
185 .....CCAAGTTGACATATACATGATGATGCAACCTCGAATGGCCCT 229
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
166 eValProThrThrThrThrThrTrpSerAspGlnProProProThr 182
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
230 GGAGCTATAGAACTGGCTTTCGTAAACGACCTTTCGAGGAAGTCA 279
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
183 ThrThrThrThrThrValTrpThrAspProThrAlaThrThrThrHi 199
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
199 sAlaProThrThrThrThrThrTrpSerAspLeuProProProPro 216
330 TGATGGCC.....TGTCAGAGAAAAAGAGTTCAAGGTAAGGCC 370
216 hThrThrThrThrThrValTrpIleAsp..... 224
371 CAGGGGACCCACCTCCCAAGACCTGAGTACTCACTCAACCCCAAGCA 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
225 .....ProThrAlaThrThrThrThrThrHiAlaProThrThr 236
421 GTGACACACTGGACAAAGTTGGAAATGCA 451
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
236 rThrThrThrThrThrSerAspLeuProProPro 246
seq_name: sp_invertebrate:Q9NL38

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seq_documentation_block:
ID Q9NL38 PRELIMINARY; PRT; 568 AA.
AC Q9NL38;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE M66 MATRIX PROTEIN.
OS Pinctada maxima.
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pterioidea;
OC Pterioidea; Pteridae; Pinctada.
NCBI_TaxID=104660;
RX MEDLINE=20160475; PubMed=10694502;
RA Kono M., Hayashi N., Samata T.;
RT "Molecular mechanism of the nacreous layer formation in pinctada
RT maxima."
RL Biochem. Biophys. Res. Commun. 269:213-218(2000).
DR EMBL: AB032613; BAA90540.1; -.
DR HSP: P23589; IDWY.
DR InterPro: IPR001148; Carb_anhydriase.
DR InterPro: IPR002952; Eggshell.
DR Pfam: PF00194; carb_anhydriase; 1.
DR PRINTS: PR01228; EGGSHELL.
DR PRODOM: PD000865; Carb_anhydriase; 2.
KW Matrix protein.
SQ SEQUENCE 568 AA; 62377 MW; 4AD9242A96EB642F CRC64;

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alignment_scores:
Quality: 89.50 Length: 177
Ratio: 1.053 Gaps: 8
Percent Similarity: 48.023 Percent Identity: 23.164
alignment_block:
US-09-821-726-17 x Q9NL38 ..
Align seg 1/1 to: Q9NL38 from: 1 to: 568

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124 GAGGCAACAGTGTGGAAGTGGCAGCAGTCACTGAGTCAACATGA 173
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
392 AsnGlyAsnAsnGlyGlyAsnGly.....AsnAsnG 402
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
174 ACACAACTGGCCAAAGTTGACATTAACATNGATGGAATCCCGAANTG 223
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```



```

      :|||  |||  :|||:|||||:|||||:  |||
402 yasnasnGLyAspAsnGLyAsnGLyAspAsnGLyTyrAsnGLyAspAsnG 419
224 CC.....CTCTGGAGCTATAGAACCTGGCTTGGCT 252
419 LysAsnSerAspGLyArgLeuArgArgTyrAspLeuAlaAsn..... 432
253 GTAACCAAGACTCTTCAGAGAAAG.....TCATGCAATGGT 287
|||  |||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:
433 ValArgArgMetHisAlaGLuArgTyrHisPheSerGlyGlyCysIleVal 449
288 GCACAAATGAAGAAGAACCCATGCCCTCCCTTCAGACCCCTTGATGGGC 337
|||  |||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:
449 LysLysAlaLysArgLeuSer.....ArgIleLeuGlyCysA 462
338 TGGTCAGGAAGAAGACTTCAG.....GCTAAGGGCCCA 372
|||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
462 LArgArgHisLysLysValArgGLuPheLysArgAsnGLyGLuLys 478
373 GGGGG.ACCACCTCCCAAGAGCCCTGAGGTACTCACTCAACCCCAACAGAG 421
|||  |||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:
479 GlyLeuAspValAspIleThrProIleMetValLeuProPromeLysTyr 495
422 TCGA.....CAAC 429
|||  |||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:
495 LArgHisTyrTyrThrTyrGLuGLySerLeuThrThrProCysAsnG 512
430 CTGGACAGATTGGAAATCCATGCTGCCATGTCCAGGGGAT..... 473
|||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
512 LThrValLeuThrValValGluLysCysHisValGlnValSerArgArg 528
474 .....TCCACATACATGCTGAGAGATTCAGAGACCA 508
|||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
529 ValLeuAspAlaLeuArgAsnValGluLysTyrGluAspGLyThrThrLe 545
509 ACCGTATTTCGTACTCAGAAAAGTCATCAG 539
|||  |||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:
545 uSerLysTyrGLyThrArgArgProThrGln 555

seq_name: sp_bacteria:Q9S2S3

seq_documentation_block:
ID Q9S2S3 PRELIMINARY; PRT; 266 AA.
AC Q9S2S3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE HYPOHETICAL 28.6 KDA PROTEIN.
CN SC466.36.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Seeger K.J., Harris D.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Bentley S.D., Parkhill J., Barrett B.G., Rajandream M.A.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA MEDLINE=97000351; PubMed=8843436;
RX Redenbach M., Kieser H.M., Denapante D., Eichner A., Cullum J.,
RA Kinasli H., Hopwood D.A.;
RT A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb streptomyces coelicolor A3(2) chromosome.*;
RL Mol. Microbiol. 21:77-96(1996).
DR EMBL, AL096884, CAB51459.1, -

```

```

KW Hypothetical protein.
SQ SEQUENCE 266 AA; 28612 MW; 83FADF6EBE18118A CRC64;

alignment_scores:
  Quality: 89.00 Length: 173
  Ratio: 1.085 Gaps: 8
  Percent Similarity: 47.399 Percent Identity: 26.012

alignment_block:
US-09-821-726-17 x Q9S2S3
Align seg 1/1 to: Q9S2S3 from: 1 to: 266

28 GGTACACCAAGATGAAGTTACACATTCCTTGTCTGCACTCTTGCTGT 77
|||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
125 GLYAspTyrLysLeuSerPheThrVal.....GlyThr 135
78 CTTCCTGACTCTGCCCTTCTGCTGACTATATCAGTTCAGTCAGCAGCAGC 127
|||  |||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:
135 rPheLeu.....AspG 139
128 GCACACAGTGTGAGAGTGGGAGAGTCACTG.....AGTGTCAACAT 171
|||  |||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:
139 LysAsnLeuGlyGlyGlySerLysAsnAlaLeuSerAlaLeuGlyAla 155
172 GAACACACAGTGGCCCAAGCTTGACATATGATGATGACATCTGGAA 221
|||  |||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:
156 AlaLeuAsnVal.....SerProG 162
222 TGGCTCTGCACTATATGAACTGAGCTTGTGCTGTAACCAAGCTCTTGAGA 271
|||:  |||:  |||:  |||:  |||:  |||:  |||:  |||:
162 uAlaPheValAspTyrLysThrAlaLeuTyrSerThrLysTyrHisProG 179
272 AGAAGTCATGCATTGTGCACAAATGAGAGAGAACCATGCCCTCTT 321
|||  |||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:
179 LysLysSerThrAspGLuPheAlaLysAspAspTyrLeuIleLysValAla 195
322 CAAGCCCTGATGCCCTGCTCAAGGAAAGACCTTCAGGT..... 363
|||  |||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:
196 AspSerValAspAlaLeuLysGlyAsnLysLysPheGlnAspAlaValG 212
364 AAGGCCCAAGGGGAGC.....CACTGCCA 388
|||  |||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:
212 uLysGly.ThrTyrAspAlaThrPalaMetArgMetSerLysSerPheAsp 228
389 AGAGCCTGAGTACTCAGTCAACCCCAACAGAGTCGACAACTGGACAG 438
|||  |||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:
229 LysAlaGluGlyValGlnSerThrProThrIleLysIleAsnAspLysVa 245
439 TTGGAAATATCCATCGTTGCCATGTCGAAGGGGATTCACACATACATGGC 488
|||  |||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:
245 ValGluThrProSerThrProAspAla.....TrpG 256
489 TGAAGAGATTCAGAGAG 505
|||  |||:  :|||:  :|||:  :|||:  :|||:  :|||:  :|||:
256 LysLysAlaLeuLysAsp 261

seq_name: sp_invertebrate:Q9VSD9

seq_documentation_block:
ID Q9VSD9 PRELIMINARY; PRT; 700 AA.
AC Q9VSD9; Q9U4A1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE UBIQUITIN-LIKE PROTEIN ACTIVATING ENZYME (SMT3 ACTIVATING ENZYME 2).
GN UBA2 OR SAE2 OR CG7528.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydriidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;

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DE NADH DEHYDROGENASE SUBUNIT II.
 OS Leptotlebias minimus.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Leptolebias.
 NCBI_TaxID=60314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hixek T., Larson A.;
 RT "The evolution of diapause in the killifish family Rivuliidae
 RT (Atherinomorpha, Cyprinodontiformes): A molecular phylogenetic and
 RT biogeographic perspective."
 CC Evolution 53:1200-1216(1999).
 CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
 DR EMBL: AF092364; AF092961;
 DR InterPro: IPR001750; Oxidored_q1.
 DR Pfam: PF00361; Oxidored_q1.
 DR Mitochondrion: NAD; Oxidoreductase; Ubiquinone.
 KM SEQUENCE 348 AA; 38796 MW; 5CB874C84B87723E CRC64;
 SQ

alignment_scores:
 Quality: 87.00 Length: 171
 Ratio: 1.036 Gaps: 11
 Percent Similarity: 49.123 Percent Identity: 32.164

alignment_block:
 US-09-821-726-17/rev x Q9TD56 ..

Align seg 1/1 to: Q9TD56 from: 1 to: 348

548 ATATTGGCACTGATGCACTTTCTGAGTACGAATACGTTTGTCTG 499
 |||||:|||||:|||||
 198 lIleuAlaIheIeuAlaPhe..... 204
 498 AATCTCTCAGCCATGATGTGGAATC.....CCCTGGCAATGGCAA 455
 :|||:|||||:|||||
 205ValMetIyValGlyIeuThrMetProValAlaValMetAlaL 218
 454 CG.....ATGATTTTCCAACTGTGTCAGGTTGCG..... 423
 |||||:|||||:|||||
 218 euSntIyMetGlnThrIySAsnIleAsnIleuSerIleSerArgSer 234
 422ACTCTGTTGGGTTGACTGACTGACTGAGGCT 391
 :|||:|||||:|||||
 235 LysAlaIProPheIeuPheSerMetIeuProIeu.....TyrIeuIeuSe 249
 390 CTTGGGAGGTGTCCTCCCT.....GGGCCCTTACCTGAGGCTTCTT 348
 |||||:|||||:|||||
 249 rIeuGlyGlyIeuProPheSerGlyIeuPheIeuProIySTIPMeIleL 266
 347TCCCTGACCAAGGCTTGAAGGAGGAGGAGGAGGCTTCC 303
 :|||:|||||:|||||
 266 euAspIySleuThrAspIyAlaIalalysProValAlaValMetAlaIa 282
 302 TTCTTCATTTTGTGCACATGACTTCTTCTCGAAGAGTGTGTTAC 253
 :|||:|||||:|||||
 283 LeuPheThrIeuIeuSerLeuPheThrIeuIeuIeuSerIyThrTh 299
 252 AGCA.....AAGCCAGTTCTATAGTCCACAGAGG 224
 |||||:|||||:|||||
 299 rAlaIeuThrThrProPheAsnAsnAsnProValThrIeuSerIyParg 315
 223 CATTCACAGAGTCCATCATTTGATTGTGCACAGTGGCCACGTTGTGT 174
 :|||:|||||:|||||
 316PheProIeuIeuIySProAlaIeu.....LeuIeu 325
 173 TCATTGTGACACTGACGACTGCTGCCACTTCCACCAGTGTGGCTG 124
 :|||:|||||:|||||
 326 AlaIeuIeuThrProIeuSerMetCys.....LeuIleProIeuIeuProSe 341

123 GTCCTTGACACTG 111
 | :|||
 341 rPheMetSerIeu 345

seq_name: sp_bacteria:Q9RUJ7

seq_documentation_block:

ID Q9RUJ7 PRELIMINARY; PRT; 369 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE PUTATIVE INTEGRAL MEMBRANE PROTEIN.

GN SCF41.22.

OS Streptomyces coelicolor.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomycetes.

OX NCBI_TaxID=1902;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=A3(2);

RA Saunders D.C., Harris D.;

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=A3(2);

RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=A3(2);

RA Redenbach M., Kieser H.M., Denapalte D., Eichner A., Cullum J.,

RT Kinshshi H., Hopwood D.A.;

RT "A set of ordered cosmid and a detailed genetic and physical map for

RT the 8 Mb Streptomyces coelicolor A3(2) chromosome."

RT Mol. Microbiol. 21:77-96(1996).

DR EMBL: AL117387; CAB55725.1; -

DR InterPro: IPR000567; SRP Bac.1.

DR Pfam: PF01547; SRP_bacterial_1;

DR SEQUENCE 369 AA; 39349 MW; F12CFB607EA641B CRC64;

alignment_scores:
 Quality: 87.00 Length: 123
 Ratio: 1.611 Gaps: 7
 Percent Similarity: 43.902 Percent Identity: 30.081

alignment_block:
 US-09-821-726-17 x Q9RUJ7 ..

Align seg 1/1 to: Q9RUJ7 from: 1 to: 369

197 ATACCATGATGGAATCTCTGGAATGCCCTCTGAGACTATAGAACTGCC 246
 :|||:|||||:|||||
 239 ValThrIaGlyIaGlyArgProGlySerThrIeuGlyIaIaGlyIleAl 255
 247 TTTCCTTAACCAAGACTCTTCGAGAGAACTCATGCTTGTGCACAAAT 296
 :|||:|||||:|||||
 255 Aleu.....SerAlaArgCysVal..... 261
 297 GAAGAGAGAGAGCCATGCCCTCCCTTCAGCCCTTGTAGCGCTGTCAAG 346
 |||||:|||||:|||||
 262ProSerProGluIeuIeuAlaHisMetIaGlyTP..... 272
 347 AAAAGAGCTTCAGGTAAGGCCCAAGGGAGACCACTCCCAAGAGCTG 396
 :|||:|||||:|||||
 273LeuMetSerProGluIaIaGlyIaSPheIeuIeuProIaGlyHis 287
 397 AGTACTCAGTCAACCCACAGAGTGCACACACCTGACGACAACTTTGAAA 446
 :|||:|||||:|||||
 287 rGly.....GlnProSerAlaIaArgThrAlaIaTPThrSer..... 298

1

170 sleuIeThrLysIleValL

170 sleuilethrllysilevallysglu 178

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129 ValAspGluAsnAspIleSerClyAspGlnClyValThrAspProGluPr 145
130 |||::: ::::||| :::||| ||| ||
131
132 ValAspGluAsnAspIleSerClyAspGlnClyValThrAspProGluPr 145
133 |||::: ::::||| :::||| ||| ||
134
135 CAGACCGTGAAGCTACTACGTCAACCCCAACAAGATTC...GACAACTGG 433
136 ::::: ::::: ||| ::: ||||||
137
138 OAlaProValGIuAlaGluAlaValProAlaLysTYrHisAspAsnIlaA 162
139 ::::: ::::: ||| ::: ||||||
140
141 ACAAGTTTGAAAATCCATTGCTGCCATGTGCAGAACGGAGATTCCAACATAC 483
142 |||||::: ::::: |||||| |:::
143
144 LethrLaclLysLeuLeuPheAspSerProLysGlySerMetValG 178
145 ::::: ::::: ||| |||||
146
147 ATGCTCAAGAAGATTCCAAGA.....GCCAACCTGAT 515
148 ||| :::::
149 SerAlaThrValValLysAspProAlaHisProGlyLysSerAsnMetVa 195
150 ::::: :::::
151 TTGCTATCCAGAAAGTGCATCATGCTGCCATATATCTC.....TGCATTC 559
152 : ::::: |||||:::
153
154 ITPHTPLALAGLYscysVALHISalagLYsserGLYTrpTYra 212
155 : ::::: |||||:::
156
157 TTAACATTTCCTTC 573
158 |||||:::~|||
159
160 rgsAntLeaLphe 216
161
seq_name: sp_plant:Q945S6
seq_documentation_block:
ID Q945S6 PRELIMINARY; PRT: 1297 AA.
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DF 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE IZC-5.
GN IZC-5.
OS Lycopersicon pimpinellifolium (Current tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxId=1084;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=2141641; PubMed=11523783;
RA Sela-Buurlage M.B., Budai-Hadrian O., Pan Q., Carmel-Goren L.,
RA Vunsci R., Zamir D., Fluhr R.,
RA "genome-wide dissection of Fusarium resistance in tomato reveals
RA multiple complex loci.",
RA Mol. Genet. Genomics 265:1104-1111(2001).
RL EMBL: AF408704; AAL01986.1; -.
SQ SEQUENCE 1297 AA; 147917 MW; 76F5C220D953181 CRC64;
alignment_scores:
Quality: 84.50 Length: 214
Ratio: 0.918 Gaps: 11
Percent Similarity: 42.991 Percent Identity: 23.832
alignment_block:
US-09-821-726-17 x Q945S6 ..
Align seg 1/1 to: Q945S6 from: 1 to: 1297
22 TGcATTgGTGAAGccAAGATGAAGTTCACATTCCTTCTGTGACTTCT 71
|||:::~|||::: |||||:::~|||:::
238 cysvalsercrlvaltyraspalahetherlilethr...lysclyleuve 253
|||:::~|||::: |||||:::~|||:::
72 T.....GGTGTCTTCtGACTTCtGCCCTTGTGTGACTATATATCA 112
||| |||
253 uglngluileglylysphe..... 259
113 GTGTCAAGAGCAGCAGCAAGTGGTGAAGTGGGAGCAGCAGTCACTAGTACT 162
:::~|||::: ~|||:::
260 .....aspserlyasp 263
163 GTCAACATAAGAACACAAGCTGGCCAAAGCTT..... 192
```

```

|||||:|||||:|||||:|||||:
264 ValHisAsnLeuAsnGlnLeuGlnValLysLeuLysGlnSerLeu 280
193 .....GACAA.....AACATGATGA 211
280 sglLysLysPheLeuIleValLeuAspAspValTyrAsnGlnAspTyr 297
212 ACTCTGGAATGCCCTC.....TGGACTATAGACT 243
297 sncLutPrpAsnAspLeuArgAsnIlePheValGlnGlnLysArgLysSer 313
244 GCGTTGCTGTAACCAAGACTCTTGCAGAGAGTCAATGCATTCGCACA 293
314 LysIleIleValThr.....ThrArgLysAspSerValAlaLeu 327
294 AATGAGAGAGAGCCATGCC.....TCCCTTCAAGCCCTTG 311
327 tMetGlnAsnGlnGlnIleSerMetGlnAsnLeuSerThrGlnAlaSer 344
332 ATGGCTGTGTCAAGAAAGAGCTTCAGGGTAAGGCCAGGGGAGCA 381
344 rPseLysPheLysArgHisAlaPheGlnAsnMetAspPrometGlnHis 360
382 CCTCCCAAGAGCCCTGAGGTACTCAGTCAACCCCAACAGAGTGCAGACCT 421
361 Pro.....TCCCTTCAAGCCCTTG 363
432 GCACAGATTGGAATATCATGTCGTCATGTCAGAGGAGTTCACAT 481
363 uGlnGlnValGlnArgGlnIleAlaLysCysLysGlnLeuPro.... 378
482 ACATGCTGGAAGAGTTCAGAGCAAACTGATTTCGTACTCGAA... 528
379 ..LeuAlaLeuLysThrLeuAlaGlyMetLeuArgProLysSerGlnIle 394
529 .....AAGTCATCAGTGCATATATCTGATTTCT 561
395 AspGlnThrLysCysIleLeuArgSerGlnIleThrGlnLeu 408

seq_name: sp_invertebrate:0952B0
seq_documentation_block:
ID 0952B0; PRELIMINARY; PRT; 1328 AA.
AC 0952B0;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE POSSIBLE MAJOR AMPULATE SPIDROIN 2-LIKE PROTEIN (FRAGMENT).
GN L3747.01.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RX MEDLINE=98146435; PubMed=9477341;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
DR EMBL; AL596273; CAC44730.1; -.
FT NON_TER 1328
SQ SEQUENCE 1328 AA; 138537 MW; 689EA0758A424434 CRC64;

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alignment_scores: quality: 84.50 Length: 168

Ratio: 1.225 Gaps: 9
Percent Similarity: 41.071 Percent Identity: 27.976
Alignment_block:
us-09-821-726-17/rev x 0952B0 ..
Align seg 1/1 to: 0952B0 from: 1 to: 1328

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523 AGTACGAATCAGGTTTCCTCTGAAATCTCTCAGCCATGATGTGGA 474
|||||:|||||:|||||:|||||:
213 SerSerProSerLysSerSerThrSerSerSerGlnProCysSerProPr 229
473 ATCCCTTGCACATAGGCAACGATGATTTCCAACTGTTCACAGTTGC 424
229 cArgGlnProArgAlaGlnIleArgTyrGlnCysLeuAsnCys.....CysA 244
423 GACTGTGTTGGGTTGACTGAGTACCTCAGGCTCTTGGGAGAGTGCCCC 374
244 rArgCys.....GlySerCysAspSerValGly 253
373 CTGGGCCCTTACCT.....GAAGCTTCTTT 348
254 Leu...ProCysProValAsnAlaHisGlnHisArgSerArgGlnThrAl 269
347 TCCTTGACCAAGGCATCAAGGCTTGAAGGAGGCA..... 311
269 aAlaGlnAlaAlaHisGlnArgCysHisAlaArgSerSerProAlaArg 286
310 ....TGGCTCTCTCTCATTTGTGCA..... 287
286 LysArgThrLeuSerSerAlaAspCysAlaAlaThrAsnLysAspSerAla 302
286 .....CAATGCATGACTTCTTCTCGAAGAGTGTGTT 255
303 ProAlaAlaSerLysThrAlaThrValAspSerProArgLeuGlnThrPle 319
254 ACAGCA.....AGCCAGTTCTATGTGCCACAGGAGCAT 220
319 uGlnGlnLeuProAlaThrProSerArgArgProSerProGlnGlnLeu 336
219 SCAGAGTTCATCATCTGTTATTGTCAAGCTTGGCCAGCTGTGTTCAT 170
336 eSerSerGlnValArgCysArgSerThrArg.....ArgValArgHis 350
169 TGTTGACACTGACTGCTGCCAC...TTCACCACTGTTCGCCGTG 123
351 ArgArgArgGlnGlnSerProAlaHisAspArgHisCysCysHisAs 367
122 TCGT 119
367 Patg 368

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2002, 16:46:12; Search time 57.74 Seconds
(Without alignments)
77.837 Million cell updates/sec

Title: US-09-821-726-16

Perfect score: 993

Sequence: 1 MKLTFVVGILGLAAPGFA.....TADILMLRMSFCGTVETTY 184

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents_AA:*

1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*

2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*

3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*

4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*

5: /cgn2_6/ptodata/2/1aa/6C.COMB.pep:*

6: /cgn2_6/ptodata/2/1aa/6D.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	91	9.2	553	3	US-09-083-351-2
2	91	9.2	553	4	US-09-083-352-2
3	85.5	8.6	346	1	US-08-213-403-2
4	85.5	8.6	346	1	US-08-458-077-2
5	85.5	8.6	346	1	US-08-460-741-2
6	85.5	8.6	346	1	US-08-747-240-2
7	85.5	8.6	346	1	US-08-299-567-6
8	79	8.0	336	1	US-08-436-044-2
9	79	8.0	336	2	US-08-436-054-2
10	79	8.0	336	5	PCR-US95-08812-2
11	77.5	7.8	428	3	US-09-118-319-5
12	76	7.7	775	4	US-09-305-640-2
13	75	7.6	334	1	US-08-241-465B-19
14	75	7.6	334	1	US-08-241-465B-20
15	73	7.4	238	4	US-09-216-295-12
16	72	7.3	333	1	US-08-436-044-4
17	72	7.3	333	2	US-08-436-054-4
18	72	7.3	333	4	US-08-271-948-2
19	72	7.3	333	5	PCT-US95-08534-2
20	72	7.3	333	5	PCT-US95-08812-4
21	72	7.3	478	3	US-08-155-888-2
22	71	7.2	193	1	US-08-616-368A-1
23	71	7.2	193	4	US-08-616-368A-1
24	71	7.2	193	4	US-08-818-655-1
25	70	7.0	193	1	US-08-616-368A-8
26	70	7.0	193	1	US-08-616-368A-13
27	70	7.0	193	2	US-08-739-485-1

28	70	7.0	193	2	US-08-739-485-9	Sequence 9, Appl1
29	70	7.0	193	4	US-09-054-298-8	Sequence 8, Appl1
30	70	7.0	193	4	US-09-054-298-13	Sequence 13, Appl1
31	70	7.0	193	4	US-08-818-655-8	Sequence 8, Appl1
32	70	7.0	193	4	US-08-818-655-13	Sequence 13, Appl1
33	70	7.0	312	1	US-08-525-505A-4	Sequence 4, Appl1
34	70	7.0	314	1	US-08-525-505A-2	Sequence 2, Appl1
35	70	7.0	992	1	US-08-127-499A-1	Sequence 1, Appl1
36	70	7.0	992	1	US-08-482-847-1	Sequence 1, Appl1
37	69.5	7.0	197	1	US-08-044-621D-29	Sequence 29, Appl1
38	69.5	7.0	197	1	US-08-709-912-9	Sequence 9, Appl1
39	69.5	7.0	197	2	US-09-047-370-9	Sequence 9, Appl1
40	69.5	7.0	348	4	US-09-216-295-16	Sequence 16, Appl1
41	68	6.8	221	1	US-08-032-848C-13	Sequence 13, Appl1
42	68	6.8	239	4	US-09-216-295-7	Sequence 7, Appl1
43	68	6.8	259	4	US-09-216-295-5	Sequence 5, Appl1
44	68	6.8	580	4	US-08-913-159-10	Sequence 10, Appl1
45	68	6.8	1046	1	US-08-386-727-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-09-083-351-2
Sequence 2, Application US/09083351
Patent No. 6087107
GENERAL INFORMATION:
APPLICANT: Sheffield, Val C.
APPLICANT: Alward, Wallace L.W.
APPLICANT: Stone, Edwin M.
APPLICANT: Nishimura, Darryl
APPLICANT: Patel, Shiva
TITLE OF INVENTION: THERAPEUTICS AND DIAGNOSTICS FOR
TITLE OF INVENTION: CONGENITAL HEART DISEASE BASED ON A NOVEL HUMAN
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,351
FILING DATE: 22-MAY-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UTA-029.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-083-351-2

Query Match 9.2%; Score 91; DB 3; Length 553;
Best Local Similarity 19.6%; Pred. No. 0.089;
Matches 38; Conservative 21; Mismatches 57; Indels 78; Gaps 9;

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OY      14 LAAGFAYVININGNDGNDGSGOQSYISINGVHVA-----NIDNNNGW----- 57
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      76 MVKPPSYIALIT--MAIONAPDKKTTLNGITFOITMDREFPFYRDKNQGNQNSIRNLISL 132
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      58 -----DSNNSIMDYENS--FATRLFSKSCIVHRMKDAM 91
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      133 NECFVKVPRDDKKPKGKGSYWTLLDPDSYNM--FENGSEFLRRRRRFRKKKDAVVKDEEKDRL 189
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      92 -----PSLDDLTMYKEQKGGKPGGAPKDDMYSYNPNRVEDLNFEGKIGMCRGIP 144
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      190 HLKEPPPPGRPPAPPAPQADGNAPGQPP-----PVRIQDIKTEN-----GTC----- 253
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      145 TYVABEIGPNQPL 158
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      234 -----PSPQPL 240
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT      2
US-09-083-352-2
Sequence 2, Application US/09083352
Patent No. 6207450
GENERAL INFORMATION:
APPLICANT: Sheffield, Val C.
APPLICANT: Alward, Wallace L.M.
APPLICANT: Stone, Edwin M.
APPLICANT: Nishimura, Darryl
APPLICANT: Patil, Shiva
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
TITLE OF INVENTION: BASED ON A NOVEL HUMAN TRANSCRIPTION FACTOR
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESSES:
ADDRESSER: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,352
FILING DATE: 22-MAY-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-029,01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-083-352-2

Query Match      9.2%; Score 91; DB 4; Length 553;
Best Local Similarity 19.6%; Pred. No. 0.089;
Matches 39; Conservative 21; Mismatches 57; Indels 78; Gaps 9.

OY      14 LAADGAYVYVINGNDGNDGSGOQSYISINGVHVA-----NIDNNNGW----- 57
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      76 MVKPPSYIALIT--MAIONAPDKKTTLNGITFOITMDREFPFYRDKNQGNQNSIRNLISL 132
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      58 -----DSNNSIMDYENS--FATRLFSKSCIVHRMKDAM 91
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      133 NECFVKVPRDDKKPKGKGSYWTLLDPDSYNM--FENGSEFLRRRRRFRKKKDAVVKDEEKDRL 189
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      92 -----PSLDDLTMYKEQKGGKPGGAPKDDMYSYNPNRVEDLNFEGKIGMCRGIP 144
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      190 HLKEPPPPGRPPAPPAPQADGNAPGQPP-----PVRIQDIKTEN-----GTC----- 253
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      145 TYVABEIGPNQPL 158
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      234 -----PSPQPL 240
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db      133 NECFVKVPRDDKKPKGKGSYWTLLDPDSYNM--FENGSEFLRRRRRFRKKKDAVVKDEEKDRL 189
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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QY      92  -----PSIQDDLTWKEQKGGPGGAPPKDMLSYNPRFVDELMTFPGKRIAGMGRGIP 144
Db      190  HLKEPPPGGQPPPPAPPEQADGNAPGPP-----PVRIDITEN-----GTC----- 233
QY      145  TYVAEIIPGNOPL 158
Db      234  -----PSPQPL 240

RESULT      3
: Sequence 2, Application US/08213403
: Patent No. 5512457
: GENERAL INFORMATION:
:   APPLICANT: Lyman, Stewart D
:   APPLICANT: Beckmann, M. Patricia
:   APPLICANT: Baum, Peter R
:   APPLICANT: Carpenter, Melissa
:   TITLE OF INVENTION: No. 5512457el cytokine Designated elk Ligand
:   NUMBER OF SEQUENCES: 2
:   CORRESPONDENCE ADDRESS:
:   ADDRESSEE: Immunex Corporation
:   STREET: 51 University Street
:   CITY: Seattle
:   STATE: Washington
:   COUNTRY: USA
:   ZIP: 98101
:   COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   COMPUTER: Apple Macintosh
:   OPERATING SYSTEM: Apple System 7.1
:   SOFTWARE: Microsoft Word for Apple, Version 5.1a
:   CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/08/213,403
:   FILING DATE: 15-MAR-1994
:   CLASSIFICATION: 435
:   PRIOR APPLICATION DATA:
:   APPLICATION NUMBER: US 07/977,693
:   FILING DATE: 13-NOV-1992
:   ATTORNEY/AGENT INFORMATION:
:   NAME: Seese, Kathryn A.
:   REGISTRATION NUMBER: 32,172
:   REFERENCE/DOCKET NUMBER: 2807-A
:   TELECOMMUNICATION INFORMATION:
:   TELEPHONE: (206) 587-0430
:   TELEFAX: (206) 233-0644
:   INFORMATION FOR SEQ ID NO: 2:
:   SEQUENCE CHARACTERISTICS:
:   LENGTH: 346 amino acids
:   TYPE: amino acid
:   TOPOLOGY: linear
:   MOLECULE TYPE: protein
:
US-08-213-403-2

```

[illegible]


```

1  APPLICANT: Baum, Peter R
2  APPLICANT: Carpenter, Melissa
3  TITLE OF INVENTION: No. 5670625e1 Cytokine Designated elk Ligand
4  NUMBER OF SEQUENCES: 2
5  CORRESPONDENCE ADDRESS:
6  ADDRESSEE: Immunex Corporation
7  STREET: 51 University Street
8  CITY: Seattle
9  STATE: Washington
10 COUNTRY: USA
11 ZIP: 98101
12
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: Apple Macintosh
16 OPERATING SYSTEM: Apple System 7.1
17 SOFTWARE: Microsoft Word for Apple, Version 5.1a
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/08/460,741
20 FILING DATE: 02-JUN-1995
21 CLASSIFICATION: 530
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: US 08/213,403
24 FILING DATE: 15-MAR-1994
25 APPLICATION NUMBER: US 07/977,693
26 FILING DATE: 13-NOV-1992
27 CLASSIFICATION: 530
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Seese, Kathryn A.
30 REGISTRATION NUMBER: 32,172
31 REFERENCE/DOCKET NUMBER: 2807-A
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: (206) 587-0430
34 TELEFAX: (206) 233-0644
35 INFORMATION FOR SEQ. ID NO: 2:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 346 amino acids
38 TYPE: amino acid
39 TOPOLOGY: linear
40 MOLECULE TYPE: protein
41
42 US-08-460-741-2
43
44 Query Match 8.6%; Score 85.5; DB 1; Length 346;
45 Best Local Similarity 23.1%; Pred. No. 0.19;
46 Matches 40; Conservative 23; Mismatches 61; Indels 49; Gaps 11.
47
48 QY 16 APGEATYVNIINGNDGVDGSGQGSVSIINGVHVAVIDNNNG-MDSWNSLMDYENSF-AAT 73
49   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
50 Db 195 APG-----SRGLGSDSK-----HEVTQGEKSGPGAGSCGSSDDPGGFRNSKY 238
51
52 QY 74 RLSK-KSCIV-----HRNKDAMPSTLQDLDTYVKQKGGPGGAP 113
53   ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
54 Db 239 ALFAAVGAGCVILFLIIFLTVLLLRKRHRKHTQGRRAALSLSTLSPKSGSGTAGTE 298
55
56 QY 114 PKDIASVNVTFREDLNTFGP---KIAGCRGIPYVAEELPGNPQ--LYSK 161
57   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
58 Db 299 PSDIITLRTTE---NNYCPHYEKVSG-DYGHPIYIVQEMP-POSPANITYK 345
59
60 RESULT 6
61 US-08-747-240-2
62 ; Sequence 2, Application US/08747240
63 ; Patent No. 5728813
64 ;
65 GENERAL INFORMATION:
66 ;
67 APPLICANT: Lyman, Stewart D.
68 APPLICANT: Beckmann, M. Patricia
69 APPLICANT: Baum, Peter R
70 APPLICANT: Carpenter, Melissa
71 TITLE OF INVENTION: No. 5728813e1 Cytokine Designated elk Ligand
72 NUMBER OF SEQUENCES: 2
73 CORRESPONDENCE ADDRESS:
74 ADDRESSEE: Immunex Corporation
75 STREET: 51 University Street

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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-436-044-2

Query Match 8.0%; Score 79; DB 1; Length 336;
Best Local Similarity 24.6%; Pred. No. 0.97;
Matches 34; Conservative 21; Mismatches 47; Indels 36; Gaps 9;

QY 49 ANIDNNNGDMSNLSMDYENSFAATRLFS--KKSCIV-----HRMKNK 88
DB 209 SSTDGNASAGHSGNNLLGSE-----VALFAGIASGCIIFIVIIITLVLLKTRRRHRKHS 263
QY 89 DAMPSLQDDLTMYKEQKGGKGGAPPKDLMYSVNPTRVEDLNTFGP---KIAGMCRGIPT 145
DB 264 PQHTTTLSTLATPKRGNGNNGSEPSDV---IIPLRAD-SVFCPHYEKVSG-DYGHV 318
QY 146 YVAEELPGNPQ--LYSK 161
DB 319 YIVQEMP-POSPANIYYK 335

RESULT 9
US-08-436-054-2
Sequence 2, Application US/08436054
Patent No. 5864020
GENERAL INFORMATION:
APPLICANT: Bennett, Brian D.
APPLICANT: Matthews, William
TITLE OF INVENTION: HTK LIGAND
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436, 054
FILING DATE: 05-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/277722
FILING DATE: 20-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 902D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-436-054-2

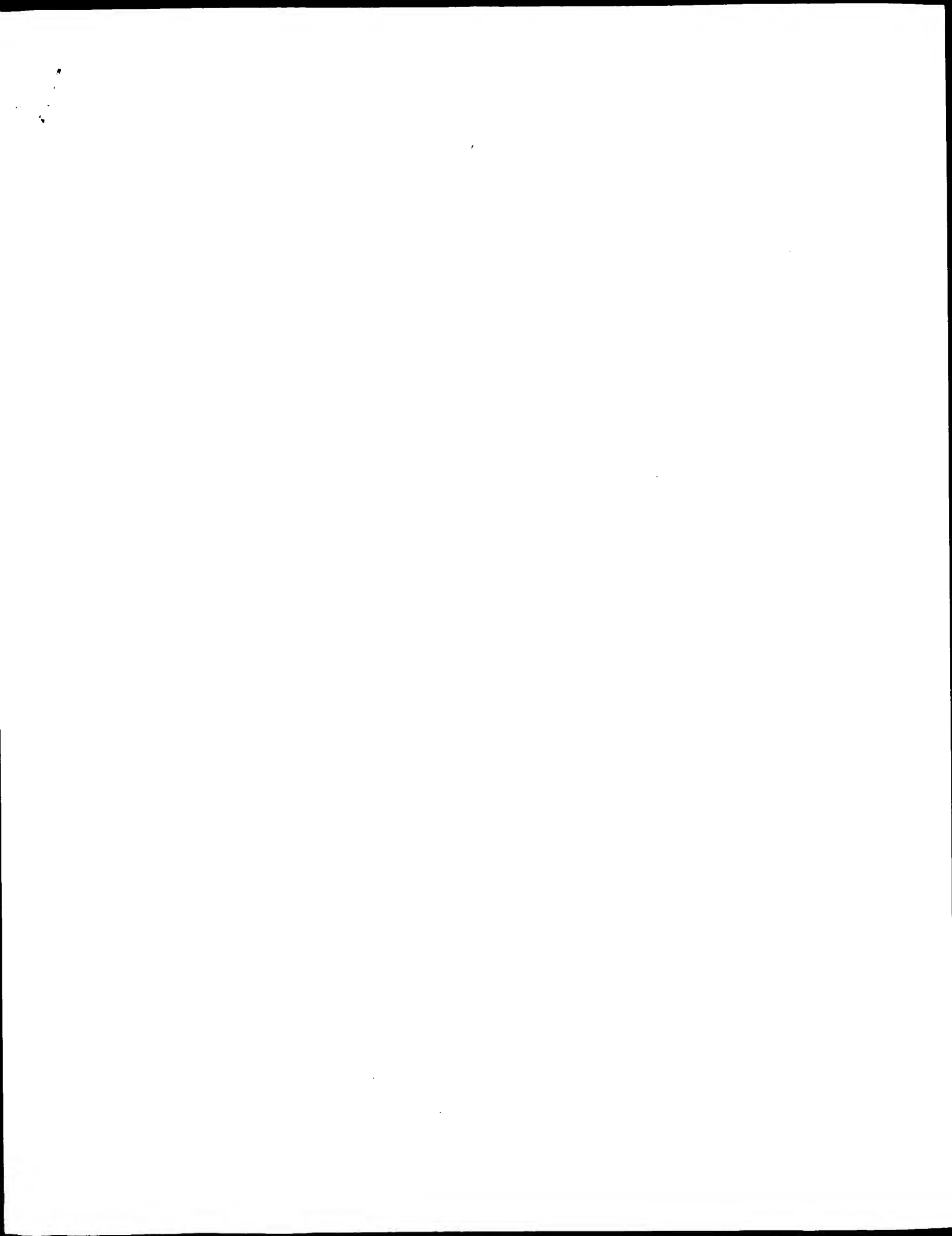
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Best Local Similarity 24.6%; Pred. No. 0.97;
Matches 34; Conservative 21; Mismatches 47; Indels 36; Gaps 9;

QY 49 ANIDNNNGDMSNLSMDYENSFAATRLFS--KKSCIV-----HRMKNK 88
DB 209 SSTDGNASAGHSGNNLLGSE-----VALFAGIASGCIIFIVIIITLVLLKTRRRHRKHS 263
QY 89 DAMPSLQDDLTMYKEQKGGKGGAPPKDLMYSVNPTRVEDLNTFGP---KIAGMCRGIPT 145
DB 264 PQHTTTLSTLATPKRGNGNNGSEPSDV---IIPLRAD-SVFCPHYEKVSG-DYGHV 318
QY 146 YVAEELPGNPQ--LYSK 161
DB 319 YIVQEMP-POSPANIYYK 335

RESULT 10
PCT-US95-08812-2
Sequence 2, Application PC/TUS9508812
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: HTK LIGAND
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08812
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 902PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US95-08812-2

Query Match 8.0%; Score 79; DB 5; Length 336;
Best Local Similarity 24.6%; Pred. No. 0.97;
Matches 34; Conservative 21; Mismatches 47; Indels 36; Gaps 9;

QY 49 ANIDNNNGDMSNLSMDYENSFAATRLFS--KKSCIV-----HRMKNK 88
DB 209 SSTDGNASAGHSGNNLLGSE-----VALFAGIASGCIIFIVIIITLVLLKTRRRHRKHS 263
QY 89 DAMPSLQDDLTMYKEQKGGKGGAPPKDLMYSVNPTRVEDLNTFGP---KIAGMCRGIPT 145
DB 264 PQHTTTLSTLATPKRGNGNNGSEPSDV---IIPLRAD-SVFCPHYEKVSG-DYGHV 318
QY 146 YVAEELPGNPQ--LYSK 161
DB 319 YIVQEMP-POSPANIYYK 335



GenCore version 4.5
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OM protein - protein search, using SW model

Run on: September 4, 2002, 16:59:21 ; Search time 704.77 Seconds

(without alignments)
91.894 Million cell updates/sec

Title: US-09-821-726-16

Perfect score: 993
Sequence: 1 MKLTFVVGGLGLAAPGFA.....TADILILMSFGTSVETV 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Pending Patents_AA_Main:*

1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US083_COMB.pep.*
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25: /cgn2_6/ptodata/2/paa/US101_COMB.pep.*
26: /cgn2_6/ptodata/2/paa/US060_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	640	64.5	185	15	US-09-130-189-18
4	640	64.5	185	20	US-09-684-524-105
5	640	64.5	185	21	US-09-709-238-211
6	640	64.5	185	21	US-09-746-783-146
7	640	64.5	185	23	US-09-941-992-211

8	640	64.5	185	23	US-09-989-279-211	Sequence 211, App
9	640	64.5	185	23	US-09-989-293A-211	Sequence 211, App
10	640	64.5	185	23	US-09-989-721-211	Sequence 211, App
11	640	64.5	185	23	US-09-989-722-211	Sequence 211, App
12	640	64.5	185	23	US-09-989-723-211	Sequence 211, App
13	640	64.5	185	23	US-09-989-724-211	Sequence 211, App
14	640	64.5	185	23	US-09-989-725-211	Sequence 211, App
15	640	64.5	185	23	US-09-989-726-211	Sequence 211, App
16	640	64.5	185	23	US-09-989-727-211	Sequence 211, App
17	640	64.5	185	23	US-09-989-728-211	Sequence 211, App
18	640	64.5	185	23	US-09-989-729A-211	Sequence 211, App
19	640	64.5	185	23	US-09-989-730-211	Sequence 211, App
20	640	64.5	185	23	US-09-989-731-211	Sequence 211, App
21	640	64.5	185	23	US-09-989-732-211	Sequence 211, App
22	640	64.5	185	23	US-09-989-734-211	Sequence 211, App
23	640	64.5	185	23	US-09-989-735-211	Sequence 211, App
24	640	64.5	185	23	US-09-989-862-211	Sequence 211, App
25	640	64.5	185	23	US-09-990-427-211	Sequence 211, App
26	640	64.5	185	23	US-09-990-436-211	Sequence 211, App
27	640	64.5	185	23	US-09-990-442-211	Sequence 211, App
28	640	64.5	185	23	US-09-990-443-211	Sequence 211, App
29	640	64.5	185	23	US-09-990-444-211	Sequence 211, App
30	640	64.5	185	23	US-09-990-439-211	Sequence 211, App
31	640	64.5	185	23	US-09-990-440-211	Sequence 211, App
32	640	64.5	185	23	US-09-990-442-211	Sequence 211, App
33	640	64.5	185	23	US-09-990-443-211	Sequence 211, App
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35	640	64.5	185	23	US-09-990-456-211	Sequence 211, App
36	640	64.5	185	23	US-09-990-562-211	Sequence 211, App
37	640	64.5	185	23	US-09-990-711-211	Sequence 211, App
38	640	64.5	185	23	US-09-990-726-211	Sequence 211, App
39	640	64.5	185	23	US-09-991-073-211	Sequence 211, App
40	640	64.5	185	23	US-09-991-157-211	Sequence 211, App
41	640	64.5	185	23	US-09-991-163-211	Sequence 211, App
42	640	64.5	185	23	US-09-991-172-211	Sequence 211, App
43	640	64.5	185	23	US-09-991-181-211	Sequence 211, App
44	640	64.5	185	23	US-09-991-854-211	Sequence 211, App
45	640	64.5	185	23	US-09-992-521-211	Sequence 211, App

ALIGNMENTS

RESULT 1
US-09-821-726-16
Sequence 16, Application US/09821726
GENERAL INFORMATION:
APPLICANT: MARTIN, TERENCE E.
APPLICANT: TOBACK, F. GARY
APPLICANT: POWELL, C. THOMAS
APPLICANT: AGARWAL, KAN
TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
FILE REFERENCE: 21459/90913
CURRENT APPLICATION NUMBER: US/09/821,726
CURRENT FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 184
TYPE: PRT
ORGANISM: Mus sp.
US-09-821-726-16

Query Match 100.0%; Score 993; DB 22; Length 184;
Best Local Similarity 100.0%; Pred. No. 2, 2e-100;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MKLTFVVGGLGLAAPFAFATVNINGDGVDSGOOSVINGVHVNATIDNNNGDSW 60
OY 61 NSLWTEVSFAATVLFSSKSCIVHRNKKDAMPSLDDIDTVMKEQKGGKPGGAPPKDLMYS 120

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DB 61 NSIMDYENSAFATRLFSKSKSCIVHRMKNKDAMPSLDDLTMTVEQKGGAPPDLMIS 120
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DB 121 VNPTRVEDLNTGPKIAGMCRGIPITYVAEIPGNOPLYSKKCYADILMLIRMSFCGTS 180
      |||
QY 181 VETV 184
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DB 181 VETV 184

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RESULT 2
PCT-US98-16318-18
; Sequence 18, Application PC/TUS9816318
; GENERAL INFORMATION:
; APPLICANT: McCoy, John M.
; APPLICANT: McCoy, John M.
; APPLICANT: Lavalie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: G16051A
; CURRENT APPLICATION NUMBER: PCT/US98/16318
; CURRENT FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US98-16318-18

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Query Match 64.5%; Score 640; DB 1; Length 185;
Best Local Similarity 63.8%; Pred. No. 1,6e-61;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

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QY 1 MKLTMFVVGGLGLAAPGFA-YTVNINGNDGNDVSGQOQSVSINGVHNVANIDNNNGWDS 59
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DB 1 MKFTIVFAGLGLVFLAPALANYINVN-DDNNNAGSGQOQSVSVNNEHNVANVDNNNGWDS 59
      |||
QY 60 WNSLMDYENSAFATRLFSKSKSCIVHRMKNKDAMPSLDDLTMTVEQK--GKGGGAPPKDL 117
      |||
DB 60 WNSIMDYNGNGFAATRLFFQKTCIVHRMKNKEVMPISQSLDALVYKCKLOGKGGPPPKGL 119
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QY 118 MYSVNPTRVEDLNTGPKIAGMCRGIPITYVAEIPGNOPLYSKKCYADILMLIRMSFC 177
      |||
DB 120 MYSVNPKNKYVDLSKFGKNIANMCRGIPITYMAEEMQEASLFFSGCTTTSVLMIVDISFC 179
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QY 178 GTSVE 182
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DB 180 GDTVE 184

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RESULT 3
US-09-130-189-18
; Sequence 18, Application US/09130189
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavalie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.

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; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: G16051A
; CURRENT APPLICATION NUMBER: US/09/130,189
; CURRENT FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-130-189-18

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Query Match 64.5%; Score 640; DB 15; Length 185;
Best Local Similarity 63.8%; Pred. No. 1,6e-61;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

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QY 1 MKLTMFVVGGLGLAAPGFA-YTVNINGNDGNDVSGQOQSVSINGVHNVANIDNNNGWDS 59
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DB 60 WNSIMDYNGNGFAATRLFFQKTCIVHRMKNKEVMPISQSLDALVYKCKLOGKGGPPPKGL 119
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QY 118 MYSVNPTRVEDLNTGPKIAGMCRGIPITYVAEIPGNOPLYSKKCYADILMLIRMSFC 177
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DB 120 MYSVNPKNKYVDLSKFGKNIANMCRGIPITYMAEEMQEASLFFSGCTTTSVLMIVDISFC 179
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QY 178 GTSVE 182
      |||
DB 180 GDTVE 184

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RESULT 4
US-09-684-524-105
; Sequence 105, Application US/09684524
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/09/684,524
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-684-524-105

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DB 120 MTSVNPKNVDJLSKFGKNIANMCRGIPYMAEMQEASLFFYSTCTTSLMIVDISFC 179
QY 178 GSTVE 182
I : : :
DB 180 GDTE 184

RESULT 5
US-09-709-238-211
Sequence 211, Application US/09709238
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Yuan, Jean
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding the Same
FILE REFERENCE: P2730R1C1
CURRENT APPLICATION NUMBER: US/09/709,238
CURRENT FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: US 60/087,607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: US 60/087,609
PRIOR FILING DATE: 1998-06-02
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,021
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: US 60/091,982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: US 60/092,182
PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: US 60/092,472
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: US 60/093,339
PRIOR FILING DATE: 1998-07-20
PRIOR APPLICATION NUMBER: US 60/094,651
PRIOR FILING DATE: 1998-07-30

Query Match 64.5%; Score 640; DB 21; Length 185;
Best Local Similarity 63.8%; Pred. No. 1.6e-61;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

QY 1 MKLTFVVGILGLAEPFA-YTVNINNGDGVDSGGQSVSINGVHVANIDNNNGDS 59
DB 1 MKFTIVFAGLGVFLAPLANININ-NDDNNAGSGQSVSNNEHVANIDNNNGDS 59
QY 60 WNSLMDYENSFAATRLFSKSCIVHRMKNKDAMPISLDDITVYKBEK--GKGPAGAPPKDL 117

DB 60 WNSLMDYENSFAATRLFSKSCIVHRMKNKEVPSISLALVKEKKLGKGGPPPKDL 119
QY 118 MYSVNPTRVEDLNTFGKILAGKCRGPTTYAEELIPBNOPLYSKCYTDIILMISC 177
DB 120 MYSVNPTRVEDLNTFGKILAGKCRGPTTYAEELIPBNOPLYSKCYTDIILMISC 179
QY 178 GTSYE 182
DB 180 GDTVE 184

RESULT 6
US-09-746-783-146
Sequence 146, Application US/09746783
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
McCoy, John M.
LaValle, Edward R.
Racie, Lisa A.
Treacy, Maurice
Spaulding, Vikki
Agostino, Michael J.
Howes, Steven H.
Fechtel, Kim
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
ENCODING THEM
NUMBER OF SEQUENCES: 231
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/746,783
FILING DATE: 21-Dec-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Milasincic, Debra J.
REGISTRATION NUMBER: 46,931
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 742-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 146:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 146:
US-09-746-783-146

Query Match 64.5%; Score 640; DB 21; Length 185;
Best Local Similarity 63.8%; Pred. No. 1.6e-61;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

QY 1 MKLTFVVGILGLAEPFA-YTVNINNGDGVDSGGQSVSINGVHVANIDNNNGDS 59
DB 1 MKFTIVFAGLGVFLAPLANININ-NDDNNAGSGQSVSNNEHVANIDNNNGDS 59
QY 60 WNSLMDYENSFAATRLFSKSCIVHRMKNKDAMPISLDDITVYKBEK--GKGPAGAPPKDL 117
DB 60 WNSLMDYENSFAATRLFSKSCIVHRMKNKEVPSISLALVKEKKLGKGGPPPKDL 119

us-09-821-726-16.ram

Page 5

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RESULT 7
US-09-941-992-211
: Sequence 211, Application US/09941992
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gertlisen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Napier, Mary A.
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: TITLE OF INVENTION: Acids Encoding the Same
: FILE REFERENCE: P2730P1c1
: CURRENT APPLICATION NUMBER: US/09/941,992
: CURRENT FILING DATE: 2001-08-28
: PRIOR APPLICATION NUMBER: 60/049787
: PRIOR FILING DATE: 1997-06-16
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/065186
: PRIOR FILING DATE: 1997-11-12
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066770
: PRIOR FILING DATE: 1997-11-24
: PRIOR APPLICATION NUMBER: 60/075945
: PRIOR FILING DATE: 1998-02-25
: PRIOR APPLICATION NUMBER: 60/078910
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/083322
: PRIOR FILING DATE: 1998-04-28
: PRIOR APPLICATION NUMBER: 60/084600
: PRIOR FILING DATE: 1998-05-07
: PRIOR APPLICATION NUMBER: 60/087106
: PRIOR FILING DATE: 1998-05-28
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: PRIOR FILING DATE: 1998-06-02
: PRIOR APPLICATION NUMBER: 60/087609
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: PRIOR APPLICATION NUMBER: 60/088021
: PRIOR FILING DATE: 1998-06-04
: PRIOR APPLICATION NUMBER: 60/088025

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PRIOR FILING DATE: 1998-07-09
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Query Match 64.58; Score 640; DB 23; Length 185;
Best Local Similarity 63.88; Pred. No. 1; Ge-61;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

Oy 1 MKLMEVVGILGLAARPEA-YTVNINGNDGNGVSGOOSVINGVHNVANIDNNNGWDS 59
db 1 MKFTIVAGLGLVFLAPALANTNINVN-DDNNNGSGOOSVYVNEHNVANVDDNNNGWDS 59

Oy 60 WNSLMDYENSFAADRLFSKSCIVHRNKNKDAMPSLODLTMVKEQK--GKPGGAPPKDL 117
db 60 WNSLMDYGNFATRLFRQKTCIVHKNNKRYMPSISLDAIVKEKLLQKGGPGPPKDL 119
Oy 118 MYSVNPTRVEDLNTFGFKIAGMCRGIPTVYAEIIPGPNOLYSKKCYTADIIMILMMSQC 177
db 120 MYSVNPTRVEDLNTFGFKIAGMCRGIPTVYAEIIPGPNOLYSKKCYTADIIMILMMSQC 179
Oy 178 GTSYE 182
db 180 GDIVE 184

RESULT 8
US-09-989-279-211
Sequence 211, Application US/09989279
GENERAL INFORMATION:
APPLICANT: Askenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Collin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC56
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 2001-11-19
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02

Query Match	64.5%;	Score 640;	DB 23;	Length 185;
Best Local Similarity	63.8%;	Pred. No. 1.6e-61;		

PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
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PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182

PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: 60/092472
Query Match 64.5%; Score 640; DB 23; Length 185;
Best Local Similarity 63.8%; Pred. No. 1,6e-61;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;
QY 1 MKLMEFVGLGLAAGFA-YIVNINGNGNVDGSGQSVSINGVHNANIDNNNGWDS 59
Db 1 MKETIVFAGLGVFLAALANYNINVN-DDNNNAGSQQSVSNHNANVNNNGWDS 59
QY 60 WNSLMDYENSFAATRLFSKSCIVHRMKNKDAMPLODDITMVEOK--GKPGGAPPKDI 117
Db 60 WNSIMDYGNGFAATRLFPQKTCIVHKNNKVEPSIQSLDLYVEKKLQCKGPGGPPKGI 119
QY 118 MYSVNPTRVEDLNTFGKTIAGKMGCRGPTVVAEETPGBNOPLYSKKCYTADILILMSFC 177
Db 120 MYSVNPKNVDLSKFGKNIANMCRGIPTYVAEEMQEASLFFYSGTCYTTSVLMTVIDISFC 179
QY 178 GTSYE 182
Db 180 GDIVE 184

RESULT 10
US-09-989-721-211
Sequence 211, Application US/09989721
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerder, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC55
CURRENT APPLICATION NUMBER: US/09/989,721
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28

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Page 10

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71	PRIOR FILING DATE: 1998-07-02


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PRIOR FILING DATE: 1998-07-01
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: 60/092472

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Query Match          64.5%; Score 640; DB 23; Length 185;
Best Local Similarity 63.8%; Pred. No. 1,6e-61;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

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QY 1 MKLTMYVYGLGLIAPGFA-YVNVINGNDGNDVSGQGSYSVINGVHNVANDNNNGMDS 59
   1 MKFTVFAGLLGVFLAPALANNVNNV-DNNNAGSGQGSVSNNEHNVANDNNNGMDS 59
Db 1 WNSLMDYENSFAATRLFSKSCIVHRNNKDAMPLODLDTMYEOK--GKPGGAPPKDL 117
   60 WNSLMDYENSFAATRLFSKSCIVHRNNKDAMPLODLDTMYEOK--GKPGGAPPKDL 117
Db 60 WNSLMDYENSFAATRLFSKSCIVHRNNKDAMPLODLDTMYEOK--GKPGGAPPKDL 119
   60 WNSLMDYENSFAATRLFSKSCIVHRNNKDAMPLODLDTMYEOK--GKPGGAPPKDL 119
QY 118 MYSVNPTRVEDLNTFGPKIAGMCRGPTFYVAEIPGPNOLYKCCYTADILMLKMSFC 177
   120 MYSVNPTRVEDLNTFGPKIAGMCRGPTFYVAEIPGPNOLYKCCYTADILMLKMSFC 179
Db 120 MYSVNPTRVEDLNTFGPKIAGMCRGPTFYVAEIPGPNOLYKCCYTADILMLKMSFC 179
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QY 178 GTSYE 182
   180 GTSYE 184
Db 180 GTSYE 184

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RESULT 12
US-09-989-723-211
Sequence 211, Application US/09989723
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zhenli
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC62
CURRENT APPLICATION NUMBER: US/09/989,723
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1997-11-12

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28	PRIOR FILING DATE: 1998-06-04	28	PRIOR APPLICATION NUMBER: 60/090252
29	PRIOR APPLICATION NUMBER: 60/088028	29	PRIOR FILING DATE: 1998-06-22
30	PRIOR FILING DATE: 1998-06-04	30	PRIOR APPLICATION NUMBER: 60/090254
31	PRIOR APPLICATION NUMBER: 60/088029	31	PRIOR FILING DATE: 1998-06-22
32	PRIOR FILING DATE: 1998-06-04	32	PRIOR APPLICATION NUMBER: 60/090349
33	PRIOR APPLICATION NUMBER: 60/088030	33	PRIOR FILING DATE: 1998-06-23
34	PRIOR FILING DATE: 1998-06-04	34	PRIOR APPLICATION NUMBER: 60/090355
35	PRIOR APPLICATION NUMBER: 60/088033	35	PRIOR FILING DATE: 1998-06-23
36	PRIOR FILING DATE: 1998-06-04	36	PRIOR APPLICATION NUMBER: 60/090429
37	PRIOR APPLICATION NUMBER: 60/088326	37	PRIOR FILING DATE: 1998-06-24
38	PRIOR FILING DATE: 1998-06-04	38	PRIOR APPLICATION NUMBER: 60/090431
39	PRIOR APPLICATION NUMBER: 60/088167	39	PRIOR FILING DATE: 1998-06-24
40	PRIOR FILING DATE: 1998-06-05	40	PRIOR APPLICATION NUMBER: 60/090435
41	PRIOR APPLICATION NUMBER: 60/088202	41	PRIOR FILING DATE: 1998-06-24
42	PRIOR FILING DATE: 1998-06-05	42	PRIOR APPLICATION NUMBER: 60/090444
43	PRIOR APPLICATION NUMBER: 60/088212	43	PRIOR FILING DATE: 1998-06-24
44	PRIOR FILING DATE: 1998-06-05	44	PRIOR APPLICATION NUMBER: 60/090445
45	PRIOR APPLICATION NUMBER: 60/088217	45	PRIOR FILING DATE: 1998-06-24
46	PRIOR FILING DATE: 1998-06-05	46	PRIOR APPLICATION NUMBER: 60/090472
47	PRIOR APPLICATION NUMBER: 60/088655	47	PRIOR FILING DATE: 1998-06-24
48	PRIOR FILING DATE: 1998-06-09	48	PRIOR APPLICATION NUMBER: 60/090535
49	PRIOR APPLICATION NUMBER: 60/088734	49	PRIOR FILING DATE: 1998-06-24
50	PRIOR FILING DATE: 1998-06-10	50	PRIOR APPLICATION NUMBER: 60/090540
51	PRIOR APPLICATION NUMBER: 60/088738	51	PRIOR FILING DATE: 1998-06-24
52	PRIOR FILING DATE: 1998-06-10	52	PRIOR APPLICATION NUMBER: 60/090542
53	PRIOR APPLICATION NUMBER: 60/088742	53	PRIOR FILING DATE: 1998-06-24
54	PRIOR FILING DATE: 1998-06-10	54	PRIOR APPLICATION NUMBER: 60/090557
55	PRIOR APPLICATION NUMBER: 60/088810	55	PRIOR FILING DATE: 1998-06-24
56	PRIOR FILING DATE: 1998-06-10	56	PRIOR APPLICATION NUMBER: 60/090676
57	PRIOR APPLICATION NUMBER: 60/088824	57	PRIOR FILING DATE: 1998-06-25
58	PRIOR FILING DATE: 1998-06-10	58	PRIOR APPLICATION NUMBER: 60/090678
59	PRIOR APPLICATION NUMBER: 60/088826	59	PRIOR FILING DATE: 1998-06-25
60	PRIOR FILING DATE: 1998-06-10	60	PRIOR APPLICATION NUMBER: 60/090690
61	PRIOR APPLICATION NUMBER: 60/088858	61	PRIOR FILING DATE: 1998-06-25
62	PRIOR FILING DATE: 1998-06-11	62	PRIOR APPLICATION NUMBER: 60/090694
63	PRIOR APPLICATION NUMBER: 60/088861	63	PRIOR FILING DATE: 1998-06-25
64	PRIOR FILING DATE: 1998-06-11	64	PRIOR APPLICATION NUMBER: 60/090695
65	PRIOR APPLICATION NUMBER: 60/088876	65	PRIOR FILING DATE: 1998-06-25
66	PRIOR FILING DATE: 1998-06-11	66	PRIOR APPLICATION NUMBER: 60/090696
67	PRIOR APPLICATION NUMBER: 60/089105	67	PRIOR FILING DATE: 1998-06-25
68	PRIOR FILING DATE: 1998-06-12	68	PRIOR APPLICATION NUMBER: 60/090862
69	PRIOR APPLICATION NUMBER: 60/089440	6	

PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
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PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: 60/092472

Query Match 64.5% Score 640; DB 23: Length 185;
Best Local Similarity 63.8% Pred. No. 1,6e-61;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

QY 1 MLETFEYVGLGILAPGFA-YTVNINSGDGVDSGQSVSINGVHVANIDNNNGWDS 59
DB 1 MFTTFVAGLGVFLAPALANNINVN-DDNNNAGSGQSVSVNNEHVANNVNNNGWDS 59
QY 60 WNSLDYENSFAATRLFSKSCIVHRMKNKAMPISLQDIDTMKEOK--GKGGGAPPKDL 117
DB 60 WNSIMWYNGFAATRLFOKKTCTVHRMKNKEMPISIOSDALVKEKLGKGGGPPPGGL 119
QY 118 MYSVNTREDINTGKRGJAGMCRGIPYVAEIRPGNOLPFSKRCYATDILMIRMSFC 177
DB 120 MYSVNPKNVDLSKRGKNTIANNCRGIPYMAEDMGASLFFESGCTTSTVIMVIDISPC 179

QY 178 GTSVE 182
DB 180 GDTVE 184

RESULT 13
US-09-989-724-211
Sequence 211, Application US/09989724
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnuyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C67
CURRENT APPLICATION NUMBER: US/09/989,724
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12

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Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

Db 60 WNSIMDYGNGFAATRLFQKCTIVHKMKEVMPISQSLDALVKEKKLQGGKPGGPPKGL 119

20 120 MISVNPNAVDDLSKFGKNLANMCRGIPITYMAEEMQEASLFFYSGTCYTTSVLWIVDISFC 179

Db 180 GDIVE 184

US-09-989-725-211

; GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Desnoyers, Luc

APPLICANT: Ferrara, Napoleone

APPLICANT: Gerber, Hanspeter

APPLICANT: Goddard, Audrey

APPLICANT: Grimaldi, J. Chri

APPLICANT: Kljavin, Ivar J.

APPLICANT: Pan, James

APPLICANT: Roy, Margaret A

APPLICANT: Jumas, Daniel
: APPLICANT: Watanabe, Colin

APPLICANT: Williams, P. M1

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2730PIC71
 CURRENT APPLICATION NUMBER: US/09/989,725
 CURRENT FILING DATE: 2001-11-20
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/065186
 PRIOR FILING DATE: 1997-11-12
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066770
 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/075945
 PRIOR FILING DATE: 1998-02-25
 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/084600
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 PRIOR APPLICATION NUMBER: 60/087106
 PRIOR FILING DATE: 1998-05-28
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 PRIOR APPLICATION NUMBER: 60/087609
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 PRIOR APPLICATION NUMBER: 60/087759
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 PRIOR APPLICATION NUMBER: 60/087827
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 PRIOR APPLICATION NUMBER: 60/088021
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 PRIOR APPLICATION NUMBER: 60/088025
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088026
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088028
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088029
 PRIOR FILING DATE: 1998-06-04
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 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088033
 PRIOR FILING DATE: 1998-06-04
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 PRIOR APPLICATION NUMBER: 60/088167
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 PRIOR APPLICATION NUMBER: 60/088202
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088212
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088217
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088655
 PRIOR FILING DATE: 1998-06-09
 PRIOR APPLICATION NUMBER: 60/088734
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088738
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088742
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088810
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088824
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 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088858
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088861

PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088876
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/089105
 PRIOR FILING DATE: 1998-06-12
 PRIOR APPLICATION NUMBER: 60/089440
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 PRIOR APPLICATION NUMBER: 60/090254
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 PRIOR APPLICATION NUMBER: 60/090349
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 PRIOR APPLICATION NUMBER: 60/090429
 PRIOR FILING DATE: 1998-06-24
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 PRIOR APPLICATION NUMBER: 60/090435
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090444
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 PRIOR FILING DATE: 1998-06-24
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 PRIOR APPLICATION NUMBER: 60/090690
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090694
 PRIOR FILING DATE: 1998-06-25

;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090862
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
;; PRIOR APPLICATION NUMBER: 60/092472

Query Match 64.5%; Score 640; DB 23; Length 185;
Best Local Similarity 63.8%; Pred. No. 1.6e-61;

Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

QY 1 KKLMEVYGLGLAAGFA-YTVYVINGNDGNDGSGQSVSINGVHNVANIDNNNGMDS 59
Db 1 MKETIVEGGLGLVLAALANYNINNV-DNNNAGSGQSVSNNEHNVANVDNNNGMDS 59
QY 60 WNSLMDENSEFAATRLFSKSCSYHRNNKRAMSLDLDITMVEOK--CKGPGAPPKDL 117
Db 60 WNSLMDGNGFAATRLFSKSCSYHRNNKRAMSLDLDITMVEOK--CKGPGAPPKDL 119
QY 118 MYSVNPTRVEDLNTFGKTAGMCRGIPTYVAERIPGPNOPLYSKCYTADILMLMSFC 177
Db 120 MYSVNPKNVDLDLSEKFGKNIANMCRGIPTYVAERIPGPNOPLYSKCYTADILMLMSFC 179
QY 178 GTSYE 182
Db 180 GDTVE 184

RESULT 15

US-09-989-726-211

;; Sequence 211, Application US/09989726

;; GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gertsitsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel

;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730PIC60
;; CURRENT APPLICATION NUMBER: US/09/989,726
;; PRIOR FILING DATE: 2001-11-19
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/065186
;; PRIOR FILING DATE: 1997-11-12
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/066770
;; PRIOR FILING DATE: 1997-11-24
;; PRIOR APPLICATION NUMBER: 60/075945
;; PRIOR FILING DATE: 1998-02-25
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/087106
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;; PRIOR APPLICATION NUMBER: 60/087607
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087609
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;; PRIOR APPLICATION NUMBER: 60/087759
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087827
;; PRIOR FILING DATE: 1998-06-03
;; PRIOR APPLICATION NUMBER: 60/088021
;; PRIOR FILING DATE: 1998-06-04
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;; PRIOR APPLICATION NUMBER: 60/088026
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088028
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088029
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088030
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088033
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088326
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088167
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088202
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088212
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088217
;; PRIOR FILING DATE: 1998-06-05
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;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088810
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088824
;; PRIOR FILING DATE: 1998-06-10

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2	PRIOR FILING DATE: 1998-06-10
3	PRIOR APPLICATION NUMBER: 60/088588
4	PRIOR FILING DATE: 1998-06-11
5	PRIOR APPLICATION NUMBER: 60/088861
6	PRIOR FILING DATE: 1998-06-11
7	PRIOR APPLICATION NUMBER: 60/088876
8	PRIOR FILING DATE: 1998-06-11
9	PRIOR APPLICATION NUMBER: 60/089105
10	PRIOR FILING DATE: 1998-06-12
11	PRIOR APPLICATION NUMBER: 60/089440
12	PRIOR FILING DATE: 1998-06-16
13	PRIOR APPLICATION NUMBER: 60/089512
14	PRIOR FILING DATE: 1998-06-16
15	PRIOR APPLICATION NUMBER: 60/089514
16	PRIOR FILING DATE: 1998-06-16
17	PRIOR APPLICATION NUMBER: 60/089552
18	PRIOR FILING DATE: 1998-06-17
19	PRIOR APPLICATION NUMBER: 60/089538
20	PRIOR FILING DATE: 1998-06-17
21	PRIOR APPLICATION NUMBER: 60/089598
22	PRIOR FILING DATE: 1998-06-17
23	PRIOR APPLICATION NUMBER: 60/089599
24	PRIOR FILING DATE: 1998-06-17
25	PRIOR APPLICATION NUMBER: 60/089600
26	PRIOR FILING DATE: 1998-06-17
27	PRIOR APPLICATION NUMBER: 60/089653
28	PRIOR FILING DATE: 1998-06-17
29	PRIOR APPLICATION NUMBER: 60/089801
30	PRIOR FILING DATE: 1998-06-18
31	PRIOR APPLICATION NUMBER: 60/089907
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33	PRIOR APPLICATION NUMBER: 60/089908
34	PRIOR FILING DATE: 1998-06-18
35	PRIOR APPLICATION NUMBER: 60/089947
36	PRIOR FILING DATE: 1998-06-19
37	PRIOR APPLICATION NUMBER: 60/089948
38	PRIOR FILING DATE: 1998-06-19
39	PRIOR APPLICATION NUMBER: 60/089952
40	PRIOR FILING DATE: 1998-06-19
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44	PRIOR FILING DATE: 1998-06-22
45	PRIOR APPLICATION NUMBER: 60/090254
46	PRIOR FILING DATE: 1998-06-22
47	PRIOR APPLICATION NUMBER: 60/090349
48	PRIOR FILING DATE: 1998-06-23
49	PRIOR APPLICATION NUMBER: 60/090355
50	PRIOR FILING DATE: 1998-06-23
51	PRIOR APPLICATION NUMBER: 60/090429
52	PRIOR FILING DATE: 1998-06-24
53	PRIOR APPLICATION NUMBER: 60/090431
54	PRIOR FILING DATE: 1998-06-24
55	PRIOR APPLICATION NUMBER: 60/090435
56	PRIOR FILING DATE: 1998-06-24
57	PRIOR APPLICATION NUMBER: 60/090444
58	PRIOR FILING DATE: 1998-06-24
59	PRIOR APPLICATION NUMBER: 60/090445
60	PRIOR FILING DATE: 1998-06-24
61	PRIOR APPLICATION NUMBER: 60/090472
62	PRIOR FILING DATE: 1998-06-24
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66	PRIOR FILING DATE: 1998-06-24
67	PRIOR APPLICATION NUMBER: 60/090542
68	PRIOR FILING DATE: 1998-06-24
69	PRIOR APPLICATION NUMBER: 60/090557
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71	PRIOR APPLICATION NUMBER: 60/090676
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80	PRIOR FILING DATE: 1998-06-25
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86	PRIOR FILING DATE: 1998-06-25
87	PRIOR APPLICATION NUMBER: 60/090678
88	PRIOR FILING DATE: 1998-06-25
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91	PRIOR APPLICATION NUMBER: 60/090678
92	PRIOR FILING DATE: 1998-06-25
93	PRIOR APPLICATION NUMBER: 60/090678
94	PRIOR FILING DATE: 1998-06-25
95	PRIOR APPLICATION NUMBER: 60/090678
96	PRIOR FILING DATE: 1998-06-25
97	PRIOR APPLICATION NUMBER: 60/090678
98	PRIOR FILING DATE: 1998-06-25
99	PRIOR APPLICATION NUMBER: 60/090678
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1 PRIOR FILING DATE: 1998-06-25
2 PRIOR APPLICATION NUMBER: 60/090690
3 PRIOR FILING DATE: 1998-06-25
4 PRIOR APPLICATION NUMBER: 60/090694
5 PRIOR FILING DATE: 1998-06-25
6 PRIOR APPLICATION NUMBER: 60/090695
7 PRIOR FILING DATE: 1998-06-25
8 PRIOR APPLICATION NUMBER: 60/090696
9 PRIOR APPLICATION NUMBER: 60/090696
10 PRIOR FILING DATE: 1998-06-25
11 PRIOR APPLICATION NUMBER: 60/090682
12 PRIOR FILING DATE: 1998-06-26
13 PRIOR APPLICATION NUMBER: 60/090683
14 PRIOR FILING DATE: 1998-06-26
15 PRIOR APPLICATION NUMBER: 60/091360
16 PRIOR APPLICATION NUMBER: 60/091478
17 PRIOR FILING DATE: 1998-07-01
18 PRIOR APPLICATION NUMBER: 60/091544
19 PRIOR FILING DATE: 1998-07-01
20 PRIOR APPLICATION NUMBER: 60/091519
21 PRIOR FILING DATE: 1998-07-02
22 PRIOR APPLICATION NUMBER: 60/091626
23 PRIOR FILING DATE: 1998-07-02
24 PRIOR APPLICATION NUMBER: 60/091633
25 PRIOR FILING DATE: 1998-07-02
26 PRIOR APPLICATION NUMBER: 60/091978
27 PRIOR FILING DATE: 1998-07-07
28 PRIOR APPLICATION NUMBER: 60/091984
29 PRIOR FILING DATE: 1998-07-07
30 PRIOR APPLICATION NUMBER: 60/092182
31 PRIOR FILING DATE: 1998-07-09
32 PRIOR APPLICATION NUMBER: 60/092472

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Query Match	64.58;	Score 640;	DB 23;	Length 185;
Best Local Similarity	63.88;	Pred. No. 1.6e-61;		
Matches 118;	Conservative 24;	Mismatches 39;	Indels 4;	Gaps 3

[illegible]

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Search completed: September 4, 2002, 16:59:21
Job time: 1042 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2002, 17:04:24 ; Search time 166.13 Seconds
(Without alignments)
272.394 Million cell updates/sec

Title: US-09-821-726-16

Perfect score: 993

Sequence: 1 MKLTMFVGLGLAAGFA.....TADILILMSFGCTSVETY 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 76338 seqs, 245939087 residues

Total number of hits satisfying chosen parameters: 76338

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_AA_New.*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	640	64.5	185	5	US-09-991-150-211
2	640	64.5	185	5	US-09-720-533-49
3	640	64.5	185	6	US-10-119-480-148
4	640	64.5	185	6	US-10-216-159A-148
5	640	64.5	185	6	US-10-216-162-148
6	640	64.5	185	6	US-10-216-163-148
7	640	64.5	185	6	US-10-216-164-148
8	640	64.5	185	6	US-10-216-165-148
9	640	64.5	185	6	US-10-216-166-148
10	640	64.5	185	6	US-10-216-167-148
11	640	64.5	185	6	US-10-216-168-148
12	640	64.5	185	6	US-10-216-160-148
13	640	64.5	185	6	US-10-218-849-148
14	640	64.5	185	6	US-10-218-930-148
15	640	64.5	185	6	US-10-219-003-148
16	640	64.5	185	6	US-10-218-612-148
17	640	64.5	185	6	US-10-218-956-148
18	640	64.5	185	6	US-10-219-010-148
19	640	64.5	185	6	US-10-218-765-148
20	640	64.5	185	6	US-10-218-784-148
21	640	64.5	185	6	US-10-219-061-148
22	640	64.5	185	6	US-10-219-062-148
23	640	64.5	185	6	US-10-219-063-148
24	640	64.5	185	6	US-10-219-064-148
25	640	64.5	185	6	US-10-219-065-148
26	640	64.5	185	6	US-10-219-066-148

27	640	64.5	185	6	US-10-219-070-148	Sequence 148, App
28	640	64.5	185	6	US-10-219-071-148	Sequence 148, App
29	640	64.5	185	6	US-10-219-072-148	Sequence 148, App
30	640	64.5	185	6	US-10-219-073-148	Sequence 148, App
31	640	64.5	185	6	US-10-219-074-148	Sequence 148, App
32	640	64.5	185	6	US-10-219-075-148	Sequence 148, App
33	640	64.5	185	6	US-10-219-077-148	Sequence 148, App
34	640	64.5	185	6	US-10-219-464-148	Sequence 148, App
35	640	64.5	185	6	US-10-219-465-148	Sequence 148, App
36	640	64.5	185	6	US-10-219-466-148	Sequence 148, App
37	640	64.5	185	6	US-10-219-467-148	Sequence 148, App
38	640	64.5	185	6	US-10-219-470-148	Sequence 148, App
39	640	64.5	185	6	US-10-219-471-148	Sequence 148, App
40	640	64.5	185	6	US-10-219-474-148	Sequence 148, App
41	640	64.5	185	6	US-10-219-475-148	Sequence 148, App
42	640	64.5	185	6	US-10-219-476-148	Sequence 148, App
43	640	64.5	185	6	US-10-219-478-148	Sequence 148, App
44	640	64.5	185	6	US-10-219-479-148	Sequence 148, App
45	640	64.5	185	6	US-10-219-480-148	Sequence 148, App

ALIGNMENTS

RESULT 1
US-09-991-150-211

Sequence 211, Application US/09991150

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Matanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PLC48
CURRENT APPLICATION NUMBER: US/09/991,150
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 532
SEQ ID NO 211
LENGTH: 185
TYPE: PRT
ORGANISM: Homo sapiens
US-09-991-150-211

Query Match 64.5%; Score 640; DB 5; Length 185;

Best Local Similarity 63.8%; Pred. No. 6,8e-60;

Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

DB 1 MKLTMFVGLGLAAGFA-VTVNINGNDDGVSQGSISNGVHRVYANIDNNNGDS 59
1 MKTTFVAGLGLFALPALANTINVN-DDNNNGSGQGSVYNNEHNVANVDNNGMDS 59

```

OY 60 WNSLWDYENSEFAATRLFSKSCIVHRMKNKDAMPSLDLDITMVEOK--GKGPGGAPPKDL 117
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 WNSLWDYNGNGAATRLFPKCTCIYHKMKKEVMPISLOSLDLVKEKKLOGKPGGPPPKGL 119
OY 118 MYSVNPTRVEDLNTFGPKIAGMCRGIPTYAAEEIPGPNQPLYSKKCTADILMILRMSFC 177
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 MYSVNPKNVDLSKFGKNIAMNCRGIPTYAAEEMOEASLFFYSCTCYTTSVLMIVDISFC 179
OY 178 GTSVE 182
    |:||
Db 180 GDIVE 184

```

```

RESULT 2
US-09-720-533-49
; Sequence 49, Application US/09720533
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: LAL, Preeti
; APPLICANT: TANG, Y. Tom
; APPLICANT: GORGONE, Gina A.
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AKERBLUM, Ingrid E.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: YUE, Henry
; APPLICANT: PATTERSON, Chandra
; APPLICANT: REDDY, Roopa
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: BANDMAN, Olga
; TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
; FILE REFERENCE: Pf-0541 PCT
; CURRENT APPLICATION NUMBER: US/09/720,533
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/090,762; 60/094,983; 60/102,686; 60/112,129
; PRIOR FILING DATE: 1998-06-26; 1998-07-31; 1998-10-01; 1998-12-11
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PERL Program
; SEQ ID NO 49
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte Clone No: 2593853
US-09-720-533-49

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Query Match 64.5%; Score 640; DB 5; Length 185;
Best Local Similarity 63.8%; Pred. No. 6, 8e-60;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

OY 1 MKLTMEVYGLGLAAGFA-YTVNINNGDNGVDSGQOSVSYNGVHNANIDNNNGMS 59
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MKFTIVAGLGLVLAAPALANYNINVN-DDNNNAGSGQOSVSYNNHNANVDNNNGMS 59
OY 60 WNSLWDYENSEFAATRLFSKSCIVHRMKNKDAMPSLDLDITMVEOK--GKGPGGAPPKDL 117
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 WNSLWDYNGNGAATRLFPKCTCIYHKMKKEVMPISLOSLDLVKEKKLOGKPGGPPPKGL 119
OY 118 MYSVNPTRVEDLNTFGPKIAGMCRGIPTYAAEEIPGPNQPLYSKKCTADILMILRMSFC 177
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 MYSVNPKNVDLSKFGKNIAMNCRGIPTYAAEEMOEASLFFYSCTCYTTSVLMIVDISFC 179
OY 178 GTSVE 182
    |:||
Db 180 GDIVE 184

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RESULT 3
US-10-119-480-148

```

; Sequence 148, Application US/10119480
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C1
; CURRENT APPLICATION NUMBER: US/10/119,480
; CURRENT FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 246
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-119-480-148

```

```

Query Match 64.5%; Score 640; DB 6; Length 185;
Best Local Similarity 63.8%; Pred. No. 6, 8e-60;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

OY 1 MKLTMEVYGLGLAAGFA-YTVNINNGDNGVDSGQOSVSYNGVHNANIDNNNGMS 59
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MKFTIVAGLGLVLAAPALANYNINVN-DDNNNAGSGQOSVSYNNHNANVDNNNGMS 59
OY 60 WNSLWDYENSEFAATRLFSKSCIVHRMKNKDAMPSLDLDITMVEOK--GKGPGGAPPKDL 117
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 WNSLWDYNGNGAATRLFPKCTCIYHKMKKEVMPISLOSLDLVKEKKLOGKPGGPPPKGL 119
OY 118 MYSVNPTRVEDLNTFGPKIAGMCRGIPTYAAEEIPGPNQPLYSKKCTADILMILRMSFC 177
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 MYSVNPKNVDLSKFGKNIAMNCRGIPTYAAEEMOEASLFFYSCTCYTTSVLMIVDISFC 179
OY 178 GTSVE 182
    |:||
Db 180 GDIVE 184

```

```

RESULT 4
US-10-216-159A-148
; Sequence 148, Application US/10216159A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C6
; CURRENT APPLICATION NUMBER: US/10/216,159A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17

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; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-159A-148
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Query Match
Best Local Similarity 64.5%; Score 640; DB 6; Length 185;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

Qy 1 MKLIMFVYGLGLAARGFA-YTYININGNDGNDVSGQOSVSINGVHNYANDNNNGWDS 59
Db 1 MKFTIVAGLLGVLAALANYNINVA-DDNNNAGSQOSVSYNNEHNYANDNNNGWDS 59
Qy 60 WNSLMDYENSFATRLFSKSCIVHRNKKDAMPSTLDDLTMYEOK--GKGFGAPPKDL 117
Db 60 WNSLMDYENSFATRLFSKSCIVHRNKKDAMPSTLDDLTMYEOK--GKGFGAPPKDL 117
Qy 60 WNSLMDYENSFATRLFSKSCIVHRNKKDAMPSTLDDLTMYEOK--GKGFGAPPKDL 117
Db 60 WNSLMDYENSFATRLFSKSCIVHRNKKDAMPSTLDDLTMYEOK--GKGFGAPPKDL 117
Qy 118 MYSVNPFRVDELNTEGKTIAGMCRGIPYVAEIPGPNOPLYSKCYTADIIILMSFC 177
Db 120 MYSVNPFRVDELNTEGKTIAGMCRGIPYVAEIPGPNOPLYSKCYTADIIILMSFC 177
Qy 178 GTSYE 182
Db 180 GDIVE 184
```

```
RESULT 5
US-10-216-162-148
; Sequence 148, Application US/10216162
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Geritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC2
; CURRENT APPLICATION NUMBER: US/10/216,162
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
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; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-162-148
```

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Query Match
Best Local Similarity 64.5%; Score 640; DB 6; Length 185;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

Qy 1 MKLIMFVYGLGLAARGFA-YTYININGNDGNDVSGQOSVSINGVHNYANDNNNGWDS 59
Db 1 MKFTIVAGLLGVLAALANYNINVA-DDNNNAGSQOSVSYNNEHNYANDNNNGWDS 59
Qy 60 WNSLMDYENSFATRLFSKSCIVHRNKKDAMPSTLDDLTMYEOK--GKGFGAPPKDL 117
Db 60 WNSLMDYENSFATRLFSKSCIVHRNKKDAMPSTLDDLTMYEOK--GKGFGAPPKDL 117
Qy 60 WNSLMDYENSFATRLFSKSCIVHRNKKDAMPSTLDDLTMYEOK--GKGFGAPPKDL 117
Db 60 WNSLMDYENSFATRLFSKSCIVHRNKKDAMPSTLDDLTMYEOK--GKGFGAPPKDL 117
Qy 118 MYSVNPFRVDELNTEGKTIAGMCRGIPYVAEIPGPNOPLYSKCYTADIIILMSFC 177
Db 120 MYSVNPFRVDELNTEGKTIAGMCRGIPYVAEIPGPNOPLYSKCYTADIIILMSFC 177
Qy 178 GTSYE 182
Db 180 GDIVE 184
```

```
RESULT 6
US-10-216-163-148
; Sequence 148, Application US/10216163
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Geritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC3
; CURRENT APPLICATION NUMBER: US/10/216,163
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
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PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 148
LENGTH: 185
TYPE: PRT
ORGANISM: Homo Sapien
US-10-216-163-148

Query Match 64.5%; Score 640; DB 6; Length 185;
Best Local Similarity 63.8%; Pred. No. 6.8e-60;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

OY 1 MKLTFVVGILGLAAGFA-YTVNINGDGNVDGSGQGSVSYNGVHVNANIDNNNGWDS 59
1 MKTTFVAGLGLVFLPALANYNINVN-DNNNAGSGQGSVSNNEHNVANVDNNNGWDS 59
DB 60 WNSLMDYENSFATRFLEKSKSCIVHRNKKDAMPISLQDIDTWYKQK--GKGGGAPPKDL 117
118 MYSVNPTRVEDLNTFGPKTAGMCRGIPTYVAEIPGPNQPLYSKCYTADILMLRMSFC 177
OY 118 MYSVNPTRVEDLNTFGPKTAGMCRGIPTYVAEIPGPNQPLYSKCYTADILMLRMSFC 177
DB 120 MYSVNPKNVDLSKFGKNIANMCRGIPTYMAEMQASLFFSGCYTTSVLMIVDISFC 179
OY 178 GTSVE 182
1 : : :
DB 180 GDTVE 184

RESULT 7
US-10-216-164-148
Sequence 148, Application US/10216164
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PIC5
CURRENT APPLICATION NUMBER: US/10/216,164
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294

PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 148
LENGTH: 185
TYPE: PRT
ORGANISM: Homo Sapien
US-10-216-164-148

Query Match 64.5%; Score 640; DB 6; Length 185;
Best Local Similarity 63.8%; Pred. No. 6.8e-60;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

OY 1 MKLTFVVGILGLAAGFA-YTVNINGDGNVDGSGQGSVSYNGVHVNANIDNNNGWDS 59
1 MKTTFVAGLGLVFLPALANYNINVN-DNNNAGSGQGSVSNNEHNVANVDNNNGWDS 59
DB 60 WNSLMDYENSFATRFLEKSKSCIVHRNKKDAMPISLQDIDTWYKQK--GKGGGAPPKDL 117
118 MYSVNPTRVEDLNTFGPKTAGMCRGIPTYVAEIPGPNQPLYSKCYTADILMLRMSFC 177
OY 118 MYSVNPTRVEDLNTFGPKTAGMCRGIPTYVAEIPGPNQPLYSKCYTADILMLRMSFC 177
DB 120 MYSVNPKNVDLSKFGKNIANMCRGIPTYMAEMQASLFFSGCYTTSVLMIVDISFC 179
OY 178 GTSVE 182
1 : : :
DB 180 GDTVE 184

RESULT 8
US-10-216-165-148
Sequence 148, Application US/10216165
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PIC7
CURRENT APPLICATION NUMBER: US/10/216,165
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26

```

? Sequence 148, Application US/10216167
? GENERAL INFORMATION:
? APPLICANT: Baker, Kevin P.
? APPLICANT: Desnoyers, Luc
? APPLICANT: Gerltsen, Mary
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Grimaldi, J. Christopher
? APPLICANT: Gurney, Austin L.
? APPLICANT: Smith, Victoria
? APPLICANT: Stephan, Jean-Philippe F.
? APPLICANT: Watanabe, Colin L.
? APPLICANT: Wood, William I.
? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
? FILE OF INVENTION: ACIDS ENCODING THE SAME
? FILE REFERENCE: P3530P1C4
? CURRENT APPLICATION NUMBER: US/10/216,167
? PRIOR FILING DATE: 2002-08-09
? PRIOR FILING DATE: 2002-04-09
? PRIOR APPLICATION NUMBER: 60/059113
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/062287
? PRIOR FILING DATE: 1997-10-17
? PRIOR APPLICATION NUMBER: 60/063549
? PRIOR FILING DATE: 1997-10-28
? PRIOR APPLICATION NUMBER: 60/064103
? PRIOR FILING DATE: 1997-10-31
? PRIOR APPLICATION NUMBER: 60/069873
? PRIOR FILING DATE: 1997-12-17
? PRIOR APPLICATION NUMBER: 60/078910
? PRIOR FILING DATE: 1998-03-20
? PRIOR APPLICATION NUMBER: 60/079294
? PRIOR FILING DATE: 1998-03-25
? PRIOR APPLICATION NUMBER: 60/079656
? PRIOR FILING DATE: 1998-03-26
? PRIOR APPLICATION NUMBER: 60/079728
? PRIOR FILING DATE: 1998-03-27
? Remaining Prior Application data removed - See File Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 246
? SEQ ID NO 148
? LENGTH: 185

```

```

; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-167-148

```

Query Match	64.5%	Score 640;	DB 6;	Length 185;
Best Local Similarity	63.8%;	Pred. No. 6.8e-60;		
Matches 118; Conservative	24;	Mismatches 39;	Indels 4;	Gaps 3

[illegible]

RESULT 11
US-10-216-168-148

; Sequence 148, Application US/10216168
; GENERAL INFORMATION:
;

Query Match	64.5%	Score 640;	DB 6;	Length 185;
Best Local Similarity	63.8%	Pred. No. 6.8e-60;		
Matches 118;	Conservative 24;	Mismatches 39;	Indels 4;	Gaps 3;

[illegible]

RESULT 12
US-10-216-160-148
: Sequence 148, Application US/10216160

GENERAL INFORMATION:

Query Match	64.5%;	Score 640;	DB 6;	Length 185;
Best Local Similarity	63.8%;	Pred. No. 6.8e-60;		
Matches 118; Conservative	24;	Mismatches 39;	Indels 4;	Gaps 3

QY	1	MKLTFYVGLGLLAAGFA-YYTNINGNDGNDGSGQSVSLNGVNNANIDNNMGDS	59
	1		
Db	1	MKFTVFAGLGVFLAALANYNTNV-DQNNNAGSGQSVYNNENNVANVDNNMGDS	59
	1		
QY	60	WNSLWDYENSEFATRLFSKSCIVHRNNKDKAMPDLQDITWKEQK--GKPGGAPPKDL	117
	60		
Db	60	WNSLTDYDNGGTAALRLQKTCIYHNNKKEMVPSIQSLDALVYKEKKIQGKGPGGAPPKGL	119
	60		
QY	118	MYSNVPFVEDLNTFGKRIAGCMGCIPIYYAAELPGNQPILYSKKCYADIIWILRSFC	177
	118		
Db	120	MYSNVPKNVDDLSTFGKRIANMCGIPIYYAAEOMEASLEFYSCTYTSVLMIWIDISFC	179
	120		
QY	178	GSFVE	182
	178		
Db	180	GVTFE	184
	180		

```

; LENGTH: 185
; TYPE: PRF
; ORGANISM: Homo Sapien
us-10-218-930-148

Query Match
Best Local Similarity      64.5%; Score 640; DB 6; Length 185;
                           63.8%; Pred.No. 6,8e-6;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

QY    1 MKLTFFVGVGLGTLAAGFA--YTVINNGNDGNVDVGSGQOVSINGVNHNVIDNNMGDS 59
      | | :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1 MKFTTFVGGLLIGVLAPLALANTNIVN--DDNNNGSGQOVSYNHNEHVANVDNNMGDS 59

QY    60 WNSLMDYDNSPAATRLRFESKSCSIVHRNRKDAMPISLDIDTWVKDOK--GKGPGCAPPKDL 117
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    60 WNSIIDYNGGFAAATRLRFQKKTCIVHKMK EVMPSIQSLDALYRKXKLQGGKPGCPPKGL 119

QY    118 MSYVAHPFEVELNTFGPRTIACMGRGIPITYVAELTIGNOPLYSKCKCTADILMLTRMSFC 177
       |||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    120 MSYVAHPNVDDLSTFKGKIANKMGRIPTYAEEHQEASLEFFYSQTCTYSTVLMIWDISFC 179

QY    178 GTSYVE 182
       | : | |
Db    180 GDIVE 184
```

```

RESULT 15
US-10-219-003-148
: Sequence 148: Application US/10219003
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Desnoyers, Luc
: APPLICANT: Geriltsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Smith, Victoria
: APPLICANT: Stephan, Jean-Philippe F.
: APPLICANT: Watanabe, Colin L.
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3530P1C12
: CURRENT APPLICATION NUMBER: US/10/219,003
: CURRENT FILING DATE: 2002-08-12

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1 PRIOR APPLICATION NUMBER: 60/059113
 2 PRIOR FILING DATE: 1997-09-17
 3 PRIOR APPLICATION NUMBER: 60/062287
 4 PRIOR FILING DATE: 1997-10-17
 5 PRIOR APPLICATION NUMBER: 60/063549
 6 PRIOR FILING DATE: 1997-10-28
 7 PRIOR APPLICATION NUMBER: 60/064103
 8 PRIOR FILING DATE: 1997-10-31
 9 PRIOR APPLICATION NUMBER: 60/069873
 10 PRIOR FILING DATE: 1997-12-17
 11 PRIOR APPLICATION NUMBER: 60/078910
 12 PRIOR FILING DATE: 1998-03-20
 13 PRIOR APPLICATION NUMBER: 60/079294
 14 PRIOR FILING DATE: 1998-03-25
 15 PRIOR APPLICATION NUMBER: 60/079656
 16 PRIOR FILING DATE: 1998-03-26
 17 PRIOR APPLICATION NUMBER: 60/079728
 18 PRIOR FILING DATE: 1998-03-27
 19 PRIOR APPLICATION NUMBER: 60/081819
 20 PRIOR FILING DATE: 1998-04-15
 21 PRIOR APPLICATION NUMBER: 60/081955
 22 PRIOR FILING DATE: 1998-04-15
 23 PRIOR APPLICATION NUMBER: 60/082804

Thu Sep 5 11:23:30 2002

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Page 8

PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
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PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/089532
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PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089905
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090691
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/095302
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095318
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095916
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/096146
PRIOR FILING DATE: 1998-08-11
PRIOR APPLICATION NUMBER: 60/096791
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PRIOR FILING DATE: 1998-08-26
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PRIOR FILING DATE: 1998-08-31
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PRIOR FILING DATE: 1998-09-09
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PRIOR FILING DATE: 1998-09-10
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PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100038
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 60/100385
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100390
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100627
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100848
PRIOR FILING DATE: 1998-09-18
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PRIOR FILING DATE: 1998-09-17
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PRIOR APPLICATION NUMBER: 60/101786
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PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101922

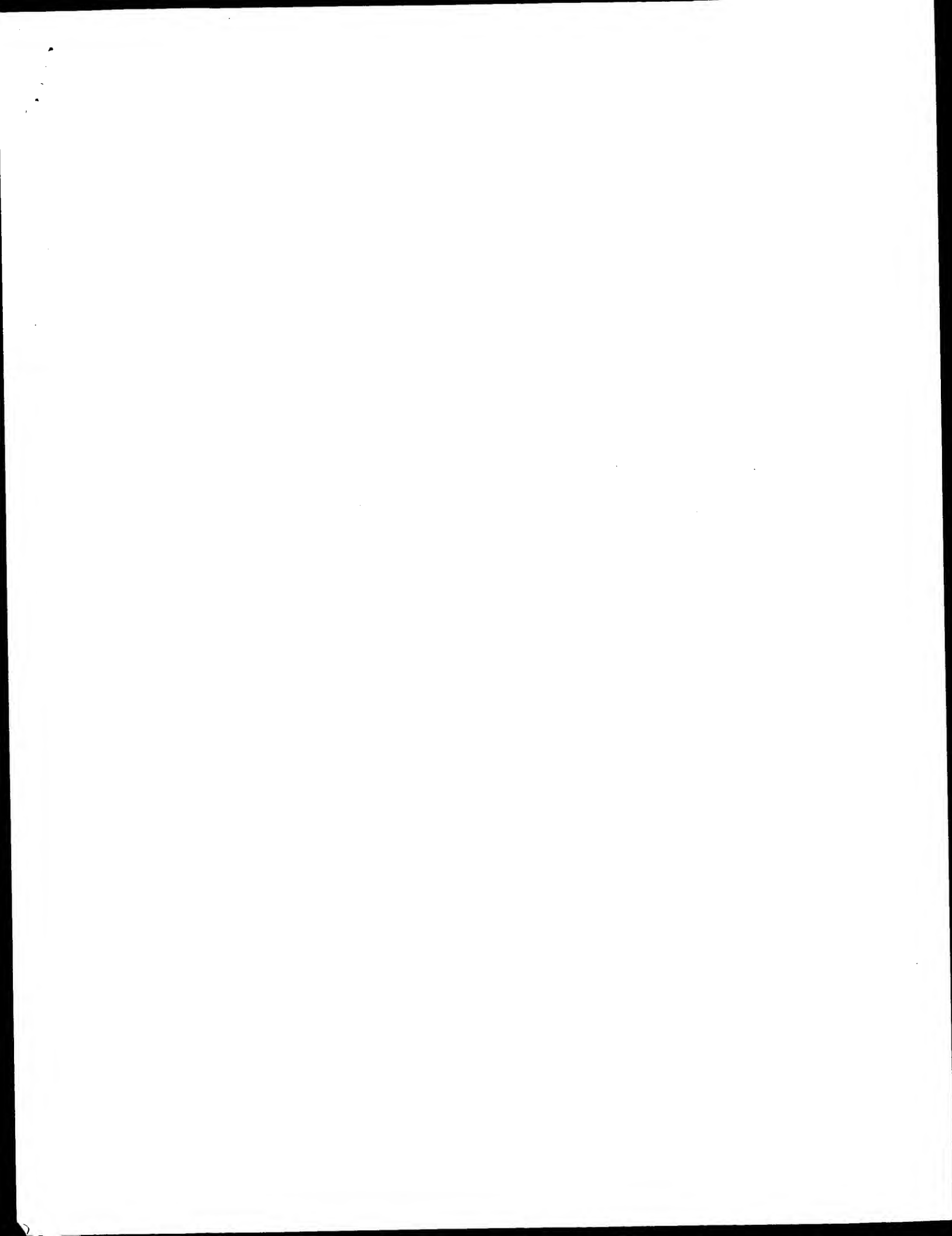
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PRIOR FILING DATE: 1998-12-22
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PRIOR FILING DATE: 1998-12-23
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PRIOR APPLICATION NUMBER: 60/119549
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PRIOR APPLICATION NUMBER: 60/123618
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/125259
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 60/125775
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/126773
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: 60/127887
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 60/130232
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131022
PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: 60/131270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131291
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131445
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PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/140650
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/140723
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146963
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/149320
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149638
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/151733
PRIOR FILING DATE: 1999-08-31

; PRIOR APPLICATION NUMBER: 60/164418
 ; PRIOR FILING DATE: 1999-11-09
 ; PRIOR APPLICATION NUMBER: 60/166361
 ; PRIOR FILING DATE: 1999-11-16
 ; PRIOR APPLICATION NUMBER: 60/169445
 ; PRIOR FILING DATE: 1999-12-07
 ; PRIOR APPLICATION NUMBER: 60/169495
 ; PRIOR FILING DATE: 1999-12-07
 ; PRIOR APPLICATION NUMBER: 60/169835
 ; PRIOR FILING DATE: 1999-12-07

Query Match 64.5%; Score 640; DB 6; Length 185;
 Best Local Similarity 63.8%; Pred. No. 6.8e-60;
 Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

QY 1 MKLTFFVYVGLGLAAGFA-YTVNINNGDNGVSGQSYSLNGVHNVANIDNNNGWDS 59
 Db 1 MKFTTFVAGLLGVFLAPALANTNINVN-DDNNNAGSGQSYSVNNEHNVANVDNNNGWDS 59
 QY 60 WNSLMDYENSFAATRLFSKSCIVHRMKNKDAMPSLQDLDITMVEOK--GKPGGAPPKDL 117
 Db 60 WNSLMDYENGFAATRLFSKSCIVHRMKNKEVMPISQSLDALVKEKKLQGGKPGGAPPKGL 119
 QY 118 MYSVNPPTVEDLNTFGKRIAGMCRGIPTYVAEITPGNPPLYSKKCYTADILWILMSFC 177
 Db 120 MYSVNPKNVDDLKSKFGKNIANMCRGIPTYMAEEMOEFASLFFYSGTCYTTSTVLWIVDISFC 179
 QY 178 GTSVE 182
 Db 180 GDTVE 184

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 Job time: 1155 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:47:37 ; Search time 75.48 Seconds
(Without alignments) 234.240 Million cell updates/sec

Title: US-09-821-726-16

Perfect score: 993

Sequence: 1 MKLTFVVGGLGLAAGFA.....TADILMLRMSFGTSVETY 184

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	DB ID	Description
1	89	9.0	345	2	148780
2	88.5	8.9	842	2	T16198
3	86.5	8.7	658	2	T41309
4	85.5	8.6	335	2	JT0569
5	85.5	8.6	346	2	S46993
6	85.5	8.6	539	2	AF0998
7	85	8.6	345	2	158406
8	84	8.5	643	2	S17997
9	83.5	8.4	782	2	S27833
10	81	8.2	617	2	H90551
11	80.5	8.1	728	2	T25478
12	80.5	8.1	728	2	S71467
13	80.5	8.1	2295	2	H71621
14	80	8.1	3194	2	D71917
15	79.5	8.0	539	2	AC0017
16	79.5	8.0	1215	2	T43916
17	79	8.0	186	2	T30918
18	79	8.0	336	2	T49766
19	78	8.0	338	2	T38170
20	78	7.9	362	2	T49528
21	78	7.9	642	2	G88087
22	77.5	7.8	407	2	S49890
23	77.5	7.8	419	2	T18420
24	77.5	7.8	459	2	T45911
25	77.5	7.8	1109	2	G75134
26	77	7.8	363	2	S75238
27	76.5	7.7	194	2	S52335
28	76.5	7.7	493	1	JH0158
29	76.5	7.7	504	2	S56745

30	76	7.7	631	2	T07670	probable protein k
31	76	7.7	1278	2	A71609	probable secreted
32	75.5	7.6	194	2	S41761	cysteine-rich prot
33	75.5	7.6	397	2	S64841	hypothetical prote
34	75.5	7.6	421	2	E64819	Yb10 protein - Esc
35	75.5	7.6	421	2	E90741	hypothetical prote
36	75.5	7.6	421	2	E85591	hypothetical prote
37	75	7.6	331	2	AG2679	conserved hypothet
38	75	7.6	352	2	E97461	hypothetical prote
39	75	7.6	423	2	T51794	MYB DNA-binding-l
40	74.5	7.5	404	2	S50648	hypothetical prote
41	74.5	7.5	624	2	B82108	flagellar hook-ass
42	74.5	7.5	747	2	S46608	YTA11 protein - ye
43	74.5	7.5	1045	2	S23570	pol polyprotein ho
44	74.5	7.5	1362	2	A75207	amylopolylalanase P
45	74	7.5	241	2	S71473	endo-1,4-beta-xy

ALIGNMENTS

RESULT 1
148780
Stral/Epig2 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: 148780; A55507; A55062; S52670
R:Bouillet, P.; Ouled-Abdelghani, M.; Vicaire, S.; Garnier, J.M.; Schunbaur, B.; Doll
Dev. Biol. 170, 420-433, 1995
A:Title: Efficient cloning of cDNAs of retinoic acid-responsive genes in P19 embryona
A:Reference number: 148780; MID:95377533
A:Accession: 148780
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-345 <RES>
A:Cross-references: EMBL:148781; NID:9747858; PIDN:CAA8695.1; PID:9747859
R:Fletcher, F.A.; Renshaw, B.; Hollingsworth, T.; Baum, P.; Lyman, S.D.; Jenkins, N.A
Genomics 24, 127-132, 1994
A:Title: Genomic organization and chromosomal localization of mouse Epig2, a gene enc
A:Reference number: A55507; MID:95203867
A:Accession: A55507
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-345 <FLR>
A:Cross-references: GB:U07598
R:Shao, H.; Lou, L.; Pandey, A.; Pasquale, E.B.; Dixit, V.M.
J. Biol. Chem. 269, 26606-26609, 1994
A:Title: cDNA cloning and characterization of a ligand for the Cdk5 receptor protein-
A:Reference number: A55062; MID:95014510
A:Accession: A55062
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-89, 91-345 <SHA>
A:Cross-references: GB:U12983; NID:9575928; PIDN:AAA3231.1; PID:9575929
C:Genetics:
A:Gene: EPLG2

Query Match 9.0%; Score 89; DB 2; Length 345;
Best local Similarity 23.1%; Pred. No. 1.2;
Matches 40; Conservative 26; Mismatches 57; Indels 50; Gaps 10;
QY 16 AGFATVAININDGNVGS-----GGQSVSINGVHNANIDNNNGMSNLSMDYENSFA 71
DB 195 AGC-----KSGQSDSOKKHETVQEKSGPAGAGGSGDSDFNSKVAL-----FA 241
QY 72 ARRLFSKSCIV-----HRMKNKAMPSTLDDDTWKKQCKGPGCAP 113
DB 242 AV-----GAGCVFLLIIFLVLLKLKRKRKHQQAALSLSTLASKGGSGTAGTE 297
QY 114 PKDLWTSNPRVRVDLNFEGP---KTAGMCGIPTTYVAELPGPNQD--LYSK 161
DB 298 PSDIILPRTTE---NNYCPHYEKVSG-DYGHPIYIVQEMP--POSPANIYYK 344

[illegible]

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Oy      52  -DNNNGWGSWSNLSMDYENSFPAT-RLFSKSKCTIYHRMKKDAMPSLQDLDTFWKEQCK 107
          ||| : : | | | | | : : : : : | | | : : | | : :
Db      380  NSSNNSSGNTSDSTFGIAAVFAAGKFYSQHSCDLAGSNKSAQEGONFLSWSE----- 436

Oy      108  GRGGAPPKDLM---YSVNPTR 125
          ||| : : | | | : :
Db      437  -----AKNLMMKNINYSANQSQ 452

RESULT   4
JT0569
chondromodulin-I precursor - bovine
M:Alternate names: 18k glycoprotein, cartilage; SCGP; small cartilage-derived glycopr
C:Species: Bos primigenius taurus (cattle)
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 05-Nov-1999
C:Accession: J00569; A33138; A36431
R:Hiraki, Y.; Tanaka, H.; Inoue, H.; Kondo, J.; Kamizono, A.; Suzuki, F.
Biochem. Biophys. Res. Commun. 175, 971-977, 1991
A>Title: Molecular cloning of a new class of cartilage-specific matrix, chondromoduli
A:Reference number: JT0569; MUID:91222210
A:Accession: JT0569
A:Molecule type: mRNA
A:Residues: 1-335 <HI>
A:Cross-references: GK:M65081; NID:g162840; PIDN:AAA3045.1; PID:g162841
A>Note: Part of this sequence, including the amino end of the mature protein, was det
R:Name, P.J.: Treep, J.T.: Young, C.N.
submitted to the Protein Sequence Database, October 1990
A:Reference number: A33138
A:Accession: A33138
A:Molecule type: protein
A:Residues: 215-220,'M',222,'NE',225-335 <NE>
A>Note: 221-Val was also found
R:Name, P.J.: Treep, J.T.: Young, C.N.
J. Biol. Chem. 265, 9628-9633, 1990
A>Title: An 18-kDa glycoprotein from bovine nasal cartilage. Isolation and primary st
A:Reference number: A36431; MUID:90277643
A:Accession: A36431
A:Molecule type: protein
A:Residues: 215-220,'MNE',224-225,227-256,'D',257-335 <NE2>
A>Note: 221-Val was also found
R:Name, P.J.: Treep, J.T.: Young, C.N.
J. Biol. Chem. 265, 22056, 1990
A:Reference number: A36535
A:Accession: A36535
A:Contents: annotation; sequence revision
C:Comment: This protein stimulates DNA synthesis of cultured growth-plate chondrocytes
C:Keywords: extracellular matrix; glycoprotein; transmembrane protein
F:43-59/Domains: transmembrane #status predicted <TM>
F:215-335/Product: chondromodulin-I #status experimental <MAT>
F:223,236/Binding site: carbohydrate (Thr) (covalent)#status experimental
F:248/Binding site: carbohydrate (Asn) (covalent)#status experimental
F:283-287,284-324/Disulfide bonds: (or 283-324,284-287)#status experimental
F:294-318,298-314/Disulfide bonds: #status experimental

Query Match      8.6%; Score 85.5; DB 2; Length 335;
Best Local Similarity 22.3%; Pred. No.2.4;
Matches 39; Conservative 29; Mismatches 70; Indels 37; Gaps 7;

Oy      7  VVGLIGLIAAPGF-----ATTVNING--NGCNVDGSGDOOSVSINGVANINDN 53
          ||| : : | | | | | | | | | | | | | | | | | | | |
Db      52  VLLILGAIGAFYFKMGSDNHLYNVHTMSINGKLQDS-----SMEIDAGNNLTFFRM 103

Oy      54  NNQGDMSNLSMDYENSFARPLFSKKSCTIYHRMKKDAMPSLQDLDTFWK-----EQGR- 107
          ::||| : : | | | | | | | | | | | | | | | | | | | |
Db      104  GSGAEAVEVNDPONGITGIRFAGEGCKTIKAQVKALIP---EVGTMTKQSISSIEGKI 160

Oy      108  GRGGAPPKDLMYSVNPTRVEDLTFGRKIAGMCRCGIPTYYAAELPGENDPLYSKK 162
          ||| : : | | | | | | | | | | | | | | | | | | | |
Db      161  MPVKYEENSLTWAGDPVKUNDSFLSSKVLELCGDDPIFWL-----KKTPRE 208

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RESULT 5
S46993
elk ligand - human
C:Species: Homo sapiens (man)
C:Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 28-May-1999
C:Accession: S46993
R:Beckmann, M.P.; Cerretti, D.P.; Baum, P.; Vanden Bos, T.; James, L.; Farrah, T.; Kozlic
EMBO J. 13, 3757-3762, 1994
A:Title: Molecular characterization of a family of ligands for eph-related tyrosine kinase
A:Reference number: S46993; MUID:94349923
A:Accession: S46993
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-346 <BEC>
A:Cross-references: GB:009304; NID:9538366; PIDN:AAA53093.1; PID:9538367

Query Match 8.6%; Score 85.5; DB 2; Length 346;
Best Local Similarity 23.1%; Pred. No. 2.5;
Matches 40; Conservative 23; Mismatches 61; Indels 49; Gaps 11;

OY 16 APGFATYVINGNDGNDGSCQSVSINGVHNVANIDNNNG-WDSNLSLDYENSF-AAT 73
DB 195 APG-----SKSLGDSGDK-----HEVYNOEKKSGPGASGSGSDPDGCFNSKY 238
OY 74 RLFSK--KSCIV-----HRNKKDAMPSLDLDITVWEQKGGPGAP 113
DB 239 ALFAVAGACVIFLLIIFLTVLLLRKRHRKHTQORAAALSLTLASPKGSGTAGTE 298
OY 114 PKDLMSVNTFRVDELNTFGP---KIAGMCRGIPTYVAEIRPGPNP--LYSK 161
DB 299 PSDIILPLRTE---NNYCPHYEYKSG-DYGHPIYIVDEMP-POSPANIYK 345

RESULT 6
AF0998
phosphoenolpyruvate carboxykinase (ATP) (EC 4.1.1.49) - Salmonella enterica subsp. enter
C:Species: Salmonella enterica subsp. enterica serovar typh
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C:Accession: AF0998
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
Th, T.; Conington, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; PMID:11677608
A:Accession: AF0998
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-539 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD08114.1; PID:G16505093; GSPDB:GN00176
C:Genetics:
A:Gene: STY4296
C:Superfamily: phosphoenolpyruvate carboxykinase (ATP)
C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 8.6%; Score 85.5; DB 2; Length 539;
Best Local Similarity 23.4%; Pred. No. 4.4;
Matches 47; Conservative 32; Mismatches 65; Indels 57; Gaps 11;

OY 1 MKLTMEV--GLGLLAAGFAATYVINGNDGNV-----DGSQOASVINGVHNVANID 52
DB 210 MKKGMFSVNNYLLPLKGLASHMGSANV-GEKGDVAVFFGLSGTGKTLSTDPKRRLLIG-D 267
OY 53 NNNKGSNLSLDYENS-FAATRLFSKRS--CIYHRNKKDAMP----- 93
DB 268 DEHGMD-DGVNFEFGGCAKTIKLSKEAPELTHAIRDALLENVYVREGTVDPPDGS 326
OY 94 -----LQDLDTVWEQKGGP-----GAPPPDLMSVNTFRVDELNT 131

DB 327 KTEHTVSYPIYHIDNYKPVSKAGHATKVIPLTADAGVLPPVSR--TANQTOYHFLSG 385
OY 132 FEGKTAGMCRGI-----PTYVA 148
DB 386 FTAKLAGEGTEGVTETPTFSA 406

RESULT 7
158406
LEKR-2 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C:Accession: 158406
R:Fletcher, F.A.; Carpenter, M.; Shilling, H.; Baum, P.; Ziegler, S.; Gimpel, S.; Hol
Oncogene 9, 3241-3248, 1994
A:Title: LEKR-2, a ligand for the receptor tyrosine kinase ELK, is evolutionarily con
A:Reference number: 158406; MUID:95022634
A:Accession: 158406
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-345 <RES>
A:Cross-references: EMBL:007560; NID:9563118; PIDN:AAA53092.1; PID:9563119
C:Genetics:
A:Gene: Epl92

Query Match 8.6%; Score 85; DB 2; Length 345;
Best Local Similarity 23.1%; Pred. No. 2.8;
Matches 40; Conservative 24; Mismatches 59; Indels 50; Gaps 10;

OY 16 APGFATYVINGNDGNDGSCQSVSINGVHNVANIDNNNGDSNLSLDYENSF 71
DB 195 APG-----RSGGDSGDKHEVYNOEKKSGPGASGSGSDTDFNSKVAL-----FA 241
OY 72 ATRLFSSKSCIV-----HRNKKDAMPSLDLDITVWEQKGGPGAP 113
DB 242 AV-----GAGCVIFLLIIFLTVLLLRKRHRKHTQORAAALSLTLASPKGSGTAGTE 297
OY 114 PKDLMSVNTFRVDELNTFGP---KIAGMCRGIPTYVAEIRPGPNP--LYSK 161
DB 298 PSDIILPLRTE---NNYCPHYEYKSG-DYGHPIYIVDEMP-POSPANIYK 344

RESULT 8
S17997
hypothetical gene COX1 intron 3 protein - yeast (Kluyveromyces marxianus var. lactis)
C:Species: mitochondrion Kluyveromyces marxianus var. lactis, Candida sphaerica
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 08-Dec-2000
C:Accession: S17997
R:Hardy, C.M.; Clark-Walker, G.D.
Curr. Genet. 20, 99-114, 1991
A:Title: Nucleotide sequence of the COX1 gene in Kluyveromyces lactis mitochondrial D
A:Reference number: S17997; MUID:92035081
A:Accession: S17997
A:Molecule type: DNA
A:Residues: 1-643 <HAR>
A:Cross-references: EMBL:X57546
C:Genetics:
A:Genome: mitochondrion
A:Genetic code: SGC2
A:Introns: 69/1, 235/3
C:Superfamily: DNA endonuclease I-SceII; COI intron 9 protein homology; cytochrome-c
F:1-324/Region: cox1 exons 1 to 3 encoded
F:325-643/Region: cox1 intron encoded

Query Match 8.5%; Score 84; DB 2; Length 643;
Best Local Similarity 26.9%; Pred. No. 7.6;
Matches 29; Conservative 20; Mismatches 39; Indels 20; Gaps 4;
OY 24 NINGNDGNDGSCQSVSINGVHNVANIDNNNGDSNLSLDYEN---SFAATRLFSKRS 80

DB 347 NNNNNNNNNRPGSPYIGNMTAGMKNKYNNSYNNSNNNNYNNKLTITGNTLIS--- 403
 QY 81 CTVHRMKNKAMPLODLDTWYKEQKGGPGCAPPKDLMSVNPFRVED 128
 DB 404 ---NLMNKETNNMTM-IKYMK-----IPNNIMYIMINGILLTD 437

RESULT 9

527833
 rhopty-associated protein 1 precursor - malaria parasite (Plasmodium falciparum)
 N:Alternate names: protective antigen
 C:Species: Plasmodium falciparum
 C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jun-2000
 C:Accession: A45514; S27833
 R:Ridley, R.G.; Takacs, B.; Lahm, H.W.; Delves, C.J.; Goman, M.; Certa, U.; Matile, H.;
 M.Ol: Biochem. Parasitol. 41, 125-134, 1990
 A:Title: Characterisation and sequence of a protective rhopty antigen from Plasmodium f.
 A:Reference number: A45514; MUID:90348711
 A:Accession: A45514
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-782 <RI2>
 A:Cross-references: GB:M32853; NID:g160656; PID:g160657
 C:Superfamily: Plasmodium falciparum rhopty-associated protein 1

Query Match 8.4%; Score 83.5; DB 2; Length 782;
 Best Local Similarity 24.0%; Pred. No. 11;
 Matches 35; Conservative 21; Mismatches 63; Indels 27; Gaps 6;

QY 26 NNDGQVSGQSVSINGVHNVANIDNNNGWMSN---LMDYENFPAATRLFSKSKC 81
 DB 18 NVADIDVNGDNNYKKT--INDDNFDDYWTYINKKEFLINSEDESSSFLFNKSS 75
 QY 82 IVHRMKNKAMPLODLDTWYKEQKGGPGCAPPK-----DLMTSVNPFRV 126
 DB 76 V-----DGGNINLDTPTSTSKSK-KGHRGSRVRSASAAILEEDSKDMEFKASPSV 129
 QY 127 EDLNTFPKTAGMCRGIPTYVAELP 152
 DB 130 KTSPTGQTGTGLKSSSPSTKSSP 155

RESULT 10

H90551
 Lipoprotein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
 C:Species: Mycoplasma pulmonis
 C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
 C:Accession: H90551
 R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallison, F.; Moszer, I.;
 Nucleic Acids Res. 29, 2145-2153, 2001
 A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pult
 A:Reference number: A99512; MUID:21267165; PMID:11353084
 A:Accession: H90551
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-617 <KUR>
 A:Cross-references: GB:A1445566; PID:g14089734; PIDN:CAC13493.1; GSPDB:GN00153
 A:Experimental source: strain UAB CTIP
 C:Genetics:
 A:Gene: MYPU_3200
 A:Genetic code: SGC3

Query Match 8.2%; Score 81; DB 2; Length 617;
 Best Local Similarity 23.4%; Pred. No. 14;
 Matches 37; Conservative 21; Mismatches 52; Indels 48; Gaps 9;

QY 31 NVDSGQSVSINGVHNVANIDNNNGWMSN---NSLMDYENFPAATRLF----- 76
 DB 352 NITSGINAKKLNINHAAN--GSVDWTSMDIRYNNSAFESSHVGILRSYDPSHSRTY 409
 QY 77 -----SKKSCIVHRMKNKAMPLODL---DTWYKEQ-KGPK---GGAPPDLMKSVN 122

DB 410 VSGNEQKKKIL-----DDEPKMEDVYWSNQTWYQKDSKPIFEYEGSS-----LVAIR 459
 QY 123 PTRVEDLNTFCKTAGMCRGIPTYVAELPCHNOLYS 160
 DB 460 TTSKRDKATL-----KLEMYEANTIPGTRKQVMS 489

RESULT 11

T25478
 hypothetical protein B0554.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T25478
 R:Graves, T.
 Submitted to the EMBL Data Library, November 1996
 A:Description: The sequence of C. elegans cosmid B0554.
 A:Reference number: Z20040
 A:Accession: T25478
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-547 <GSA>
 A:Cross-references: EMBL:U80031; PIDN:AAB37615.1; GSPDB:GN00023; CESP:B0554.2
 A:Experimental source: strain Bristol N2; clone B0554
 C:Genetics:
 A:Gene: CESP:B0554.2
 A:Map position: 5
 A:Intons: 103/2; 217/2; 339/2; 458/2

Query Match 8.1%; Score 80.5; DB 2; Length 547;
 Best Local Similarity 20.9%; Pred. No. 13;
 Matches 38; Conservative 25; Mismatches 74; Indels 45; Gaps 7;

QY 30 GNVDSGQSVSINGVHNVANIDNNNG-----WDSNLSMDYEN 68
 DB 225 GSTTTTMTKISCALAGITNDVNNGLPAENDVVPQTVAINAECSSVDSINWYV 284
 QY 69 SFAATRLFSKSKSCIVHRMKNKAMPLODLDTWYKEQKGGPG-----CAPPKDLMSY 121
 DB 285 VVACQTVKVPWTSATCOOIKDPGSPVTRSCSPALTYGMGDGMNPEYQIVTYTDFMTTA 344
 QY 122 NPTREVEDLNTFCKTAGMCRGIPTY-VAELPCHNOLY-----YSKRCYTADI 168
 DB 345 TPGTWDSVSTW--KIT--CSGIAGYNQOMELDGTTLLENAGNPNPPTVTITNVCNSADM 400

RESULT 12

S71467
 diacylglycerol kinase (EC 2.7.1.107) ATDGK1 - Arabidopsis thaliana
 N:Alternate names: protein F13624.120
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 05-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 01-Dec-2000
 C:Accession: S71467; T43617
 R:Katagiri, T.; Mizoguchi, T.; Shinzaki, K.
 Plant Mol. Biol. 30, 647-653, 1996
 A:Title: Molecular cloning of a cDNA encoding diacylglycerol kinase (DGK) in Arabidop
 A:Reference number: S71467; MUID:96189276
 A:Accession: S71467

A:Molecule type: mRNA
 A:Residues: 1-728 <KAT>
 A:Cross-references: EMBL:D63787; NID:g1374771; PIDN:BA09856.1; PID:g1374772
 R:Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voelt, M.; Robben, J.; Volckaert, G.;
 submitted to the Protein Sequence Database, December 1999
 A:Reference number: Z23009
 A:Accession: T43617
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-508, 'N', 510-728 <BEV>

Query Match	8.18;	Score 80.5;	DB 2;	Length 728;
Best Local Similarity	24.18;	Pred. No. 19;		
Matches 34;	Conservative 27;	Mismatches 57;	Indels 23;	Gaps 7

RESULT 13
P71671

Query Match	Score	DB 2	Length
8.18;	80.5;		2295;
Best Local Similarity	24.89;		
Prod No	83		

30; Conservative 10; Mismatches 44; Indels 37; Gaps 3;

QY	24	NINGANGVNDGSGOOSVSJNG-----	VHNVNIDNNNGDMSNSIMDYENSFAATR	74
Dd	540	NISEGDGEVDGGDEBDGGDDGDEGADDSVPTHHNKNDGESDVAWNLIMSYKKLANDE		599
QY	75	LFSKKSCTYHRNMKDAMSIDDLTMYKEBGKGPGGAPKDLWSVNFTRVEDLNTFGP		134
Dd	600	NFKK-----YNKTILKNLDKFLMSSSEK-----		
QY	135	K 135	EDINSYKN	631
Dd	632	K 632		

RESULT 14
D71917

C:Species: Helicobacter pylori
C:Strain: Helicobacter pylori (strain J99)
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C:Accession: D71917
R:Aim, R.A.; Lind, L.S.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Lives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.

Query Match	8.1%	Score 80;	DB 2;	Length 3194;
Best Local	31.4%	Pred. No. 1.4e+02;		
Matches	43;	Conservative	17;	Mismatches 49;
				Indels 28;
				Gaps 9

Dy 8 VGLLGLAAPCAVTYVNI--NDGNVDGS-QGQSVS----NCVHNANIDNNNGWTSW 60
 | : | : - : : | | | | : : | | | |
Db 2066 VFYLGYINAFKAKNIIYTGTIGSGNAMWGSGGSANVSSESATNLVLNQANID-AQGTD-- 2122

[illegible]

```

2175 --KTLSSILSPTEVNNL 2189

```

RESULT	15
AC0017	

phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49) [imported] - Yersinia pestis (a
C.Species: Yersinia pestis
C.Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C.Accession: AG0017
R.Parthill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.;
deno-Farrago, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,
Nature 413, 523-527, 2001
A.Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A.Reference number: AB0001; MUID:21470413; PMID:11586360
A.Accession: AG0017
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-539 >KUP>
A.Cross-references: GB:AL590842; PIDD:CAC89001.1; PID:g15978243; GSPDB:GN00175
C.Genetics:
A.Gene: pckA
C.Superfamily: phosphoenolpyruvate carboxykinase (ATP)
C.Keywords: carbon-carbon lyase; carboxy-lyase

Query Match	Score	DB 2	Length
Best Local Similarity	8.08	79.5	539
Best Local Similarity	33.48	79.5	539

Local Similarity	22.46;	Pred. NO. 1b;
Matches	45;	Conservative
	34;	Mismatches
	65;	Indels
	57;	Gaps
	11;	

1 MRLIMF V V - - G L L G L L A A P G F A Y T V N I N G N D G N V - - - - - D G S G Q Q S V S I N G V H N V A N I D 52

[illegible][illegible]

94 -----IOPDPTMYKFOKKGKBP-----CCADDEETUVGUVDEUEUEETUM 122

Db 327 K T E N T R V S Y P I Y H I D N I V K P V S K A G H A T K V T F I T A D A E C V I P V S B I - T A N O T O V U U I C S 366

QY 132 FGPKIAGMCRGI---PTYVA 148

Db 386 FTAKLAGTGVTEPTFSA 406

Thu Sep 5 11:23:30 2002

us-09-821-726-16.rpr

Page 6

Search completed: September 4, 2002, 16:47:39
Job time: 375 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 17:01:41 : Search time 124.34 Seconds

(without alignments)
256,000 Million cell updates/sec

Title: US-09-821-726-16

Perfect score: 993

Sequence: 1 MKLTFVVGILGLAAGFA.....TADILILRMFCGTSVFTY 184

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SP_RMBL_19:*
2: SP_Archaea:*
3: SP_Bacteria:*
4: SP_Fungi:*
5: SP_Human:*
6: SP_Invertebrate:*
7: SP_Mammal:*
8: SP_Mhc:*
9: SP_Organelle:*
10: SP_Phage:*
11: SP_Plant:*
12: SP_Rodent:*
13: SP_Virus:*
14: SP_Vertebrate:*
15: SP_Unclassified:*
16: SP_Virus:*
17: SP_Bacteriophage:*
17: SP_Archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	234	23.6	191	11	Q9D077
2	167.5	16.9	184	11	Q9C056
3	93	9.4	618	5	Q9V629
4	91	9.2	577	5	Q961R5
5	89.5	9.0	292	5	Q25762
6	88.5	8.9	860	5	Q19852
7	88	8.9	2206	12	Q99F74
8	88	8.9	2206	12	Q99F74
9	86.5	8.7	658	3	Q99F75
10	86	8.7	531	2	Q93JF5
11	85	8.6	2206	12	Q99F75
12	84	8.5	319	8	Q34834
13	83.5	8.4	782	5	Q94431
14	83.5	8.4	782	5	Q94431
15	83.5	8.4	782	5	Q94431
16	83.5	8.4	782	5	Q94431
					Q25730

17	83.5	8.4	782	5	Q26007	Q26007 plasmodium
18	82.5	8.3	493	9	Q9JMM8	Q9JMM8 bacterioph
19	82	8.3	602	6	Q9GL34	Q9GL34 bos taurus
20	81	8.2	553	11	Q9OWR9	Q9OWR9 mus musculu
21	81	8.2	617	16	Q98Q21	Q98Q21 mycoplasma
22	80.5	8.1	547	5	P91006	P91006 caenorhabdi
23	80.5	8.1	728	10	Q9SD92	Q9SD92 arabidopsis
24	80.5	8.1	782	5	Q25875	Q25875 plasmodium
25	80.5	8.1	782	5	Q9U430	Q9U430 plasmodium
26	80.5	8.1	1332	5	Q9BN17	Q9BN17 drosophila
27	80.5	8.1	2295	5	Q9TV98	Q9TV98 plasmodium
28	80	8.1	2009	5	Q9VXW0	Q9VXW0 drosophila
29	80	8.1	3194	16	Q9ZLM3	Q9ZLM3 helicobacte
30	79.5	8.0	494	2	Q05527	Q05527 comamonas a
31	79.5	8.0	1215	1	Q9UMR7	Q9UMR7 pyrococcus
32	79.5	8.0	1960	5	Q9U0R8	Q9U0R8 homo sapien
33	79.5	8.0	2432	12	Q91OP4	Q91OP4 anopheles g
34	79	8.0	2432	12	Q91OP4	Q91OP4 anopheles g
35	79	8.0	338	4	Q15333	Q15333 neurospora
36	78.5	7.9	501	5	Q9BID4	Q9BID4 caenorhabdi
37	78	7.9	319	3	Q96U67	Q96U67 neurospora
38	78	7.9	642	5	Q17169	Q17169 caenorhabdi
39	78	7.9	664	5	Q27435	Q27435 plasmodium
40	77.5	7.8	419	5	Q77316	Q77316 plasmodium
41	77.5	7.8	428	3	Q12646	Q12646 neocallimias
42	77.5	7.8	439	3	Q92401	Q92401 agaricus bi
43	77.5	7.8	458	10	Q9FVH2	Q9FVH2 arabidopsis
44	77.5	7.8	459	10	Q9M354	Q9M354 arabidopsis
45	77.5	7.8	782	5	Q26104	Q26104 plasmodium

ALIGNMENTS

RESULT 1
Q9D077 PRELIMINARY: PRT: 191 AA.
ID Q9D077
AC Q9D077
DT 01-JUN-2001 (TREMURel. 17, Created)
DT 01-JUN-2001 (TREMURel. 17, Last sequence update)
DE 01-JUN-2001 (TREMURel. 17, Last annotation update)
GN 1190003M12RIK PROTEIN.
GN 1190003M12RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirni L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boiffell D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gutschalk S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Hayashizaki Y., Yoshida K., Hasegawa Y., Kawai J., Kohsaki S.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK004474; BAB23320.1;
DR MGI: 1916138; 1190003M12RIK.

SEQUENCE 191 AA; 20772 MW; 76D7DB4796AE8B4D CRC64;

Query Match 23.68; Score 234; DB 11; Length 191;
Best Local Similarity 31.1%; Pred. No. 6,3e-15;
Matches 56; Conservative 40; Mismatches 66; Indels 18; Gaps 7;

QY 3 LTMFVGLLGLLAAPGFATYVINGNDG-NVDS-SINGVHVANIDNNNGMDSW 60
DB 21 VTEFLV-----PALALT---NTSDSYPLDSSVGTOTIHVDLRGVSLRDSVQSEW 69
QY 61 NSLMDYENSFATRLFSKSCIVHRMKNKAMPSTLQD-LTWKQKQKGGAPKRLM 119
DB 70 DGVMDYKNDLLAAKLFKMACVLAKMPAAPPSTLDTLQALGKQASGHP---PTRGILTY 126
QY 120 SVNPRVVDLTFFGPKINGMCRGIPITYA-EEIPGPNQPLYSKRCYADILMLRSCFG 178
DB 127 TVLPSRIKNAQYGVPIKDLCRAPVTFYFARQOREGALTMDPDCSELQGLSTFGCLSTIG 186

RESULT 2

Q9C0S6 PRELIMINARY; PRT; 184 AA.

AC Q9C0S6; MEDLINE=21085660; PubMed=11217851;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE 1810036H07RIK PROTEIN.
CN 1810036H07RIK
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=STOMACH, AND PANCREAS;
RA MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Akakawa T., Hara A., Fukunishi K., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schmitt L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balarelli R., Barsh G.,
RA Blake J., Boilelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohitsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL: AK008986; BAB26008.1;
DR EMBL: AK007451; BAB25046.1;
DR EMBL: AK007705; BAB25201.1;
DR MGD: MGI:1913534; 1810036H07RIK.
SQ SEQUENCE 184 AA; 20469 MW; 612A18FABE652230 CRC64;

Query Match 16.98; Score 167.5; DB 11; Length 184;
Best Local Similarity 25.7%; Pred. No. 1.7e-08;
Matches 46; Conservative 46; Mismatches 76; Indels 11; Gaps 5;

QY 5 MFVVGILGLLAAPGFATYVINGNDGSGQSVSINGVHVANIDNNNGMDSWMSLW 64
DB 8 LVVLSIFGISOAEIFNFIYPSKNG---GNIGETVITIDNQGNATLNIHSGSCSSTIF 64
QY 65 DYENSFATRLFSKSCIVHRMKNKAMPSTLQD-LTWKQKQKGGAPKRLMYSNP- 123

DB 65 DYKRGITASRVLSRACVYIKMDHKAIPALDKLQGFVKEQGMNAIDS-PEYTWRYNPL 123

QY 124 ---TRVEDLTNFGPKIACMCRGIPITYAAEELPGNPLYSKRCYADILMLRSCFG 178
DB 124 KSLITKYV-DWFLFGSPITROLCKHMPLYEGEVATKPKRE-VSTGCAKVGILGLTGVSTIG 180

RESULT 3
Q9V6Z9 PRELIMINARY; PRT; 618 AA.

AC Q9V6Z9; MEDLINE=20196006; PubMed=10731132;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CG8547 PROTEIN.
GN CG8547.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Ceuliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananthides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.H.C., Baxter E.G., Helt R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Dwyer E., Helt R.G., Nelson C.R., Miles G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Planck C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Botkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke S., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dublin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flosser C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Gloder A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Relibert K., Remington K., Saunders R.D.C., Scheefer F., Shen H.,
RA Shne B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtkars R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003815; AAF58267.2;
DR FlyBase: FBgn003919; CG8547.
DR InterPro: IPR001230; Prentylin.
DR PROSITE: PS00294; PRENYLATION;
SQ SEQUENCE 618 AA; 68023 MW; 7C82273A67F32C6C CRC64;

Query Match 9.4%; Score 93; DB 5; Length 618;
Best Local Similarity 21.7%; Pred. No. 1.3;

ID	RESULT	4
0961R5		
AC	0961R5	PRELIMINARY; PRT; 577 AA.
DT	01-DEC-2001 (TREMBLrel. 19, Created)	
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)	
DE	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
CG	CG9547.	
OS	Drosophila melanogaster (Fruit fly).	
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
OC	Ephydroidea; Drosophilidae; Drosophila.	
OX	NCBI_TaxID=7227;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Y, CN BW SP;	
RA	Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,	
RA	Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,	
RA	Gonzalez M., Guatin H., Li P., Liao G., Miranda A., Mungall C.J.,	
RA	Nimmo J., Paclt J., Paragas V., Park S., Phouanavong S., Wan K.,	
RA	Yu C., Lewis S.E., Rubin G.M., Celisner S.;	
RL	Submitted (AUG-2001) to the EMBL/Genbank/DBD databases.	
DR	EMBL: AF051417; AAK92811.1;	
SQ	SEQUENCE 577 AA; 63582 MW; 8581CCB5BD1D026A CRC64;	

Query Match	9.2%	Score 91:	DB 5;	Length 577;
Best Local Similarity	20.7%;	Pred. NO.	1.9;	
Matches	34;	Conservative	133;	Mismatches 51; Indels 46; Gaps 8;
DQ	12	GLLAAPGFAATVAINCNDGNV--DSGGQSVSINCIVHVAANIIDNNNCWDSNLSIMDYENS	69	
		::	:	::: ::
Dd	215	GILPAPTKVTTVTRTYRYEIPATCGSNSTIINRTH---TLNSN--TLLSSRYKHES	268	
		::	:	::: ::
QY	70	FATRLFSKKSCIVH-----RKMKDA-MPSLDDDTJWKEDK----	105	
		::: ::	:	::: ::
Dd	269	HNSQNFQSOLSPVHPDPQSHVPQTIVNTESYTILNRHSDDRPVYSNOSYIERHKETTR	328	
		::	:	::: ::
QY	106	-----GCGPGCAPP-KDLMTSYNP-LRVEDLNITFGXP	135	
		::	:	::: ::
Dd	329	GVSFPQRPLPLCGGPAGTPPGNRTVIYNIRKTDHVNTVNELPPQ	372	
		::	:	::: ::
RESULT	5			
ID	025762	PRELIMINARY:	PRT:	292 AA.
AC	025762;			
DT	01-NOV-1996	(TREMBLrel. 01,	Created)	
DT	01-NOV-1996	(TREMBLrel. 01,	Last sequence update)	
DT	01-DEC-2001	(TREMBLrel. 19,	Last annotation update)	
DE	P02	(FRAGMENT).		
CN	RAP-I...			
CS	Plasmodium falciparum.			

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=INDU (INDIAN ISOLATE D);
 RX MEDLINE=92244303; Pubmed=1574089;
 RA Howard R.F.;
 RT "The sequence of the p82 rhoptry protein is highly conserved between
 RT two Plasmodium falciparum isolates."; 1992.
 RL Mol. Biochem. Parasitol. 51:327-330(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=INDD (INDIAN ISOLATE D);
 RX MEDLINE=96379224; Pubmed=8784775;
 RA Howard R.F.; Peterson C.;
 RT "Limited RAP-1 sequence diversity in field isolates of Plasmodium
 RT falciparum."; Parasitol. 77:95-98(1996).
 RL Mol. Biochem. Parasitol. 77:95-98(1996).
 DR EMBL; U041074; AAC47090.1; -;
 FT NON_TER 1 1
 FT 292 292
 SO SEQUENCE 292 AA; 32345 MW; A35C979C3FEC3019 CR664;

Query Match	9.0%;	Score 89.5;	DB 5;	Length 292;
Best Local Similarity	24.7%;	Pred. No. 1.1;		
Matches	36;	Conservative	20;	Mismatches 63; Indels 27; Gaps 6;
QY	26	NCNDG-NDVDSGGQSVSINGVHNVANIDNNNGWDSWNS---	LMDYENSFAATRLFSKSC	81
DB	12	NVADGIVNADNNNGYKTI--INNDENFDDYVNWPIPKKEFLNSYENVEFSSEFLENKSS	69	
QY	82	IYHRMKNKDAMPSTLDDTDYVKKQKKGGGAGAPK-----	DLMTSVNPTRY	126
DB	70	V-----DDGNNINLTDTSTSNKSSK-KGGRKSRVKSASAAALIEEDDSKDDMEFKASPSVY	123	
QY	127	EDLNTFGPKIAGNCRCGIPPTVAAEETP	152	
DB	124	KTSPSGTQTSGLKSSPSITFKSSP	149	
RESULT	6			
ID	019852	PRELIMINARY;	PRT;	860 AA.
DC	019852;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-OCT-2001 (TREMBLrel. 18, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	HYPOTHEICAL 96.1 KDA PROTEIN.			
GN	F28B4.2.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditya; Rhabditidae;			
OC	Rhabdillidae; Peloderinae; Caenorhabditis.			
OX	NCBI_TaxID=6239;			
RN	[1]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN-BRISTOL N2.			
RC	MEDLINE=99069613; PubMed=9851915;			
RA	None.			
RT	"Genome sequence of the nematode C. elegans: a platform for			
RT	investigating biology. The C. elegans Sequencing Consortium."			
RX	science 282:2012-2018(1998).			
RN	[2]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN-BRISTOL N2;			
RC	Leinbach D.;			
RA	"The sequence of C. elegans cosmid F28B4."			
RT	Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN-BRISTOL N2;			
RC	Waterston R.;			
RA	"Direct Submission."			

DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE HYPOTHEICAL 69.7 KDA ASN/THR-RICH PROTEIN C320.02C IN CHROMOSOME
 DE 11.
 GN SPCC320.02C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 ON NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Wood V., Rajandream M.A., Barrell B.G., Medler H., Wambutt R.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 468-658 FROM N.A.
 RC STRAIN=972;
 RA Wood V., Rajandream M.A., Barrell B.G., Murphy L., Harris D.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL022245; CAA18304.1; -
 DR EMBL; AL031764; CAA21105.1; -
 KM Hypothetical protein.
 SQ SEQUENCE 658 AA; 69695 MW; 63082230B6488AC5 CRC64;

Query Match 8.7%; Score 86.5; DB 3; Length 658;
 Best Local Similarity 25.4%; Pred. No. 6.1;
 Matches 36; Conservative 26; Mismatches 53; Indels 27; Gaps 7;

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 DB 321 METTINIVGNDSTSPSONFKSGTFVSNANSSNSN-DGSSSKSIDVGSFVNAFKQLNVND 379
 QY 52 ---DNNQWDSWNSLWYENSEFAT-RLFSKSKIVHRMKDAMPISLQDDITWYKBEKGK 107
 DB 380 NSSNNNSGNTDSTTGAAVFAAGFFSOHSCDLASGMSKSAOEGONFLSWSE--- 436
 QY 108 GPGGAPPKDLM---YSVNPTK 125
 DB 437 -----AKNLKNTKNTYSANOSQ 452

RESULT 10
 Q93JF5 PRELIMINARY; PRT; 531 AA.
 AC Q93JF5;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HYPOTHEICAL 58.7 KDA PROTEIN.
 GN STRAC16H6.07.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 ON NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Collins M.R., Harris D.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kieser H.M., Denapalpe D., Eichner A., Cullum J.,
 Kinashi H., Hopwood D.A.;

RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome."
 RL MOL. Microbiol. 21:77-96(1996).
 DR EMBL; AL596162; CAC44586.1; -
 KM Hypothetical protein.
 SQ SEQUENCE 531 AA; 58656 MW; 714F1033D5C29B3F CRC64;

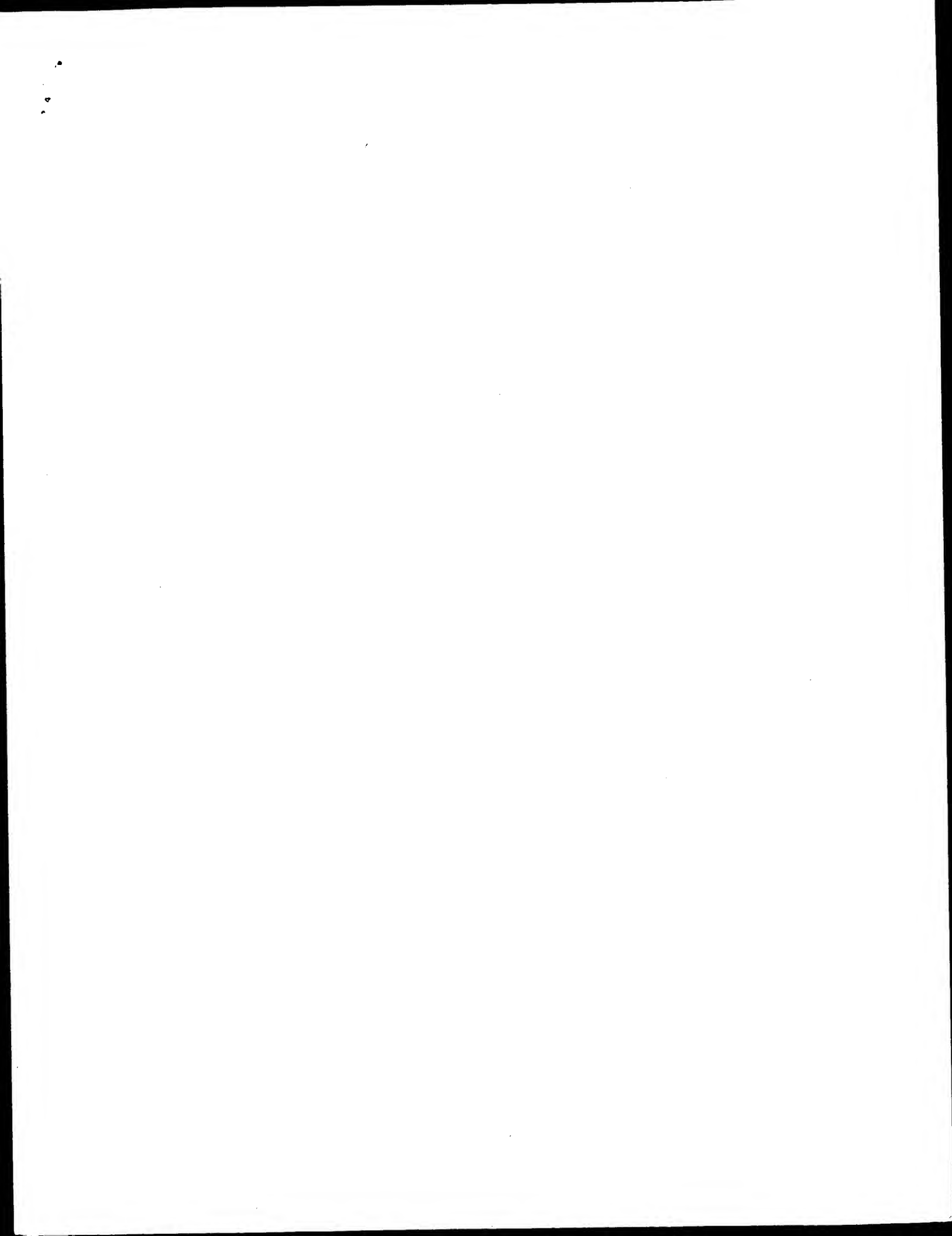
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 Best Local Similarity 28.4%; Pred. No. 5.2;
 Matches 27; Conservative 12; Mismatches 34; Indels 22; Gaps 4;

QY 96 DLDTMVEKKGKGGAPKDLWYVN--PTRVEDL-----NTEGPKTAGMKRGITPTV 147
 DB 92 DVALVVRGKGGKGGAPDPAALQYVNDPRYAASSLLAVALSVSSAMRGVCKSRPERA 151
 QY 148 AEEIP-----GPN--OPLYSKKCYTADI 168
 DB 152 AESLPLRVEIPALPARGGPDLVRLPEPLGWTVDV 186

RESULT 11
 Q99JF5 PRELIMINARY; PRT; 2206 AA.
 AC Q99JF5;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE POLYPROTEIN.
 OS Porcine teschovirus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
 OC Teschovirus.
 ON NCBI_TaxID=118140;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VIR 918-19/85;
 RX MEDLINE=21105197; PubMed=11160660;
 RA Zell R., Dauber M., Krumholz A., Henke A., Birch-Hirschfeld E.,
 Stelzner A., Prager D., Wurm R.;
 RT "Porcine Teschoviruses Comprise at Least Eleven Distinct Serotypes:
 RT Molecular and Evolutionary Aspects."
 RL J. Virol. 75:1620-1631(2001).
 DR EMBL; AF296111; AAK12405.1; -
 DR HSSP; O88590; 1TME.
 DR MEROPS; C03.UPC; -
 DR InterPro: IPR004004; Calici_pol_hel.
 DR InterPro: IPR001676; Rnv.
 DR InterPro: IPR000605; RNA_helicase.
 DR InterPro: IPR001205; RNA_pol_P3D.
 DR Pfam; PF00073; Rnv; 2.
 DR Pfam; PF00680; RNA_dep_RNA_pol; 1.
 DR Pfam; PF00910; RNA_helicase; 1.
 DR PRINTS; PR00918; CALICVIRUSN.
 SQ SEQUENCE 2206 AA; 247295 MW; 113CC439CB2C774F CRC64;

Query Match 8.6%; Score 85; DB 12; Length 2206;
 Best Local Similarity 23.6%; Pred. No. 38;
 Matches 51; Conservative 21; Mismatches 64; Indels 80; Gaps 12;

QY 4 TMFVVGGLGLAAGFAVTVNING---NDGNVDSGQSVSINGVHVANIDNNNGMD- 58
 DB 275 TRFHGGCLGVFAIPFSVSKLQGIPLTYDGNKDG-----VNSNI-----WDR 317
 QY 59 ---SWNS-----LMDYENSF-----AATRLPSKKCYH-----RAN 87
 DB 318 FTTWHNPDAFGAMWYSHAYDDKHKWYKPKLEOYGGISPSLF---CFPHOLINPRTN 373
 QY 88 KDAMPSLQDLD-----TMVKEOKGKGPGAPPKDLMYVNPTRVEDLNT 131
 DB 374 SSATLCPLPFDVCGPLTDVTVHCPMAIVVVVRLTLVALGCTPSPDINVSAPC---DVEY 430
 QY 132 FGPRTAGMCRG-IPTVVAEETPGNOLPSKKCYTA 166



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:46:10 ; Search time 57.74 Seconds

(without alignments)
78.260 Million cell updates/sec

Title: US-09-821-726-13

Sequence: 994

1 MKRTVFAGLGVFLAPALA.....YTSVLMIVDISFGDTVEN 185

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Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued_Patents-AA:*
1: /cgn2_6/plodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/plodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/plodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/plodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/plodata/2/1aa/PCTUS.COMB.pep.*
6: /cgn2_6/plodata/2/1aa/backfiles1.pep.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	89.5	8.1	652	4	US-08-559-896B-2
2	77.5	7.8	428	3	US-09-118-319-5
3	77.5	7.8	430	2	US-08-845-848-8
4	74	7.4	606	4	US-09-187-124-2
5	73.5	7.4	533	1	US-08-445-586-10
6	73	7.3	1507	3	US-08-929-329-5
7	72	7.2	334	1	US-08-241-465B-19
8	72	7.2	334	1	US-08-241-465B-20
9	72	7.2	380	2	US-08-227-108-16
10	72	7.2	380	2	US-09-073-674-16
11	71.5	7.2	432	3	US-09-118-319-2
12	71.5	7.2	533	1	US-08-484-493-13
13	71.5	7.2	533	1	US-08-484-494-13
14	71.5	7.2	533	2	US-08-345-212-13
15	71.5	7.2	533	2	US-09-249-003-13
16	71	7.1	434	3	US-08-236-311-4
17	71	7.1	434	3	US-08-457-918-4
18	71	7.1	674	4	US-09-199-637A-51
19	70.5	7.1	379	1	US-08-227-108-18
20	70.5	7.1	379	2	US-09-073-674-18
21	70.5	7.1	1181	1	US-08-053-614-4
22	70.5	7.1	1181	1	US-08-316-397B-4
23	70.5	7.1	1181	2	US-09-034-306-4
24	70.5	7.1	1181	4	US-09-259-437-4
25	70.5	7.1	1181	5	PCT-US93-09782-4
26	70.5	7.1	1220	3	US-08-930-996A-2
27	70	7.0	418	2	US-08-873-479-44

28	70	7.0	467	4	US-09-002-361-3	Sequence 3, Appl
29	70	7.0	496	4	US-09-002-361-2	Sequence 2, Appl
30	70	7.0	855	1	US-08-344-536-2	Sequence 2, Appl
31	70	7.0	855	3	US-08-920-562-2	Sequence 2, Appl
32	70	7.0	2391	2	US-08-446-855A-2	Sequence 2, Appl
33	70	7.0	2391	4	US-09-150-741-2	Sequence 2, Appl
34	69.5	7.0	1240	3	US-08-930-996A-4	Sequence 4, Appl
35	69	6.9	328	4	US-09-216-295-12	Sequence 12, Appl
36	69	6.9	259	4	US-09-041-889-28	Sequence 28, Appl
37	69	6.9	323	3	US-09-041-889-28	Sequence 29, Appl
38	69	6.9	361	1	US-08-415-751-3	Sequence 4, Appl
39	69	6.9	377	3	US-09-041-889-29	Sequence 5, Appl
40	68.5	6.9	211	4	US-08-856-253-4	Sequence 6, Appl
41	68.5	6.9	439	3	US-09-118-319-6	Sequence 2, Appl
42	68.5	6.9	459	4	US-09-286-691-2	Sequence 2, Appl
43	68.5	6.9	459	4	US-09-687-147-2	Sequence 6, Appl
44	68.5	6.9	512	4	US-08-856-253-6	Sequence 4, Appl
45	68.5	6.9	1003	1	US-08-571-758-4	

ALIGNMENTS

RESULT 1
US-08-559-896B-2
Sequence 2, Application US/0859896B
Patent No. 6310046
GENERAL INFORMATION:
APPLICANT: Patrick E. Duffy
APPLICANT: Christian F. Ockenhouse
TITLE OF INVENTION: SEQUESTRAIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: John Moran
STREET: USA MRC - MCMR-JA
CITY: FORT DETRICK, FREDERICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/559,896B
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Moran, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
TYPE: amino acid
TOPOLOGY: Linear
US-08-559-896B-2

Query Match
Best Local Similarity 23.8%; Score 80.5; DB 4; Length 652;
Matches 38; Conservative 23; Mismatches 44; Indels 55; Gaps 9;
QY 21 NYN-----DVNDNNNAGSGQGV-SVNNEN-----VANVDNNNGDSWNS 62
DB 404 NVNVFIIDNNNSNNNNNNNNRDVNNLNKKFTNNNNYNNVEVELVRRLLDKG-AKIED 462

Page 2

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				Gaps
QY	21	NYNIDVDDNNNAG-----	SGOOSVSYNNENHNAVYDNNNGDSNWSIMDYGNGEPAAT	73
DB	242	NGNNSYIGDGNNGVANGNGYNGDNGNNDGNNNGYDNGDNGDNGENGENGNGN	301	
QY	74	--RLFOKTCITVHKMKKEVWPSIQSLDALYKREKTKQGGKGGPPPKGLMYSVNEKVVDL	131	
DB	302	NGEGHHGGRVKKAK-----	HLISRI	
QY	132	SKFSKNIANNRCGIPTYMAEEMQASL-----	FFYSGT-----	CYTSVLMTIV 174
DB	336	KKVGGE-----	EGLDVHITPEKALPPLKIRHYYTIGSLTTPC--	TESLVAV 382

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RESULT      4
US-09-187-124-2
; Sequence 2, Application US/09187124A
; Patent No. 6255563
; GENERAL INFORMATION:
; APPLICANT: Emmertmann, Michael
; APPLICANT: Kossmann, Jens
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES CODING FOR DEBRANCHING ENZYMES
; TITLE OF INVENTION: FROM POTATO
; FILE REFERENCE: GFB8
; CURRENT APPLICATION NUMBER: US/09/187,124A
; CURRENT FILING DATE: 1998-11-05
; EARLIER APPLICATION NUMBER: PCT/Ep97/02292
; EARLIER FILING DATE: 1997-05-06
; EARLIER APPLICATION NUMBER: DE 196 18 125.9
; EARLIER FILING DATE: 1996-05-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentlin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 606
; TYPE: prt
; ORGANISM: Solanum tuberosum
; US-09-187-124-2

Query Match          7.4%; Score 74; DB 4; Length 606;
Best Local Similarity 35.0%; Pred. No. 5.1;
Matches 14; Conservative 10; Mismatches 16; Indels 0; Gaps 0.

OY      40  VSVNNEHNVANVDNNNGDSWNSIMWDGNGFAATRLRFÖKK 79
         |:.|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      369  VTNNKHNLANGEDNKDGENHNNNSMCGEGEPASIFVKK 408

RESULT      5
US-08-445-586-10
; Sequence 10, Application US/08445586
; Patent No. 5627050
; GENERAL INFORMATION:
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APPLICANT: Takeshita, Sunao
APPLICANT: Ito, Toshimi
APPLICANT: Otawara-Hamamoto, Yoko
APPLICANT: Amann, Egon
TITLE OF INVENTION: Bone-Related Sulfatase-Like Protein and
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESS: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,586
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/111,887
FILING DATE: 26-AUG-1993
APPLICATION NUMBER: JP 230030/92
FILING DATE: 28-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 324034/92
FILING DATE: 03-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 02481.1322-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 533 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-445-586-10

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Query Match

Best Local Similarity 7.4%; Score 73.5; DB 1; Length 533;
Matches 42; Conservative 20; Mismatches 48; Indels 47; Gaps 11;

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OY 43 NNEHVAVND-----NNGMD-----SMNSIMD-----YNGCFATRLFOKKTCTVHKMKK 88
DB 291 NNTVYIFSTDGGOTLGGNNWPLRGKKW-SLNEGGRVGVFVASPLLRKQGV---KNR 345
OY 89 EVMPSIOGLDALVK-----EKKLOG-----KGGGPPPK-GIMSVNPNKYVDLSK 133
DB 346 ELIHSMQLPLVLARGHNGTKPLDGFDMKKTISEGSPRIELHLHIDNFDVDS-SP 404
OY 134 FGKNIANNCRGIPYMAEMQEAFLFFYSGTCYTTSV 170
DB 405 CPRN-----SMAPAKDDSLPEYS--AFNTSV 429

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RESULT 6

US-08-929-329-5

Sequence 5, Application US/08929329

PATENT NO. 6120770

GENERAL INFORMATION:

APPLICANT: Adams, John H

APPLICANT: Dalton, John P

APPLICANT: Kappe, Stefan

```

TITLE OF INVENTION: Plasmodium Proteins Useful for Preparing
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESS: Barnes & Thornburg
STREET: 11 S Meridian
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
ZIP: 46204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/929,329
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Breen, John P
REGISTRATION NUMBER: 38,833
REFERENCE/DOCKET NUMBER: 835910-28685
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 231-7745
TELEFAX: (317) 231-7433
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1507 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium yoelii
US-08-929-329-5

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Query Match

Best Local Similarity 7.3%; Score 73; DB 3; Length 1507;
Matches 46; Conservative 23; Mismatches 71; Indels 74; Gaps 12;

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OY 19 LANYNIDVND-----NNNA-----GSGQSYSVNNEHVA-----NVDNNGMD----- 58
DB 527 LKNYNDSENFSTSFHNTVAPTHYBNSKFTGVNKKRENTYGTODLNANNYINOPKN 586
OY 59 -----SMNSIMDYGNGFAATRLFOKKTCTVHKMKK 97
DB 587 KPNPQAEYMDRFDIEKNHIYIDMKODGKRGSG---KL--KYNIIISH-----ETADTOSL 636
OY 98 -----DALKEKKLQCKGPGPPKGLMYSV-NPNKYVDLSKFGKNIANNCRG--IPTM 149
DB 637 LITDKODICPNHYSPOGAGSCPNYKGSIVVKTPESSINGNENHLSNPLNFIKGYLNKTM 696
OY 150 AEDM-----OEASLFFYSGTCYTTSVLWIVDSFC 179
DB 697 KSNVELPEYKESGLAMHNG-----DLVSC 719

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RESULT 7

US-08-241-465B-19

Sequence 19, Application US/08241465B

PATENT NO. 5719125

GENERAL INFORMATION:

APPLICANT: Fujio SUZUKI

APPLICANT: Fujio HIRAKI

APPLICANT: Kazuhito TAKAHASHI

APPLICANT: Junko SUZUKI

APPLICANT: Jun KONDO

APPLICANT: Atsuko KOHARA

APPLICANT: Akiko MORI

APPLICANT: BI YAMADA
TITLE OF INVENTION: HUMAN CHONDROMODULIN-1 PROTEIN
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
COUNTRY: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,465B
FILING DATE: May 11, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 334 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-241-465B-19

Query Match 7.2%; Score 72; DB 1; Length 334;
Best Local Similarity 20.3%; Pred. No. 3.7; Indels 14; Gaps 4;
Matches 29; Conservative 26; Mismatches 74;
QY 21 NYNIDVNDNNAGSGQ-SVSVNNEHNVANVNDNNGSDMSNIMWYNGFAATRLFOKK 79
DB 76 HTYMSIN-----GKLDGSMELDAGNNLETFKMGSAEALVAVDFONGITGIRPAGE 129
QY 80 TCIVHKKKEVWPSIOSDALVKEKTLQK-GPGGPPKGLMYSVNPKNKVDLSKFGKNI 138
DB 130 KCIYKAQVKARIPVGAATVKOSISKLEKIMPVKTEENSLIWAVDQPVKNKNSLSKV 189
QY 139 ANMCRGI-----PTYMAEEMOE 155
DB 190 LEICGDLPIFWLKPTYPEKIORE 212

RESULT 8
US-08-241-465B-20
Sequence 20 Application US/08241465B
Patent No. 5719125
GENERAL INFORMATION:
APPLICANT: Fujio SUZUKI
APPLICANT: YUJI HIRAKI
APPLICANT: Kazuhiko TAKAHASHI
APPLICANT: Junko SUZUKI
APPLICANT: Jun KONDO
APPLICANT: Atsuko KOHARA
APPLICANT: AKIKO MORI
APPLICANT: BI YAMADA
TITLE OF INVENTION: HUMAN CHONDROMODULIN-1 PROTEIN
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
COUNTRY: D.C.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,465B
FILING DATE: May 11, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 334 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-241-465B-20

Query Match 7.2%; Score 72; DB 1; Length 334;
Best Local Similarity 20.3%; Pred. No. 3.7; Indels 14; Gaps 4;
Matches 29; Conservative 26; Mismatches 74;
QY 21 NYNIDVNDNNAGSGQ-SVSVNNEHNVANVNDNNGSDMSNIMWYNGFAATRLFOKK 79
DB 76 HTYMSIN-----GKLDGSMELDAGNNLETFKMGSAEALVAVDFONGITGIRPAGE 129
QY 80 TCIVHKKKEVWPSIOSDALVKEKTLQK-GPGGPPKGLMYSVNPKNKVDLSKFGKNI 138
DB 130 KCIYKAQVKARIPVGAATVKOSISKLEKIMPVKTEENSLIWAVDQPVKNKNSLSKV 189
QY 139 ANMCRGI-----PTYMAEEMOE 155
DB 190 LEICGDLPIFWLKPTYPEKIORE 212

RESULT 9
US-08-227-108-16
Sequence 16 Application US/08227108
Patent No. 580726
GENERAL INFORMATION:
APPLICANT: Blanchard, Claire
APPLICANT: Benicourt, Claude
APPLICANT: Julien, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,108
FILING DATE: 03-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fannucci, Allan A.
REGISTRATION NUMBER: 30,256
REFERENCE/DOCKET NUMBER: 7620-033

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 790-9090
 TELEFAX: 212 869-8864/9741
 TELEEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 380 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-227-108-16

Query Match
 Best Local Similarity 23.1%; Score 72; DB 1; Length 380;
 Matches 39; Conservative 30; Mismatches 50; Indels 50; Gaps 11;

QY 22 YNIDVN---DDNNAGSGQGSVSYNNEHN-----VANVDNN-----GMSW- 60
 Db 38 YLEVNRIPIYCKKNSGNTGQRPV-VFLQHGILASATNMWISNLPNNSLAFLIADAGYDVL 96
 QY 61 -NSTWDYNGGFAATRLFFOKTCTI-----VHKMKKEVPSIQSLDALYK---EKKLQK 109
 Db 97 GNS---KGNTWARRNLIYSPDSVEFMAAFSPDEMAKYDLP--TIDPIYKKTGQKQLHYV 151
 QY 110 GPGGPPKPG-LMYSVNNKRYDLS-----KFGKNIANMCRGIP 146
 Db 152 GHSQGTIGTIFASTNPISLAKRIKTFYALAPVATVYKTSINKLRFVP 200

RESULT 10

US-09-073-674-16
 Sequence 16, Application US/09073674
 Patent No. 5998189

GENERAL INFORMATION:

APPLICANT: Blanchard, Claire
 APPLICANT: Benicourt, Claude
 APPLICANT: Junien, Jean-Louis
 TITLE OF INVENTION: Recombinant Dog Gastric Lipase
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Warner-Lambert Company
 STREET: 2800 Plymouth Road
 CITY: Ann Arbor
 STATE: Michigan
 COUNTRY: U.S.A.
 ZIP: 48105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/073,674
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Crlsey, Todd M.
 REGISTRATION NUMBER: 37,807
 REFERENCE/DOCKET NUMBER: 5072-DI-66-TMC
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 734 622-7530
 TELEFAX: 734 622-1553
 TELEX:

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:
 LENGTH: 380 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-073-674-16

Query Match
 Best Local Similarity 23.1%; Score 72; DB 2; Length 380;
 Matches 39; Conservative 30; Mismatches 50; Indels 50; Gaps 11;

QY 22 YNIDVN---DDNNAGSGQGSVSYNNEHN-----VANVDNN-----GMSW- 60
 Db 38 YLEVNRIPIYCKKNSGNTGQRPV-VFLQHGILASATNMWISNLPNNSLAFLIADAGYDVL 96
 QY 61 -NSTWDYNGGFAATRLFFOKTCTI-----VHKMKKEVPSIQSLDALYK---EKKLQK 109
 Db 97 GNS---KGNTWARRNLIYSPDSVEFMAAFSPDEMAKYDLP--TIDPIYKKTGQKQLHYV 151
 QY 110 GPGGPPKPG-LMYSVNNKRYDLS-----KFGKNIANMCRGIP 146
 Db 152 GHSQGTIGTIFASTNPISLAKRIKTFYALAPVATVYKTSINKLRFVP 200

RESULT 11

US-09-118-319-2
 Sequence 2, Application US/09118319
 Patent No. 6114158

GENERAL INFORMATION:

APPLICANT: Li, Xin-Liang
 APPLICANT: Chen, Huizhong
 APPLICANT: Ljungdahl, Lars G.
 TITLE OF INVENTION: Orpinomyces Cellulase Celf Protein and Coding Sequences
 FILE REFERENCE: 33-98sequence listing
 CURRENT APPLICATION NUMBER: US/09/118,319
 CURRENT FILING DATE: 1998-07-17
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 2

LENGTH: 432
 TYPE: PRT
 ORGANISM: Orpinomyces sp. PC-2
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:colligonucleotide

US-09-118-319-2

Query Match
 Best Local Similarity 7.2%; Score 71.5; DB 3; Length 432;
 Matches 33; Conservative 21; Mismatches 60; Indels 9; Gaps 4;

QY 27 NDDNNAGSGQGSVSYNNEHNAVYDNNNGWDSNWSIMDYNGGFAATRLFFOKKTCIVHKM 86
 Db 64 NPSNNASNN 118
 QY 87 KEVVPSTISLDALYKKEKKGKGGPGPPKGLMYSVNNKRYDLSKF--GKNIANMCRG 144
 Db 119 IEEVNSSTPKLSMDLQAKQKVDV--PVAWLAMEGAPVEVDHLKAGSKTYVFIYV 176
 QY 145 IPT 147
 Db 177 IPT 179

RESULT 12

US-08-484-493-13
 Sequence 13, Application US/08484493
 Patent No. 5728381

GENERAL INFORMATION:

APPLICANT: Wilson, Peter J
 APPLICANT: Morris, Charles P
 APPLICANT: Anson, Donald S
 APPLICANT: Occhiodoro, Teresa
 APPLICANT: Brielickl, Julie
 APPLICANT: Clements, Peter R
 APPLICANT: Hopwood, John J
 TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
 IDURONATE 2-SULFATASE

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,493
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8416Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 533 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-484-493-13

Query Match 7.2%; Score 71.5; DB 1; Length 533;
Best Local Similarity 26.8%; Pred. No. 8.4; Indels 47; Gaps 11;
Matches 42; Conservative 20; Mismatches

OY 43 NNEHNANVND-----NNGMD-----YNGFAATRLFOKKTCTVHKMK 88
DB 291 NNIVFISTDNGGOTLAGNNMPLRGKW-SLMEGVGVGCVASPLLKQGV-----KNR 345
OY 89 EVMSIOSLDALVK-----EKKLOG-----KPGGPPPK-GLMYSVNPKNVDDLSK 133
DB 346 ELIHSDMLPTLVKLARGHTNGTKPLDGFVWKTISEGSPSPRIELHNDPFDVS-SP 404
OY 134 FGNIANMCRGIFTYMAEEMQESLFFYSGTCYTSV 170
DB 405 CPRN-----SMAPAKDSSLPETYS--AFNTSV 429

RESULT 13
US-08-484-494-13
Sequence 13, Application US/08484494
Patent No. 5798239
GENERAL INFORMATION:
APPLICANT: Wilson, Peter J
APPLICANT: Morris, Charles P
APPLICANT: Anson, Donald S
APPLICANT: Occhiodoro, Teresa
APPLICANT: Bieliicki, Julie
APPLICANT: Clements, Peter R
APPLICANT: Hopwood, John J
TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza

CITY: Garden City
STATE: New York
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,494
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8416Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 533 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-484-494-13

Query Match 7.2%; Score 71.5; DB 1; Length 533;
Best Local Similarity 26.8%; Pred. No. 8.4; Indels 47; Gaps 11;
Matches 42; Conservative 20; Mismatches

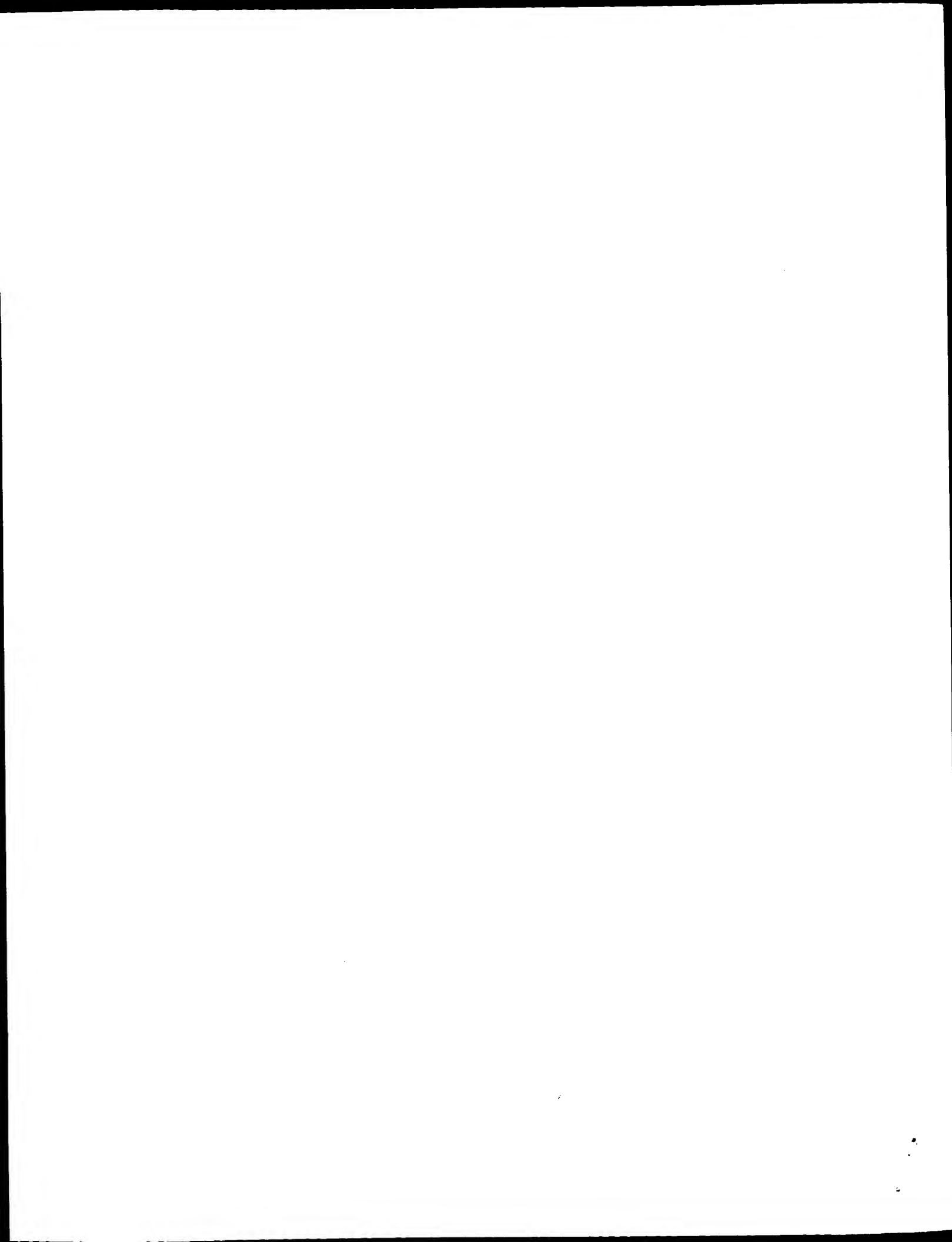
OY 43 NNEHNANVND-----NNGMD-----YNGFAATRLFOKKTCTVHKMK 88
DB 291 NNIVFISTDNGGOTLAGNNMPLRGKW-SLMEGVGVGCVASPLLKQGV-----KNR 345
OY 89 EVMSIOSLDALVK-----EKKLOG-----KPGGPPPK-GLMYSVNPKNVDDLSK 133
DB 346 ELIHSDMLPTLVKLARGHTNGTKPLDGFVWKTISEGSPSPRIELHNDPFDVS-SP 404
OY 134 FGNIANMCRGIFTYMAEEMQESLFFYSGTCYTSV 170
DB 405 CPRN-----SMAPAKDSSLPETYS--AFNTSV 429

RESULT 14
US-08-345-212-13
Sequence 13, Application US/08345212
Patent No. 5932211
GENERAL INFORMATION:
APPLICANT: Wilson, Peter J
APPLICANT: Morris, Charles P
APPLICANT: Anson, Donald S
APPLICANT: Occhiodoro, Teresa
APPLICANT: Bieliicki, Julie
APPLICANT: Clements, Peter R
APPLICANT: Hopwood, John J
TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: USA
ZIP: 11530

Query Match 7.2%; Score 71.5; DB 4; Length 533;
Best Local Similarity 26.8%; Pred. No. 8.4;
Matches 42; Conservative 20; Mismatches 48; Indels 47; Gaps 11;

Search completed: September 4, 2002, 16:46:12
Job time: 333 sec

RESULT 15
US-09-249-003-13
; Sequence 13, Application US/09249003
; Patent No. 6153188



A:Title: Molecular structure and genetic regulation of SFA, a gene responsible for resistance to streptococcal infection in *Salmonella typhimurium* DT104
A:Reference number: S31138; MUID:93247548
A:Accession: S31139
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-492, 'N', 494-719 <WEH>
A:Cross-references: EMBL:X68020; NID:g577609; PID:CAA48159.1; PID:g288590
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
R:Pohl, T.M.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67708
A:Accession: S67719
A:Molecule type: DNA
A:Residues: 1-719 <POW>
A:Cross-references: EMBL:Z74215; NID:gl431265; PID:CAA98741.1; PID:e253076; PID:gl43126
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:NRP1; ARP1
A:Cross-references: MIPS:VDL167c; SGD:S0002326
A:Map position: 4L

	Query Match	9.6%; Score 95.5; DB 2;	Length 719;
	Best Local Similarity	25.5%;	Pred. No. 0.59;
	Matches	Conservative 18;	Mismatches 62; Indels 37; Gaps 5;
Qy	22 YNIDVDDNNAGSGOOSVSVNNEIN-----VANVDNNKNGWDSNSIW 64 : : : : :		
Dd	508 YNTNNITNGGNGGNSSNNHHNNHNNHNHGHSTINSNSTNNNNNNHGNSNCNS 567 : : : : :		
Qy	65 DYNGGFAATRL-----FOKKTCIVHKMKKEVM-----PSIOSLDALVREKKLQGK--G 110 :: :: : : : : :		
Dd	568 NIGMGCGSNMPFRAGDWKCSTCTYHFNAFNVCLRCGGPKSISGDASEINHYSISFTFG 627 :: :: : : : : :		
Qy	111 PGGPPPKGLMYSNPN-----KVDDLCKFKGTANM 141 : : : : :		
Dd	628 PASRTPSNNNISVTNYNGGSNAGRTDGNDNKGRDTSIM 664 : : : : :		

RESULT 3
 H71607
 hypothetical protein PF0705w - malaria parasite (Plasmodium falciparum)
 C:Species: Plasmodium falciparum
 C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
 C:Accession: H71607
 R:Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
 .; Percec, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
 Science 282, 1126-1132, 1998
 A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
 A:Reference number: A71600; MUID:99021743
 A:Accession: H71607
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-764 <GAR>
 A:Cross-references: GB:AE001413; GB:AE001362; NID:g3845255; PIDN:AACT1930.1; PID:g3845255
 A:Experimental source: clone 3d7
 C:Genetics:
 A:Gene: PF0705w

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Query Match          9.4%; Score 93; DB 2; Length 764;
Best Local Similarity 22.6%; Pred. No. 1.1;
Matches 31; Conservative 25; Mismatches 41; Indels 40; Gaps 6;

Qy      20 ANYIDVDDNNAGSGQSQSVYNEINVANVDNNGGWDNSWNSIWDYGNGFAATRLFOKK 79
       :|::||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      335 SNHHNHNNHNSHNHNHNHNHNHNHNHNHNHNHNHNHNHNHNYYNYLYTN-----YQK- 386

Qy      80 TCIVHHKKKEVMPSIQSIDALVKELKGCGPGPPPKGLMY-SVNPNKVD-----DL 131
       ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      387 -----HKNNKIPTP-----PSGPPPPNNIKYNNVHPNNYPNPDPGGT.L 424

Ov      132 SKFGKNIANMCRGIPTY 148
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RESULT 12
B69823
conserved hypothetical protein yhcN - Bacillus subtilis
C/Species: Bacillus subtilis
C/Date: 05-Dec-1997 #text_change 15-Oct-1999
C/Acession: B69823
E/Kunst, F.; Ogasawara, N.; Moszer, I.; Alloni, G.; Azevedo,
C.; Bron, S.; Brouillet, S.; Bruschii, C.V.; Caldwell, B.; Capuano, V.; Carter,
A.; Ehrlich, S.D.; Emmerison, P.T.; Entian, K.D.; Errington, J.; Fabret, C.;
Nature 390, 249-256, 1997
A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi,
M.; Harwood, C.R.; Henaute, A.; Hilbert, H.; Holstege, F.C.;
Iech, J.; Harwood, C.R.; Henaute, A.; Hilbert, H.; Holstege, F.C.;
Iech, J.; Harwood, C.R.; Henaute, A.; Hilbert, H.; Holstege, F.C.

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:46:08 ; Search time 57.74 Seconds
(without alignments)
8.038 Million cell updates/sec

Title: US-09-821-726-5
Perfect score: 90
Sequence: 1 KKEYMPSIQSLDALVKEKK 19

Scoring table: BLOSUM62
Gapex 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
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3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	44.4	1964	2	US-08-790-912-3
2	40	44.4	2052	4	US-08-790-912-2
3	37.5	41.7	2548	4	US-09-172-422-1
4	37	41.1	24	2	US-08-491-527A-12
5	37	41.1	476	3	US-08-704-711A-21
6	37	41.1	476	4	US-08-448-489-14
7	37	41.1	498	1	US-08-470-202-59
8	37	41.1	498	1	US-08-470-202-60
9	37	41.1	498	1	US-08-471-770-59
10	37	41.1	498	1	US-08-471-770-60
11	37	41.1	498	2	US-08-468-059-59
12	37	41.1	498	2	US-08-468-059-60
13	37	41.1	498	4	US-09-109-916-59
14	37	41.1	498	4	US-09-109-916-60
15	37	41.1	568	2	US-08-835-170-4
16	37	41.1	568	4	US-09-359-257-4
17	37	41.1	588	2	US-08-835-170-2
18	37	41.1	588	4	US-09-359-257-2
19	37	41.1	1045	2	US-08-553-436A-6
20	37	41.1	1525	4	US-09-396-651B-1
21	37	41.1	1536	1	US-08-038-682-2
22	37	41.1	1536	1	US-08-302-832-2
23	37	41.1	1536	2	US-08-530-198-2
24	37	41.1	1536	2	US-08-469-880-2
25	37	41.1	1536	2	US-08-728-470-2
26	37	41.1	1536	2	US-08-617-697-2
27	37	41.1	1536	4	US-08-719-641-2

Sequence 23, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 46, Appli
Sequence 62, Appli
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Sequence 63, Appli
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Sequence 46, Appli
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Sequence 63, Appli
Sequence 8, Appli
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Sequence 12, Appli
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Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-790-912-3
; Sequence 3, Application US/08790912
; Patent No. 5976542
; GENERAL INFORMATION:
; APPLICANT: Weiser, Jeffrey N.
; APPLICANT: Plaut, Andrew G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
; TITLE OF INVENTION: OF STREPTOCOCCUS PNEUMONIAE INFECTION
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,912
; FILING DATE: 29-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,939
; FILING DATE: 23-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Leary, Kathryn
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 7600-4UI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 567-2020
; TELEFAX: (215) 567-2991
; TELEX: 831-494
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1964 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-912-3

Query Match 44.4%; Score 40; DB 2; Length 1964;
Best Local Similarity 63.6%; Pred. No. 2.6e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 KEVMPISQSLD 12
|||:|:|:|
Db 1230 KEVLPQLKLD 1240

RESULT 2

US-08-790-912-2
; Sequence 2, Application US/08790912
; Patent No. 5976542
; GENERAL INFORMATION:
; APPLICANT: Weiser, Jeffrey N.
; APPLICANT: Plaut, Andrew G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
; OF STREPTOCOCCUS PNEUMONIAE INFECTION
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,912
; FILING DATE: 29-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,939
; FILING DATE: 23-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Leary, Kathryn
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 7600-401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 567-2020
; TELEFAX: (215) 567-2991
; TELEX: 831-494
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2052 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-912-2

Query Match 44.4%; Score 40; DB 2; Length 2052;
Best Local Similarity 63.6%; Pred. No. 2.7e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 KEVMPISQSLD 12
|||:|:|:|
Db 1303 KEVLPQLKLD 1313

RESULT 3

US-09-172-422-1
; Sequence 1, Application US/09172422A
; Patent No. 6300485
; GENERAL INFORMATION:
; APPLICANT: Adams, Arwen E.
; APPLICANT: Chiu, Choi Ying
; APPLICANT: Duhl, David
; APPLICANT: Gorman, Susan W.
; APPLICANT: Leng, Song
; APPLICANT: Sheffield, Val
; APPLICANT: Welch, Juliet

; TITLE OF INVENTION: MYOSIN IXA AND CYCLIC NUCLEOTIDE GATED
; TITLE OF INVENTION: CHANNEL-15 (CNGC-15) POLYNUCLEOTIDES, POLYPEPTIDES,
; FILE REFERENCE: 200130.442
; CURRENT APPLICATION NUMBER: US/09/172,422A
; CURRENT FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2548
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-172-422-1

Query Match 41.7%; Score 37.5; DB 4; Length 2548;
Best Local Similarity 50.0%; Pred. No. 9.2e+02;
Matches 10; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 1 KKEYMPSI-QSLDALVREKK 19
|||:|:|:|:|:|:|
Db 1509 EKENMEQIRQQTDLERK 1528

RESULT 4

US-08-491-527A-12
; Sequence 12, Application US/08491527A
; Patent No. 5824483
; GENERAL INFORMATION:
; APPLICANT: Houston, Michael E.
; APPLICANT: Hodges, Robert S.
; TITLE OF INVENTION: Conformationally-Restricted Combinatorial
; TITLE OF INVENTION: Library Composition and Method
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/491,527A
; FILING DATE: 16-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,199
; FILING DATE: 15-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/245,507
; FILING DATE: 18-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 7900-0008.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: LPS epitope library peptide, Fig. 5A

US-08-491-527A-12

Query Match 41.1%; Score 37; DB 2; Length 24;
Best Local Similarity 47.4%; Pred. No. 5.1;
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 KKEVMPISQSLDALVREKK 19
||| :| :|||
Db 6 KKEHFLVQKIHLEKEIK 24

RESULT 5

US-08-704-711A-21
; Sequence 21, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,711A
FILING DATE: 20-NOV-1996
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/DE95/00357
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4438838.1
FILING DATE: 21-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-704-711A-21

Query Match 41.1%; Score 37; DB 3; Length 476;
Best Local Similarity 56.2%; Pred. No. 1.6e+02;
Matches 9; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY 6 PSIQSLDALV--KEKK 19
|:: :||| :|||
Db 382 PTIRKIDAAVSDKEKK 397

RESULT 6

US-08-448-489-14
; Sequence 14, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-14

Query Match 41.1%; Score 37; DB 4; Length 476;
Best Local Similarity 56.2%; Pred. No. 1.6e+02;
Matches 9; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY 6 PSIQSLDALV--KEKK 19
|:: :||| :|||
Db 382 PTIRKIDAAVSDKEKK 397

RESULT 7

US-08-470-202-59
; Sequence 59, Application US/08470202
; Patent No. 5759808
; GENERAL INFORMATION:
; APPLICANT: Guertler, Lutz G.
; APPLICANT: Eberle, Josef
; APPLICANT: Brunn, Albrecht v.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: Retrovirus from the HIV Group and Its
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESS: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,202
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/132,653
FILING DATE: 05-OCT-1993
APPLICATION NUMBER: DE P 42 33 646.5
FILING DATE: 06-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 42 35 718.7
FILING DATE: 22-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 42 44 541.8

; FILING DATE: 30-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 18 186.4
; FILING DATE: 01-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael J. Blake
; REGISTRATION NUMBER: 37,096
; REFERENCE/DOCKET NUMBER: 05495-0001-00000
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; US-08-470-202-59

Query Match 41.1%; Score 37; DB 1; Length 498;
Best Local Similarity 36.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 KKEVMPISQSLDALVKEKK 19
Db 455 KQVSPSPAPPMEAEVKEQE 473

RESULT 8
US-08-470-202-60
; Sequence 60, Application US/08470202
; Patent No. 5759808
; GENERAL INFORMATION:
; APPLICANT: Guertler, Lutz G.
; APPLICANT: Eberle, Josef
; APPLICANT: Brunn, Albrecht v.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: Retrovirus from the HIV Group and Its
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,202
; FILING DATE: 06-OCT-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/132,653
; FILING DATE: 05-OCT-1993
; APPLICATION NUMBER: DE P 42 33 646.5
; FILING DATE: 06-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 35 718.7
; FILING DATE: 22-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 44 541.8
; FILING DATE: 30-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 18 186.4

; FILING DATE: 01-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael J. Blake
; REGISTRATION NUMBER: 37,096
; REFERENCE/DOCKET NUMBER: 05495-0001-00000
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; US-08-470-202-60

Query Match 41.1%; Score 37; DB 1; Length 498;
Best Local Similarity 36.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 KKEVMPISQSLDALVKEKK 19
Db 455 KQVSPSPAPPMEAEVKEQE 473

RESULT 9
US-08-471-770-59
; Sequence 59, Application US/08471770
; Patent No. 5770427
; GENERAL INFORMATION:
; APPLICANT: Guertler, Lutz G.
; APPLICANT: Eberle, Josef
; APPLICANT: Brunn, Albrecht v.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: Retrovirus from the HIV Group and Its
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,770
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/132,653
; FILING DATE: 05-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 33 646.5
; FILING DATE: 06-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 35 718.7
; FILING DATE: 22-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 44 541.8
; FILING DATE: 30-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 18 186.4
; FILING DATE: 01-JUN-1993


```
;
; REGISTRATION NUMBER: 32,220
; REFERENCE/DOCKET NUMBER: 05495-0001-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-468-059-59
```

```
Query Match 41.1%; Score 37; DB 2; Length 498;
Best Local Similarity 36.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
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```
QY 1 KKEVMPISQSLDALVKEKK 19
Db 455 QKQVSPSPAPPMEAEVKEQE 473
```

```
RESULT 12
US-08-468-059-60
; Sequence 60, Application US/08468059
; Patent No. 5840480
; GENERAL INFORMATION:
; APPLICANT: Guertler, Lutz G.
; APPLICANT: Eberle, Josef
; APPLICANT: Brunn, Albrecht V.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: Retrovirus from the HIV Group and Its
; TITLE OF INVENTION: Use
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,059
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/132,653
; FILING DATE: 05-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 33 646.5
; FILING DATE: 06-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 35 718.7
; FILING DATE: 22-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 44 541.8
; FILING DATE: 30-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 18 186.4
; FILING DATE: 01-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Carol P. Einaudi
; REGISTRATION NUMBER: 32,220
```

```
;
; REFERENCE/DOCKET NUMBER: 05495-0001-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-468-059-60
```

```
Query Match 41.1%; Score 37; DB 2; Length 498;
Best Local Similarity 36.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 1 KKEVMPISQSLDALVKEKK 19
Db 455 QKQVSPSPAPPMEAEVKEQE 473
```

```
RESULT 13
US-09-109-916-59
; Sequence 59, Application US/09109916
; Patent No. 6277561
; GENERAL INFORMATION:
; APPLICANT: Guertler, Lutz G.
; APPLICANT: Eberle, Josef
; APPLICANT: Brunn, Albrecht V.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE
; FILE REFERENCE: 05495, 0001-04
; CURRENT APPLICATION NUMBER: US/09/109,916
; CURRENT FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: DE P 42 33 646.5
; EARLIER FILING DATE: 1992-10-06
; EARLIER APPLICATION NUMBER: DE P 42 35 718.7
; EARLIER FILING DATE: 1992-10-22
; EARLIER APPLICATION NUMBER: DE P 42 44 541.8
; EARLIER FILING DATE: 1992-12-30
; EARLIER APPLICATION NUMBER: DE P 43 18 186.4
; EARLIER FILING DATE: 1993-06-01
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
; US-09-109-916-59
```

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Query Match 41.1%; Score 37; DB 4; Length 498;
Best Local Similarity 36.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
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```
QY 1 KKEVMPISQSLDALVKEKK 19
Db 455 QKQVSPSPAPPMEAEVKEQE 473
```

```
RESULT 14
US-09-109-916-60
; Sequence 60, Application US/09109916
; Patent No. 6277561
; GENERAL INFORMATION:
; APPLICANT: Guertler, Lutz G.
; APPLICANT: Eberle, Josef
; APPLICANT: Brunn, Albrecht V.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 17:01:39 ; Search time 124.34 Seconds
(without alignments)
257.392 Million cell updates/sec

Title: US-09-821-726-13

Perfect score: 994

Sequence: 1 MKFTIVFAGLGVFLAPALA.....YTTSLVIVDISFGDIVEN 185

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp-archaea:*
- 2: sp-bacteria:*
- 3: sp-fungi:*
- 4: sp-human:*
- 5: sp-invertebrate:*
- 6: sp-mammal:*
- 7: sp-mhc:*
- 8: sp-organelle:*
- 9: sp-phage:*
- 10: sp-plant:*
- 11: sp-rodent:*
- 12: sp-virus:*
- 13: sp-vertebrate:*
- 14: sp-unclassified:*
- 15: sp-virus:*
- 16: sp-bacteriap:*
- 17: sp-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query		Match	Length	DB	ID	Description
SUMMARIES								
1	245	24.6	191	11	Q9D0T7			Q9D0T7 mus musculus
2	195	19.6	184	11	Q9C0S6			Q9C0S6 mus musculus
3	98	9.9	568	5	Q9NL38			Q9NL38 pinctada ma
4	97	9.8	588	5	Q964F6			Q964F6 plasmodium
5	97	9.8	1208	5	Q97101			Q97101 dictyostelli
6	96.5	9.7	1844	5	Q97287			Q97287 plasmodium
7	95.5	9.6	1318	5	Q95PH4			Q95PH4 dictyostelli
8	93	9.4	764	5	Q96234			Q96234 plasmodium
9	91.5	9.2	596	5	Q964F7			Q964F7 plasmodium
10	91.5	9.2	600	5	Q964F5			Q964F5 plasmodium
11	91.5	9.2	600	5	Q95NL3			Q95NL3 plasmodium
12	90	9.1	604	5	Q964F8			Q964F8 plasmodium
13	90	9.1	1245	5	Q96195			Q96195 plasmodium
14	89	9.0	608	5	Q97331			Q97331 plasmodium
15	88.5	8.9	186	5	Q01876			Q01876 caenorhabdi
16	88	8.9	560	5	Q00885			Q00885 dictyostelli

17	88	8.9	3619	5	Q9U573	Q9U573 dictyosteli
18	87	8.8	1650	5	Q77328	Q77328 plasmodium
19	86	8.7	346	5	Q77363	Q77363 plasmodium
20	85	8.6	915	5	Q9GN07	Q9GN07 plasmodium
21	85	8.6	1064	5	Q25773	Q25773 plasmodium
22	85	8.6	1256	5	Q25770	Q25770 plasmodium
23	84.5	8.5	720	5	Q23847	Q23847 dictyosteli
24	84.5	8.5	1855	5	Q9TX75	Q9TX75 plasmodium
25	84.5	8.5	1855	5	Q9BHN0	Q9BHN0 plasmodium
26	84.5	8.5	2188	5	Q9VXD5	Q9VXD5 plasmodium
27	84	8.5	1817	5	Q96253	Q96253 plasmodium
28	83.5	8.4	728	5	Q96422	Q96422 plasmodium
29	83.5	8.4	1979	5	Q96133	Q96133 plasmodium
30	83.5	8.4	3300	16	O06304	O06304 mycobacteri
31	83.5	8.4	3933	5	Q97239	Q97239 plasmodium
32	83	8.4	1010	5	Q9U0J3	Q9U0J3 plasmodium
33	83	8.4	1570	5	Q9U0H8	Q9U0H8 plasmodium
34	83	8.4	1960	5	Q9U0K8	Q9U0K8 plasmodium
35	83	8.4	3394	5	Q77384	Q77384 plasmodium
36	82.5	8.3	949	5	Q97306	Q97306 plasmodium
37	82.5	8.3	1225	5	O15784	O15784 dictyosteli
38	82.5	8.3	1225	5	Q95P12	Q95P12 dictyosteli
39	82	8.2	359	3	Q96X44	Q96X44 saccharomyc
40	82	8.2	419	5	Q25774	Q25774 plasmodium
41	82	8.2	622	5	Q9U0K4	Q9U0K4 plasmodium
42	81.5	8.2	865	15	Q9ICT2	Q9ICT2 chimpanzee
43	81.5	8.2	877	5	Q23853	Q23853 dictyosteli
44	81.5	8.2	1090	3	Q9P5J0	Q9P5J0 neurospora
45	81.5	8.2	1486	5	Q9XZS0	Q9XZS0 dictyosteli

ALIGNMENTS

RESULT 1
Q9D0T7 PRELIMINARY; PRT; 191 AA.
AC Q9D0T7;
DT 01-JUN-2001 (TREMELREL. 17, Created)
DT 01-JUN-2001 (TREMELREL. 17, Last sequence update)
DE 1190003M12RIK PROTEIN.
DE 1190003M12RIK (Last annotation update)
GN 1190003M12RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamazaki I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochava H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikolaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK004474; BAB23320.1; -;
DR MGD; MGI:1916138; 1190003M12RIK.

[illegible]

	9	RESULT	
ID	Q964F7	PRT;	596 AA.
ID	Q964F7	PRELIMINARY;	
AC	Q964F7;		
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DT	01-DEC-2001	(TREMBLrel . 19, Last sequence update)	
DT	01-DEC-2001	(TREMBLrel . 19, Last annotation update)	
DE	MEROZOITE SURFACE PROTEIN 8.		
DE	MSP8.		
GN	Plasmodium falciparum.		
OS	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.		
OC	[1]		
OX	NBI_TaxID=5833;		
RN	SEQUENCE FROM N.A.		
RP	STRAIN=D10;		
RC			

ID	Q95NL3	PRELIMINARY;	PK1	000 RA.
AC	Q95NL3;			
DT	01-DEC-2001	(REMBLrel. 19, Created)		
DT	01-DEC-2001	(REMBLrel. 19, Last sequence update)		
DT	01-DEC-2001	(REMBLrel. 19, Last annotation update)		
DE	MEROZOITE SURFACE PROTEIN 8.			
GN	MSP8.			
OS	Plasmodium falciparum.			
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.			
OX	NCBI_TaxID=5833;			
RP	[1]			
RP	SEQUENCE FROM N.A.			

ID	Q95NL3	PRELIMINARY;	PK1	000 RA.
AC	Q95NL3;			
DT	01-DEC-2001	(REMBLrel. 19, Created)		
DT	01-DEC-2001	(REMBLrel. 19, Last sequence update)		
DT	01-DEC-2001	(REMBLrel. 19, Last annotation update)		
DE	MEROZOITE SURFACE PROTEIN 8.			
GN	MSP8.			
OS	Plasmodium falciparum.			
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.			
OX	NCBI_TaxID=5833;			
RP	[1]			
RP	SEQUENCE FROM N.A.			


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Search completed: September 4, 2002, 17:01:41
Job time: 1162 sec
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RESULT 9
66572
    yandoline receptor type 3 - chicken
    ;;Species: Gallus gallus (chicken)
    ;;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
    ;;Accession: S66572
    ;;Title: Alpha and beta isoforms of yandoline receptor from chicken skeletal muscle are
    ;;Reference number: S66572; MUID:96207583
    ;;Accession: S66572
    ;;Status: preliminary; nucleic acid sequence not shown
    ;;Molecule type: mRNA
    ;;Residues: 1-4869 <OTT>
    ;;Cross-references: EMBL:X95287; NID:gl1212911; PID:gl1212912
    ;;Superfamily: yandoline receptor; transcription initiation factor sigma region 1 homolog

```

-3-hydroxy-2-naphthoate isomerase - Pseudomonas putida plasmid NAH7

C:Species: Pseudomonas putida
C:Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 29-Sep-1999
C:Accession: C55552

R:Eaton, R.W.
J. Bacteriol. 176, 7757-7762, 1994
A:Title: Organization and evolution of naphthalene catabolic pathways: sequence of the p from the NAH7 plasmid.

A:Reference number: A55552; MUID:95095951

A:Accession: C55552

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-203 <EAT>

A:Cross-references: GB:U09057; NID:g483790; PIDN:AAA66358.1; PID:g483793

C:Genetics:

A:Gene: nahD

A:Genome: plasmid

A:Start codon: GTG

C:Superfamily: 2-hydroxychromene-2-carboxylate isomerase

Query Match 46.7%; Score 42; DB 2; Length 203;
Best Local Similarity 53.3%; Pred. No. 29;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 VMPISQSLDALVKEK 18

:|:|:|:|:|:|

Db 118 IAPDLESPLAVSEK 132

RESULT 13

hypothetical protein RC0442 [imported] - Rickettsia conorii (strain Malish 7)

C:Species: Rickettsia conorii

C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001

C:Accession: B97755

R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R

Science 293, 2093-2098, 2001

A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.

A:Reference number: A97700; MUID:21442074; PMID:11557893

A:Accession: B97755

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-339 <KUR>

A:Cross-references: GB:AE006914; PIDN:AAL02980.1; PID:g15619513; GSPDB:GN00173

C:Genetics:

A:Gene: RC0442

C:Superfamily: yceG protein

Query Match 46.7%; Score 42; DB 2; Length 339;
Best Local Similarity 57.1%; Pred. No. 51;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 PSIOSLDALVKEK 19

:|:|:|:|:|:|

Db 276 PSLKSLEAVVKS 289

RESULT 14

T41207

hypothetical protein SPCC1902.02 - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T41207

R:Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, March 1999

A:Reference number: Z21928

A:Accession: T41207

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-574 <SEE>

A:Cross-references: EMBL:AL049521; PIDN:CAB40004.1; GSPDB:GN00068; SPDB:SPCC1902.02

A:Experimental source: strain 972h-; cosmid c1902

C:Genetics:
A:Gene: SPCC663.16c; SPDB:SPCC1902.02

A:Map position: 3

A:Introns: 14/1; 68/1

Query Match 46.7%; Score 42; DB 2; Length 574;
Best Local Similarity 40.0%; Pred. No. 89;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 3 EVMPISQSLDALVKE 17

:|:|:|:|:|:|

Db 90 KILPSVYNLDTAIKE 104

RESULT 15

AC2477

hypothetical protein all5371 [imported] - Anabaena sp. (strain PCC 7120)

C:Species: Anabaena sp.

A:Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002

C:Accession: AC2477

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.;

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AC2477

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-130 <KUR>

A:Cross-references: GB:BA000019; PIDN:BA077070.1; PID:g17134510; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: all5371

Query Match 45.6%; Score 41; DB 2; Length 130;
Best Local Similarity 62.5%; Pred. No. 26;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 KEVMPISQSLDALVKE 17

:|:|:|:|:|:|

Db 52 KEVMASPGELDPLVRE 67

Search completed: September 4, 2002, 16:47:35

Job time: 371 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2002, 17:01:37 ; Search time 124.34 Seconds
(without alignments)
26.435 Million cell updates/sec

Title: US-09-821-726-5
Perfect score: 90
Sequence: 1 KKEYMPSIQSLDALVKEK 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriaph.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	54.4	592	5 Q9VZW4	Q9VZW4 drosophila
2	47	52.2	2895	10 O65551	O65551 arabidopsis
3	46	51.1	388	16 Q92P38	Q92P38 rhizobium m
4	45	50.0	430	16 Q25052	Q25052 helicobacte
5	45	50.0	431	16 Q92M60	Q92M60 helicobacte
6	45	50.0	1712	5 Q9VSV99	Q9VSV99 drosophila
7	45	50.0	1716	5 Q961N2	Q961N2 drosophila
8	45	50.0	1912	5 Q9NGV1	Q9NGV1 drosophila
9	45	50.0	5081	13 O13054	O13054 makaira nig
10	44.5	49.4	1676	10 Q23332	Q23332 arabidopsis
11	44	48.9	1336	5 Q21216	Q21216 caenorhabdi
12	43	47.8	156	10 Q9LJV3	Q9LJV3 arabidopsis
13	43	47.8	283	4 Q9NSK3	Q9NSK3 homo sapien
14	43	47.8	489	4 Q9BR76	Q9BR76 homo sapien
15	43	47.8	4869	13 Q90985	Q90985 gallus gall
16	42.5	47.2	299	3 Q9UVK3	Q9UVK3 candida alb

ALIGNMENTS

RESULT 1

ID	Q9VZW4	PRELIMINARY;	PRT;	592 AA.
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	CG2077 PROTEIN.			
GN	CG2077.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7227;			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RP	STRAIN=BERKELEY.			
RX	MEDLINE=20196006; PubMed=10731132;			
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Amantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,			
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
RA	Sutton G.G., Wortman J.R., Vandeil M.D., Zhang O., Chen L.X.,			
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,			
RA	Wap K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,			
RA	Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,			
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,			
RA	Beeson K.Y., Benos P.V., Beriman B.P., Bhandari D., Bolshakov S.,			
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,			
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,			
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,			
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,			
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,			
RA	Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,			
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,			
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,			
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,			


```

RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RL pylori.";
RL Nature 388:539-547(1997).
DR EMBL: AE000546; AAD07339.1; -.
DR TIGR: HF0275; -.
DR InterPro: IPR002885; PPR.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 430 AA; 49684 MW; E702669D4297A52C CRC64;

Query Match 50.0%; Score 45; DB 16; Length 430;
Best Local Similarity 42.1%; Pred. No. 41;
Matches 8; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 KKEVMPISQSLDALVKEKK 19
Db 313 KEEMLP1QKLEQATKERQ 331
|:::| | | |:::|

RESULT 5
Q92MG0 PRELIMINARY; PRT; 431 AA.
AC Q92MG0;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PUTATIVE.
GN JHP0260.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Dolg P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RA "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori."
RL Nature 397:176-180(1999).
DR EMBL: AE001463; AAD05839.1; -.
DR InterPro: IPR002885; PPR.
KW Complete proteome.
SQ SEQUENCE 431 AA; 49895 MW; E4095C519A52DAC CRC64;

Query Match 50.0%; Score 45; DB 16; Length 431;
Best Local Similarity 42.1%; Pred. No. 41;
Matches 8; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 KKEVMPISQSLDALVKEKK 19
Db 314 KEEMLP1QKLEQATKERQ 332
|:::| | | |:::|

RESULT 6
Q9VS99 PRELIMINARY; PRT; 1712 AA.
AC Q9VS99;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE SP2523 PROTEIN.
GN SP2523 OR CG7493.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RT STRAIN=Y, CN BW SP;

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[1]
RN SEQUENCE FROM N.A.
RP STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer V.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.D., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Gibbs R.H., Myers E.W., Rubin G.M., Venter J.C.;
RA "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003558; AAF50528.2; -.
DR FlyBase: FBgn0035808; SP2523.
SQ SEQUENCE 1712 AA; 187520 MW; 35D189F958AAE030 CRC64;

Query Match 50.0%; Score 45; DB 5; Length 1712;
Best Local Similarity 45.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 8; Mismatches 1; Indels 2; Gaps 1;

QY 1 KKEVWPS--IOSLDALVKEK 18
Db 1450 RTEVVPSSQVESIEALLKQK 1469
|:::| |:::| |:::|

RESULT 7
Q961N2 PRELIMINARY; PRT; 1716 AA.
ID Q961N2
AC Q961N2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GH14650P.
GN SP2523.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RT STRAIN=Y, CN BW SP;

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```

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.,
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY051490; AAK92914.1; -
SQ SEQUENCE 1716 AA; 187955 MW; 63ACE8D1339E5396 CRC64;

Query Match 50.0%; Score 45; DB 5; Length 1716;
Best Local Similarity 45.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 8; Mismatches 2; Indels 2; Gaps 1;

QY 1 KKEVMP--IQSLDALVKEK 18
Db 1454 RTEVPSSQVESIEALLKOK 1473
: ||:| | :|:|:|:|:|:|

RESULT 8
ID Q9NGV1 PRELIMINARY; PRT; 1912 AA.
AC Q9NGV1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE SP2523.
GN SP2523 OR CG7493.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ENDOPLASMIC RETICULUM;
RA Serano T.L., Pendleton J.D., Rubin G.M.;
RT "A reverse genetic screen for genes involved in Drosophila
RT development.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF239611; AAF63503.1; -
DR FlyBase; FBgn0035808; SP2523.
SQ SEQUENCE 1912 AA; 209847 MW; 5B124A6961B58C71 CRC64;

Query Match 50.0%; Score 45; DB 5; Length 1912;
Best Local Similarity 45.0%; Pred. No. 1.9e+02;
Matches 9; Conservative 8; Mismatches 1; Indels 2; Gaps 1;

QY 1 KKEVMP--IQSLDALVKEK 18
Db 1650 RTEVPSSQVESIEALLKOK 1669
: ||:| | :|:|:|:|:|:|

RESULT 9
ID O13054 PRELIMINARY; PRT; 5081 AA.
AC O13054;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE RYANODINE RECEPTOR RYRI ISOFORM.
GN RYRI.
OS Makaira nigricans (Blue marlin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Xiphidae; Makaira.
OX NCBI_TaxID=13604;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SKELETAL MUSCLE;
RA Franck J.P.C., Keen J.E., Londraville R.L., Morrisette J.,

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```

RA Beamsley M., Block B.A.;
RT "Cloning and characterization of fiber type-specific ryanodine
RT receptor isoforms in skeletal muscles of fish (Makaira nigricans).";
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U97329; AAB58117.1; -
DR InterPro; IPR000636; Cation_chan_non_lig.
DR InterPro; IPR001682; Channel_pore_Ca_Na.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR003608; MIR.
DR InterPro; IPR001215; Ryanodn_receptor.
DR InterPro; IPR000699; RYDR_ITPR.
DR InterPro; IPR003032; RYR.
DR InterPro; IPR003877; SPRY.
DR InterPro; IPR003878; SPRY_domain.
DR Pfam; PF00520; ion_trans; 1.
DR Pfam; PF02815; MIR; 4.
DR Pfam; PF01365; RYDR_ITPR; 2.
DR Pfam; PF02026; RYR; 4.
DR Pfam; PF00622; SPRY; 3.
DR PRINTS; PR00795; RYANODINER.
DR SMART; SM00472; MIR; 4.
DR SMART; SM00449; SPRY; 3.
KW Receptor.
SQ SEQUENCE 5081 AA; 576220 MW; 5A3D7E253CFBC09B CRC64;

Query Match 50.0%; Score 45; DB 13; Length 5081;
Best Local Similarity 56.2%; Pred. No. 5.2e+02;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 KEVMPSTQSLDALVKE 17
Db 3277 QELCPDPELDALIKE 3292
: | : | : | : | : | : |

RESULT 10
ID O23332 PRELIMINARY; PRT; 1676 AA.
AC O23332;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE CENTROMERE PROTEIN HOMOLOG.
GN AT4G14760.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98121113; PubMed-9461215;
RA Bevan M., Bancroft I., Bent E., Love K., Goodman H., Dean C.,
RA Bergkamp R., Dirkse W., van Staveren M., Stiekema W., Drost L.,
RA Ridley P., Hudson S.A., Patel K., Murphy G., Piffanelli P., Wedler H.,
RA Wedler E., Wambutt R., Weitzenegger T., Pohl T.M., Terryn N.,
RA Gielen J., Villarroel R., De Clerck R., van Montagu M., Lecharny A.,
RA Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S., Kotter P.,
RA Entian K.D., Rieger M., Schaeffer M., Funk B., Mueller-Auer S.,
RA Silvey M., James R., Montfort A., Pons A., Puigdomenech P., Douka A.,
RA Vouklatou E., Milioni D., Hatzopoulos P., Piravandi E., Obermaier B.,
RA Hilbert H., Duesterhoft A., Moores T., Jones J.D.G., Eneva T.,
RA Palme K., Benes V., Rechman S., Ansoorge W., Cooke R., Berger C.,
RA Delseny M., Voet M., Volckaert G., Mewes H.W., Klosterman S.,
RA Schueller C., Chludzis N.;
RT "Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of
RT Arabidopsis thaliana."
RL Nature 391:485-488(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z97337; CAB10255.1; -

```

DR EMBL; AL161539; CAB78518.1; -;
SQ SEQUENCE 1676 AA; 192957 MW; FEC783B8A2A047E0 CRC64;

Query Match 49.4%; Score 44.5; DB 10; Length 1676;
Best Local Similarity 55.6%; Pred. No. 2e+02;
Matches 10; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

Qy 2 KEVMPISQSLD-ALVKEK 18
||: |||::: ||||
Db 1356 KEINPSIKTIQAFVKEK 1373

RESULT 11

ID Q21216 PRELIMINARY; PRT; 1336 AA.
AC Q21216;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE K04D7.5 PROTEIN.
GN K04D7.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Wild A.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RS [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
RT Science 282:2012-2018(1998).
DR EMBL; Z69664; CAA93515.1; -;
DR InterPro; IPR001552; Acyl-CoA-dh.
DR PROSITE; PS00073; ACYL-CoA-DH_2; UNKNOWN_1.
SQ SEQUENCE 1336 AA; 152551 MW; 07057CE0B4A3F51B CRC64;

Query Match 48.9%; Score 44; DB 5; Length 1336;
Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KKEVMPISQSLDAL 14
: ||| ||| | | | |
Db 759 EKELMPSTSSIDSL 772

RESULT 12

O9LTV3
ID Q9LJV3 PRELIMINARY; PRT; 156 AA.
AC Q9LJV3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GB|AAC69115.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;

RX MEDLINE=203363099; PubMed=10907853;
RA Nakamura Y.;

RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the regions of 4,251,695 bp covered by ninety P1,
TAC and BAC clones.";
RL DNA Res. 7:217-221(2000).
DR EMBL; AP000389; BAB01424.1; -;
SQ SEQUENCE 156 AA; 17854 MW; FCPEC18EF009588E CRC64;

Query Match 47.8%; Score 43; DB 10; Length 156;
Best Local Similarity 47.4%; Pred. No. 30;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KKEVMPISQSLDALVKEK 19
| || : || | | | | |
Db 88 KSEVAVELEALQAMVKEK 106

RESULT 13

Q9NSK3
ID Q9NSK3 PRELIMINARY; PRT; 283 AA.
AC Q9NSK3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE HYPOTHETICAL 31.4 KDA PROTEIN (FRAGMENT).
GN DKFZP7621166.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-MELANOMA (MEWO CELL LINE);
RA Bloembergen H., Boecher M., Brandt P., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL162072; CAB82408.1; -;
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 283 AA; 31436 MW; 3E33782A2086E9EE CRC64;

Query Match 47.8%; Score 43; DB 4; Length 283;
Best Local Similarity 52.9%; Pred. No. 56;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KEVMPISQSLDALVKEK 18
: ||| : || | | | | |
Db 248 EEVMOELRALVKEQ 264

RESULT 14

O9BR76
ID O9BR76 PRELIMINARY; PRT; 489 AA.
AC O9BR76;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SIMILAR TO CORONIN, ACTIN BINDING PROTEIN 1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA, CHORIOCARCINOMA;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 3 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL; BC006449; AAH06449.1; -;
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 3.

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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:45:03 ; Search time 158.52 Seconds
(without alignments)
7.708 Million cell updates/sec

Title: US-09-821-726-4
Perfect score: 60
Sequence: 1 KKTCTIVHKMKK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq_032802.*

- 1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	91.7	185	20	AAW99667 Human secreted pro
2	55	91.7	185	21	AAW99667 Human PRO1005 prot
3	55	91.7	185	21	AAW99667 Human signal pepti
4	55	91.7	185	21	AAW99667 Membrane-bound pro
5	55	91.7	185	22	AAW99667 Human PRO1005 (UNQ
6	55	91.7	185	22	AAW99667 Human PRO1005 prot
7	55	91.7	186	21	AAW99667 Human secreted pro
8	55	91.7	194	19	AAW99667 Cancer associated
9	55	91.7	194	20	AAW99667 Human ovarian tumo
10	41	68.3	971	22	ABW63836 Drosophila melanog
11	39	65.0	55	21	AAW99667 Arabidopsis thalia

12	39	65.0	55	21	AAW99667 Arabidopsis thalia
13	39	65.0	107	21	AAW99667 Arabidopsis thalia
14	39	65.0	107	21	AAW99667 Arabidopsis thalia
15	39	65.0	131	22	AAW99667 Human protein sequ
16	38	63.3	86	18	AAW99667 H. pylori secreted
17	38	63.3	87	18	AAW99667 H. pylori secreted
18	38	63.3	126	22	AAW99667 Human polypeptide
19	37	61.7	141	22	AAW99667 Novel human diagno
20	37	61.7	141	22	AAW99667 Drosophila melanog
21	36	60.0	173	20	AAW99667 Feline B7-1S prote
22	36	60.0	278	22	AAW99667 Novel human diagno
23	36	60.0	292	21	AAW99667 Feline CD80 (B7-1)
24	36	60.0	292	21	AAW99667 Feline CD80 (B7-1)
25	36	60.0	292	21	AAW99667 Cat CD80 (B7-1)-TA
26	36	60.0	292	21	AAW99667 Cat CD80 (B7-1)-TA
27	36	60.0	464	22	AAW99667 Cat CD80 (B7-1)-SY
28	35	58.3	66	20	AAW99667 Drosophila melanog
29	35	58.3	128	22	AAW99667 Human prostate can
30	35	58.3	143	22	AAW99667 Novel human diagno
31	35	58.3	147	22	AAW99667 Novel human diagno
32	35	58.3	152	22	AAW99667 Novel human diagno
33	35	58.3	154	21	AAW99667 Arabidopsis thalia
34	35	58.3	161	22	AAW99667 Drosophila melanog
35	35	58.3	170	22	AAW99667 Novel human diagno
36	35	58.3	173	21	AAW99667 C. albicans caplin
37	35	58.3	173	21	AAW99667 N-terminal RNA tri
38	35	58.3	174	21	AAW99667 Arabidopsis thalia
39	35	58.3	235	20	AAW99667 Canine B7-1S prote
40	35	58.3	304	20	AAW99667 Canine B7-1 protei
41	35	58.3	336	13	AAW99667 Non-A, Non-B Hepat
42	35	58.3	385	22	AAW99667 Novel human diagno
43	35	58.3	390	22	AAW99667 Novel human diagno
44	35	58.3	492	22	AAW99667 Novel human diagno
45	35	58.3	581	22	AAW99667 Novel human diagno

ALIGNMENTS

RESULT 1

AAW99667
ID AAW99667 standard; Protein; 185 AA.

AC AAW99667;

DT 07-JUN-1999 (first entry)

XX Human secreted protein clone ej90_5 protein.

DE Human; secreted protein; nutritional; cytokine; cell proliferation;
KW differentiation; immune stimulating; vaccine; haematopoiesis regulation;
KW tissue growth; chemotactic; chemokine; haemostatic; thrombolytic;
KW anti-inflammatory; cadherin; tumour invasion suppressor;
KW tumour inhibition; gene therapy.

XX Homo sapiens.

OS Homo sapiens.

PN WO9907840-A1.

XX 18-FEB-1999.

PD 06-AUG-1998; 98WO-0516318.

PF 04-AUG-1998; 98US-0130189.

PR 06-AUG-1997; 97US-0906708.

XX (GEM) GENETICS INST INC.

PI Agostino MJ, Evans C, Jacobs K, Lavallie ER, McCoy JM;

PI Merberg D, Racie LA, Steininger RJ, Treacy M;

XX WPI; 1999-167419/14.

DR N-PSDB; AAX19493.

XX New polynucleotides encoding secreted human proteins - derived from
PT fetal kidney, adult testes, adult brain, adult heart, adult placenta
PT or adult retina cDNA libraries
XX
XX
XX Claim 34; Page 98-99; 107pp; English.
XX
XX The present sequence represents a human secreted protein. The secreted
CC protein can have activities such as: nutritional activity, cytokine and
CC cell proliferation/differentiation activity, immune stimulating (e.g. as
CC vaccines) or suppressing activity, haematopoiesis regulating activity,
CC tissue growth activity, activin/inhibin activity, chemotactic/
CC chemokinetic activity, haemostatic and thrombolytic activity, receptor/
CC ligand activity, anti-inflammatory activity, cadherin/tumour invasion
CC suppressor activity, and tumour inhibition activity. The secreted
CC protein polynucleotides and proteins are predicted to have biological
CC activities which would make them suitable for treating, preventing or
CC ameliorating medical conditions in humans and animals. The
CC polynucleotides are also stated to be useful for gene therapy.
XX
XX Sequence 185 AA;
SQ

Query Match 91.7%; Score 55; DB 20; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMKK 11
|||||||
Db 78 kktctivhkmnk 88

RESULT 2
ID AAB24067 standard; Protein; 185 AA.
XX
XX AAB24067;
XX
XX 29-JAN-2001 (first entry)
XX
XX Human PRO1005 protein sequence SEQ ID NO:34.
XX
XX Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
KW proliferation; tumorigenesis; identification; cancer; cytostatic;
KW proliferative; neuroprotective; antiinflammatory; immunosuppressive;
KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
KW neuronal disorder; glioma disorder; astrocytoma disorder; angiogenic;
KW hypothalamic disorder; glandular disorder; macrophage disorder;
KW epithelial disorder; stromal disorder; blastocoele disorder;
KW inflammatory disorder; immunologic disorder.
XX
XX Homo sapiens.
XX
XX WO200053755-A2.
XX
XX 14-SEP-2000.
XX
XX 06-JAN-2000; 2000WO-US00376.
XX
XX 08-MAR-1999; 99WO-US05028.
XX
XX 02-JUN-1999; 99WO-US12252.
XX
XX 23-JUN-1999; 99US-0141037.
XX
XX 07-JUL-1999; 99US-0143048.
XX
XX 26-JUL-1999; 99US-0145698.
XX
XX 30-NOV-1999; 99WO-US28313.
XX
XX 20-DEC-1999; 99WO-US30911.
XX
XX 05-JAN-2000; 2000WO-US00219.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
PI Watanabe CK, Wood WI;
XX
XX

DR WPI; 2000-572270/53.
XX N-PSDB; AAC58377.
XX
XX Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
PT treatment, diagnosis and prevention of cancer -
XX
XX Claim 61; Fig 22; 286pp; English.
XX
XX The present invention describes an isolated antibody that binds to
CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,
CC PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,
CC PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,
CC PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094, cell
CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell
CC growth. The PRO polypeptides and nucleotides are useful in the
CC treatment, diagnosis and prevention of cancer. The antibodies and other
CC anti-tumour compounds may be used to treat various conditions, including
CC those characterised by overexpression and/or activation of the amplified
CC PRO genes. Exemplary conditions or disorders to be treated with such
CC antibodies and other compounds include benign or malignant tumours
CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,
CC colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic
CC carcinomas, sarcomas, glioblastomas, and various disorders such as neuronal,
CC leukaemias and lymphoid malignancies, other disorders such as neuronal,
CC glioma, astrocytoma, hypothalamic and other glandular, macrophage,
CC epithelial, stromal and blastocoele disorders, and inflammatory.
CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR
CC primers and hybridisation probes used in the isolation of the human PRO
CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human
CC PRO polynucleotide and protein sequences given in the exemplification of
CC the present invention.
XX
XX Sequence 185 AA;
SQ

Query Match 91.7%; Score 55; DB 21; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMKK 11
|||||||
Db 78 kktctivhkmnk 88

RESULT 3
ID AAY87272 standard; Protein; 185 AA.
XX
XX AAY87272;
XX
XX 11-MAY-2000 (first entry)
XX
XX Human signal peptide containing protein HSPP-49 SEQ ID NO:49.
XX
XX Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
KW antimicrobial; neurotropic; neuroprotective; cardiovascular; hepatotropic;
KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
KW reproductive disorder; developmental disorder; arteriosclerosis;
KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
KW Parkinson's disease; Huntington's disease; muscular dystrophy.
XX
XX Homo sapiens.
XX
XX WO200000610-A2.
XX
XX 06-JAN-2000.
XX
XX 25-JUN-1999; 99WO-US14484.
XX
XX 26-JUN-1999; 98US-0090762.
XX

PR 31-JUL-1998; 98US-0094983.
PR 01-OCT-1998; 98US-0102686.
PR 11-DEC-1998; 98US-0112129.
PA (INCY-) INCYTE PHARM INC.
XX
XX Lal P, Tang WT, Gorgone CA, Corley NC, Guegler KJ, Baughn MR;
PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
PI Bandman O;
XX
XX WPI: 2000-160673/14.
DR N-PSDB; AA298157.
XX
XX New human signal peptide-containing proteins useful in treatment,
PT prevention and diagnosis of e.g. cancer, inflammation and
PT cardiovascular disease
XX
XX Claim 1; Page 193-194; 327pp; English.
XX
XX AA298109 to AA298242 encode AAY87224 to AAY87357 which represent the
CC human signal peptide-containing proteins Hspp-1 to Hspp-134. Hspps have
CC anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,
CC neuroprotective, cardiovascular and antiasthmatic activities, and can
CC be used in gene therapy. Hspps can be used to treat or prevent disorders
CC associated with decreased activity or function of Hspp. Antagonists of
CC Hspp are used to treat or prevent disorders associated with increased
CC activity or function of Hspp. Such diseases include cell proliferation
CC (including cancer), inflammation, cardiovascular, neurological,
CC reproductive or developmental disorders, (e.g. arteriosclerosis,
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
CC asthma, Crohn's disease, microbial or other infections, congestive or
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). Hspp
CC nucleic acids can be used for the recombinant production of Hspp, for
CC detecting Hspp in standard hybridisation and amplification assays (for
CC diagnosis and monitoring), in gene therapy, as antisense,
CC triplex-forming or ribozyme therapeutics, for detecting related sequences
CC or genetic variations, and for chromosomal mapping. Hspp are also used to
CC raise specific antibodies (Ab) and to screen for agonists and
CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
CC monitor, Hspp-related diseases (in usual immunoassays), as therapeutic
CC antagonists, in competitive drug screens, and for purification of Hspp
CC from natural sources.
XX
XX Sequence 185 AA;
SQ

Query Match 91.7%; Score 55; DB 21; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 11
| | | | | | | | | |
Db 78 Kktctivhkmmk 88

RESULT 4
AAY66686
ID AAY66686 standard; protein; 185 AA.
XX
XX AAY66686;
AC
XX
XX 05-APR-2000 (first entry)
DT
XX Membrane-bound protein PH01005.
DE
XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping.
XX
XX Homo sapiens.
OS
XX WO9963088-A2.
PN
XX

PD 09-DEC-1999.
XX
XX 02-JUN-1999; 99WO-US12252.
XX
XX 02-JUN-1998; 98US-0087607.
PR 02-JUN-1998; 98US-0087609.
PR 02-JUN-1998; 98US-0087759.
PR 03-JUN-1998; 98US-0087827.
PR 04-JUN-1998; 98US-0088021.
PR 04-JUN-1998; 98US-0088025.
PR 04-JUN-1998; 98US-0088028.
PR 04-JUN-1998; 98US-0088029.
PR 04-JUN-1998; 98US-0088030.
PR 04-JUN-1998; 98US-0088033.
PR 04-JUN-1998; 98US-0088326.
PR 05-JUN-1998; 98US-0088167.
PR 05-JUN-1998; 98US-0088202.
PR 05-JUN-1998; 98US-0088212.
PR 05-JUN-1998; 98US-0088217.
PR 09-JUN-1998; 98US-0088655.
PR 10-JUN-1998; 98US-0088722.
PR 10-JUN-1998; 98US-0088730.
PR 10-JUN-1998; 98US-0088734.
PR 10-JUN-1998; 98US-0088738.
PR 10-JUN-1998; 98US-0088740.
PR 10-JUN-1998; 98US-0088741.
PR 10-JUN-1998; 98US-0088742.
PR 10-JUN-1998; 98US-0088810.
PR 10-JUN-1998; 98US-0088811.
PR 10-JUN-1998; 98US-0088824.
PR 10-JUN-1998; 98US-0088825.
PR 10-JUN-1998; 98US-0088826.
PR 11-JUN-1998; 98US-0088858.
PR 11-JUN-1998; 98US-0088861.
PR 11-JUN-1998; 98US-0088863.
PR 11-JUN-1998; 98US-0088876.
PR 12-JUN-1998; 98US-0089090.
PR 12-JUN-1998; 98US-0089105.
PR 16-JUN-1998; 98US-0089440.
PR 16-JUN-1998; 98US-0089512.
PR 16-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089653.
PR 18-JUN-1998; 98US-0089801.
PR 18-JUN-1998; 98US-0089907.
PR 18-JUN-1998; 98US-0089908.
PR 19-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089948.
PR 19-JUN-1998; 98US-0089952.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090461.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.

PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091513.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 11-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 99US-0115565.
PR (GETH) GENENTECH INC.
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
a XX

DR WPI; 2000-072883/06.
DR N-PSDB; AAZ65023.
XX
PT Membrane-bound proteins and related nucleotide sequences
XX
PS claim 12; Fig 139; 822pp; English.
XX
CC The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC will also be useful for the preparation of PRO polypeptides, especially
CC by recombinant techniques.
XX
SQ Sequence 185 AA;
Query Match 91.7%; Score 55; DB 21; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KKTCTVHKMKK 11
Db 78 kktctvHKmkk 88
RESULT 5
AAB65209
ID AAB65209 standard; Protein; 185 AA.
XX
AC AAB65209;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO1005 (UNQ489) protein sequence SEQ ID NO:211.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic;
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay.
XX
OS Homo sapiens.
XX
PN WO2000073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US08439.
XX
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 17-AUG-1999; 99US-0149396.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 08-OCT-1999; 99US-0158663.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.

KW nootropic; antibacterial; virucide; fungicide; fungicide; ophthalmological; human;
 KW vulnery; gene therapy; infection; secreted protein.

OS Homo sapiens.

PN WO200061623-A1.

PD 19-OCT-2000.

XX 06-APR-2000; 2000WO-US08979.

XX 09-APR-1999; 99US-0128693.

PR 26-APR-1999; 99US-0130991.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Ni J, Komatsoulis GA, Rosen CA, Soppet DR, Shi Y;

PI Lafleur DW, Olsen HS, Ebner R, Florence KA, Moore PA, Birse CB;

PI Young PE;

XX WPI; 2000-647418/52.

XX New nucleic acid molecules encoding 62 human secreted proteins for
 PT diagnosing, preventing, treating or ameliorating medical conditions and
 PT used as food additives or preservatives -

XX Claim 11; Page 598; 716pp; English.

XX Sequences AAB38321-B38396 represent the amino acid sequences of 62
 CC human secreted proteins encoded by the genes AAC69512-C69587. The genes
 CC and proteins are useful for preventing, ameliorating or treating medical
 CC conditions, e.g. by protein or gene therapy. The genes are isolated from
 CC a range of human tissues disclosed in the specification. The nucleic
 CC acids, proteins, antibodies and (ant)agonists are useful in the
 CC diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.
 CC rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms
 CC of the breast or liver; (c) cardiovascular disorders e.g. cardiac
 CC arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e)
 CC angiogenesis; (f) nervous system disorders e.g. Alzheimer's disease; (g)
 CC infections caused by bacteria, viruses and fungi; and (h) ocular
 CC disorders e.g. corneal infection. The polypeptides can also be used to
 CC aid wound healing and epithelial cell proliferation, to prevent skin
 CC aging due to sunburn, to maintain organs before transplantation, for
 CC supporting cell culture of primary tissues, to regenerate tissues and in
 CC chemotaxis.

XX Sequence 186 AA;

Query Match 91.7%; Score 55; DB 21; Length 186;

Best Local Similarity 90.9%; Pred. No. 0.12;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMK 11

|||||||

Db 78 kktctvkhmk 88

RESULT 8

AAW69974
 ID AAW69974 standard; Protein; 194 AA.

XX AAW69974;

XX 16-NOV-1998 (first entry)

XX Cancer associated protein.

XX Cancer; PCR; Northern blotting; ribonuclease protection assay;

XX diagnosis; metastatic cancer.

XX Synthetic.

XX

PN WO9837187-A1.

XX 27-AUG-1998.

XX 18-FEB-1998; 98WO-JP00667.

XX 21-FEB-1997; 97JP-0052508.

XX (TAKI) TAKARA SHUZO CO LTD.

XX Asada K, Hino F, Kato I, Mukai H, Yoshikawa Y;

XX WPI; 1998-467552/40.

XX Detection of cancer cells in tissue samples - by changes in mRNA

XX expression compared to normal tissue of specific cancer-associated

XX gene sequences

XX Claim 14; Page 64-65; 92pp; Japanese.

XX The cancer associated proteins AAW69974-W69976 where used in the method

XX of the invention to detect cancer cells in tissue samples or biological

XX fluids. They are detected by monitoring the change in mRNA expression

XX as compared to normal tissue of one or more cancer-associated genes

XX whose cDNA stringently hybridises to cancer associated gene nucleic acid

XX fragments. The change in expression may be an increase or a decrease

XX compared to normal tissue. The mRNA expression may be determined by

XX PCR, Northern blotting or ribonuclease protection assay, or by

XX determining the change in the amount of protein encoded by the gene(s) as

XX compared to normal tissue, for example by using a labelled antibody

XX recognising the protein. Detection of cancer cells for cancer diagnosis,

XX including detection of metastatic cancer cells in tissues other than the

XX primary tumour site.

XX Sequence 194 AA;

XX Query Match 91.7%; Score 55; DB 19; Length 194;

XX Best Local Similarity 90.9%; Pred. No. 0.13;

XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMK 11

|||||||

Db 87 kktctvkhmk 97

RESULT 9

AAW76591

ID AAW76591 standard; Protein; 194 AA.

XX AAW76591;

XX 10-APR-2000 (first entry)

XX Human ovarian tumor EST fragment encoded protein 87.

XX Expressed sequence tag; EST; human; ovarian tumor; anticancer;

XX gene therapy; treatment.

XX Homo sapiens.

XX DE19817557-A1.

XX 21-OCT-1999.

XX 09-APR-1998; 98DE-1017557.

XX 09-APR-1998; 98DE-1017557.

XX (META-) METAGEN GES GENOMFORSCHUNG MBH.

XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;

XX

DR WPI; 1999-591920/51.
 DR N-PSDB; AAZ77487.
 XX
 PT New nucleic acid sequences expressed in ovarian, and some other, cancer
 PT tissues, and derived polypeptides, for treatment of ovarian cancer and
 PT identification of therapeutic agents.
 XX
 PS Claim 25; Page 279; 310pp; German.
 XX
 CC This invention describes novel nucleic acid (cDNA) sequences (A) which
 CC have anticancer activity and are highly expressed in ovarian tumor
 CC tissue (and some also in testis and breast cancer tissue). The products
 CC of the invention can be used for gene therapy. (A) are used (i) for
 CC recombinant expression of polypeptides (B) and (ii) to isolate complete
 CC genes. (B) are used (i) to identify agents suitable for treatment of
 CC ovarian cancer; (ii) directly for treating this form of cancer
 CC (including expression from gene therapy vectors) and (iii) for generation
 CC of specific antibodies. (A) are identified by assembling ESTs (expressed
 CC sequence tags) from a particular tissue type before comparison of
 CC expression patterns. This allows a significantly longer fragment of the
 CC gene to be revealed, so should reduce the number of failures associated
 CC with the fact that ESTs from different libraries may represent different
 CC parts of the same unknown gene, distorting the estimated frequency of
 CC occurrence in a particular tissue. AAY76505-Y76638 represent protein
 CC fragments encoded by the human ovarian tumor cDNA library derived EST
 CC fragments represented in AAZ77450-Z77572.
 XX
 SQ Sequence 194 AA;

Query Match 91.7%; Score 55; DB 20; Length 194;
 Best Local Similarity 90.9%; Pred. No. 0.13;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KKTCTVHKMKK 11
 |||||
 Db 87 kktctvhhkmk 97

RESULT 10
 ABB63836
 ID ABB63836 standard; Protein; 971 AA.
 AC ABB63836;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 18300.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 XX (PEKE) PE CORP NY.
 PA
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 XX WPI; 2001-656860/75.
 DR N-PSDB; ABL07939.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.

XX
 PS Disclosure; SEQ ID NO 18300; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).

CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 971 AA;

Query Match 68.3%; Score 41; DB 22; Length 971;
 Best Local Similarity 63.6%; Pred. No. 1.2e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KKTCTVHKMKK 11
 |||||
 Db 942 kttcavhkhkq 952

RESULT 11
 AAG22477
 ID AAG22477 standard; Protein; 55 AA.
 XX
 AC AAG22477;
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 25420.
 XX

KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

OS Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
 PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126264.
 PR 29-MAR-1999; 99US-0126785.
 PR 01-APR-1999; 99US-0127462.
 PR 06-APR-1999; 99US-0128234.
 PR 08-APR-1999; 99US-0128714.
 PR 16-APR-1999; 99US-0129845.
 PR 19-APR-1999; 99US-0130077.
 PR 21-APR-1999; 99US-0130449.
 PR 23-APR-1999; 99US-0130510.
 PR 28-APR-1999; 99US-0130891.
 PR 30-APR-1999; 99US-0131449.
 PR 30-APR-1999; 99US-0132048.
 PR 04-MAY-1999; 99US-0132407.
 PR 05-MAY-1999; 99US-0132484.
 PR 06-MAY-1999; 99US-0132485.
 PR 06-MAY-1999; 99US-0132486.
 PR 07-MAY-1999; 99US-0132487.
 PR 11-MAY-1999; 99US-0132863.
 PR 14-MAY-1999; 99US-0134256.
 PR 14-MAY-1999; 99US-0134218.

PR	14-MAY-1999;	99US-0134219.	PR	26-JUL-1999;	99US-0145276.
PR	14-MAY-1999;	99US-0134221.	PR	27-JUL-1999;	99US-0145913.
PR	14-MAY-1999;	99US-0134370.	PR	27-JUL-1999;	99US-0145918.
PR	18-MAY-1999;	99US-0134768.	PR	27-JUL-1999;	99US-0145919.
PR	19-MAY-1999;	99US-0134941.	PR	28-JUL-1999;	99US-0145951.
PR	20-MAY-1999;	99US-0135124.	PR	02-AUG-1999;	99US-0146386.
PR	21-MAY-1999;	99US-0135353.	PR	02-AUG-1999;	99US-0146388.
PR	24-MAY-1999;	99US-0135629.	PR	02-AUG-1999;	99US-0146389.
PR	25-MAY-1999;	99US-0136021.	PR	03-AUG-1999;	99US-0147038.
PR	27-MAY-1999;	99US-0136392.	PR	04-AUG-1999;	99US-0147204.
PR	28-MAY-1999;	99US-0136782.	PR	04-AUG-1999;	99US-0147302.
PR	01-JUN-1999;	99US-0137222.	PR	05-AUG-1999;	99US-0147192.
PR	03-JUN-1999;	99US-0137528.	PR	05-AUG-1999;	99US-0147260.
PR	04-JUN-1999;	99US-0137502.	PR	06-AUG-1999;	99US-0147303.
PR	07-JUN-1999;	99US-0137724.	PR	06-AUG-1999;	99US-0147416.
PR	08-JUN-1999;	99US-0138094.	PR	09-AUG-1999;	99US-0147493.
PR	10-JUN-1999;	99US-0138540.	PR	09-AUG-1999;	99US-0147935.
PR	10-JUN-1999;	99US-0138847.	PR	10-AUG-1999;	99US-0148171.
PR	14-JUN-1999;	99US-0139119.	PR	11-AUG-1999;	99US-0148319.
PR	16-JUN-1999;	99US-0139452.	PR	12-AUG-1999;	99US-0148341.
PR	16-JUN-1999;	99US-0139453.	PR	13-AUG-1999;	99US-0148565.
PR	17-JUN-1999;	99US-0139492.	PR	13-AUG-1999;	99US-0148684.
PR	18-JUN-1999;	99US-0139454.	PR	16-AUG-1999;	99US-0149368.
PR	18-JUN-1999;	99US-0139455.	PR	17-AUG-1999;	99US-0149175.
PR	18-JUN-1999;	99US-0139456.	PR	18-AUG-1999;	99US-0149426.
PR	18-JUN-1999;	99US-0139457.	PR	20-AUG-1999;	99US-0149722.
PR	18-JUN-1999;	99US-0139458.	PR	20-AUG-1999;	99US-0149723.
PR	18-JUN-1999;	99US-0139459.	PR	20-AUG-1999;	99US-0149929.
PR	18-JUN-1999;	99US-0139460.	PR	23-AUG-1999;	99US-0149902.
PR	18-JUN-1999;	99US-0139461.	PR	23-AUG-1999;	99US-0149930.
PR	18-JUN-1999;	99US-0139462.	PR	23-AUG-1999;	99US-0150566.
PR	18-JUN-1999;	99US-0139463.	PR	26-AUG-1999;	99US-0150884.
PR	18-JUN-1999;	99US-0139750.	PR	27-AUG-1999;	99US-0151065.
PR	18-JUN-1999;	99US-0139763.	PR	27-AUG-1999;	99US-0151066.
PR	21-JUN-1999;	99US-0139817.	PR	27-AUG-1999;	99US-0151080.
PR	22-JUN-1999;	99US-0139899.	PR	30-AUG-1999;	99US-0151303.
PR	23-JUN-1999;	99US-0140353.	PR	31-AUG-1999;	99US-0151438.
PR	24-JUN-1999;	99US-0140354.	PR	01-SEP-1999;	99US-0151930.
PR	24-JUN-1999;	99US-0140695.	PR	07-SEP-1999;	99US-0152363.
PR	28-JUN-1999;	99US-0140823.	PR	10-SEP-1999;	99US-0153070.
PR	28-JUN-1999;	99US-0140991.	PR	13-SEP-1999;	99US-0153758.
PR	30-JUN-1999;	99US-0141287.	PR	15-SEP-1999;	99US-0154018.
PR	01-JUL-1999;	99US-0141842.	PR	16-SEP-1999;	99US-0154039.
PR	01-JUL-1999;	99US-0142154.	PR	22-SEP-1999;	99US-0155139.
PR	02-JUL-1999;	99US-0142055.	PR	23-SEP-1999;	99US-0155486.
PR	06-JUL-1999;	99US-0142390.	PR	24-SEP-1999;	99US-0155659.
PR	08-JUL-1999;	99US-0142803.	PR	28-SEP-1999;	99US-0156458.
PR	09-JUL-1999;	99US-0142920.	PR	29-SEP-1999;	99US-0156596.
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PR	19-JUL-1999;	99US-0144331.	PR	13-OCT-1999;	99US-0159293.
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Query Match 65.0%; Score 39; DB 21; Length 55;
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QY 1 KKTCLVHKK 10
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 Db 7 kkcclfhkqk 16

RESULT 12
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AC AAG50024;
 XX
 DT 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 63347.

XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 XX termination sequence.

OS Arabidopsis thaliana.
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 PN EP1033405-A2.

XX 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

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Query Match 55.0%; Score 39; DB 21; Length 55;
Best Local Similarity 70.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 10
Db 7 kkcfcifhkqk 16

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XX AC AAG22475;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 25418.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
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PR 29-OCT-1999; 99US-0162142.

Query Match 65.0%; Score 39; DB 21; Length 107;
Best Local Similarity 70.0%; Pred. No. 31;
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Db 59 kkecfhkkq 68

RESULT 14
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AC AAG50022;
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DT 18-OCT-2000 (first entry)
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XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
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PR 07-JUN-1999; 99US-0137724.
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PR 14-JUN-1999; 99US-0139119.
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PR 22-JUN-1999; 99US-0139899.
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PR 24-JUN-1999; 99US-0140695.
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 PR 25-OCT-1999; 99US-0161404.
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 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
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 PR 26-OCT-1999; 99US-0161361.
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 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 65.0%; Score 39; DB 21; Length 107;
 Best Local Similarity 70.0%; Pred No. 31;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KKTCTVHKMK 10
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 Db 59 kkcctfkhkq 68

RESULT 15

AAH25898

ID AAH25898 standard; Protein; 131 AA.

XX AC AAH25898;

XX DT 16-OCT-2001 (first entry)

XX DE Human protein sequence SEQ ID NO:1413.

XX KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
 KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
 KW antibacterial; endocrine; cardiant; central nervous system; virucide;
 KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
 KW antiaggregant; haemostatic; vulnery; antulcer; osteopathic; eczema;
 KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
 KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
 KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
 KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
 KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
 KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
 KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
 KW allergic rhinitis; diabetes; multiple sclerosis; depression;
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
 XX KW neurological disorder.

OS Homo sapiens.

XX WO200153455-A2.

XX PD 26-JUL-2001.

XX XX 22-DEC-2000; 2000WO-US35017.

XX PR 23-DEC-1999; 99US-0471275.

XX PR 21-JAN-2000; 2000US-0488725.

XX PR 25-APR-2000; 2000US-0552317.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI: 2001-457603/49.

XX N-PSDB; AAH99839.

Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection -

Claim 20; Page 287; 1217pp: English.

XX AAH99166 to AAH99904 encode the human proteins given in AAH25225 to
 CC AAH25963. The proteins can have activities based on the tissues and
 CC cells they are expressed in, such as: antiinflammatory; antirheumatic;
 CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
 CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
 CC cardiovascular; antianaemic; antiaggregant; haemostatic; vulnery;
 CC antulcer; osteopathic; dermatological; antiallergic; antiasthmatic;
 CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
 CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
 CC encoding them can be used in gene therapy, antisense therapy and vaccine
 CC production. The proteins and polynucleotides are useful for screening for
 CC agonists or antagonists of a protein and for the treatment and diagnosis
 CC of disorders associated with the activity of a protein e.g. inflammation,
 CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
 CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
 CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
 CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
 CC osteoporosis, severe combined immunodeficiency, eczema, allergic
 CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
 CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
 CC neurological disorders.

XX Sequence 131 AA;

Query Match 65.0%; Score 39; DB 22; Length 131;
Best Local Similarity 50.0%; Pred. No. 37;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 10
: : : : :
Db 84 eetcfihk1k 93

Search completed: September 4, 2002, 16:45:03
Job time: 379 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:46:07 ; Search time 57.74 Seconds
(without alignments)
4.653 Million cell updates/sec

Title: US-09-821-726-4
Perfect score: 60
Sequence: 1 KKTICIVHKMKK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	58.3	173	3	US-09-188-579-87
2	35	58.3	173	4	US-09-315-444-87
3	34	56.7	516	3	US-08-948-564-12
4	33	55.0	399	2	US-08-742-621-3
5	33	55.0	399	2	US-08-750-134A-11
6	33	55.0	399	4	US-09-363-745-11
7	33	55.0	410	4	US-09-106-075A-88
8	33	55.0	479	4	US-09-004-838-41
9	33	55.0	483	4	US-09-004-838-117
10	33	55.0	768	1	US-08-454-455-4
11	33	55.0	1140	2	US-08-657-641-7
12	33	55.0	1140	5	PCT-US94-07233-7
13	33	55.0	1366	4	US-09-004-838-22
14	33	55.0	1890	4	US-09-004-838-88
15	32	53.3	27	4	US-09-345-468-21
16	32	53.3	50	4	US-09-052-089A-15
17	32	53.3	292	4	US-09-345-468-18
18	32	53.3	313	4	US-09-345-468-16
19	32	53.3	381	2	US-08-867-057-1
20	32	53.3	381	2	US-08-867-057-3
21	32	53.3	381	2	US-09-128-369-1
22	32	53.3	381	2	US-09-128-369-3
23	32	53.3	419	4	US-09-011-197-4
24	32	53.3	826	1	US-07-638-431-2
25	32	53.3	826	5	PCT-US92-00018-2
26	31.5	52.5	457	1	US-08-416-478A-8
27	31.5	52.5	457	2	US-08-474-988B-8

28	31.5	52.5	457	2	US-08-394-442B-8	Sequence 8, Appli
29	31	51.7	368	2	US-08-869-137-2	Sequence 2, Appli
30	31	51.7	590	1	US-08-448-196A-9	Sequence 9, Appli
31	31	51.7	600	3	US-08-860-519-12	Sequence 12, Appli
32	31	51.7	625	1	US-08-391-615-3	Sequence 3, Appli
33	30.5	50.8	1045	1	US-08-452-083-2	Sequence 2, Appli
34	30	50.0	25	4	US-09-177-249-221	Sequence 221, App
35	30	50.0	59	1	US-08-358-160-118	Sequence 118, App
36	30	50.0	59	1	US-08-358-160-119	Sequence 119, App
37	30	50.0	59	6	5466783-13	Patent No. 5466783
38	30	50.0	60	1	US-08-358-160-121	Sequence 121, App
39	30	50.0	60	6	5466783-16	Patent No. 5466783
40	30	50.0	79	1	US-08-225-757B-15	Sequence 15, Appli
41	30	50.0	80	4	US-08-714-071-2	Sequence 2, Appli
42	30	50.0	103	1	US-08-197-795-1	Sequence 1, Appli
43	30	50.0	103	5	PCT-US95-01721-1	Sequence 1, Appli
44	30	50.0	104	3	US-09-012-515A-6	Sequence 6, Appli
45	30	50.0	104	4	US-08-360-144A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-188-579-87
; Sequence 87, Application US/09188579B
; Patent No. 6107040
; GENERAL INFORMATION:
; APPLICANT: Shuman, Stewart
; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
; FILE REFERENCE: D6185
; CURRENT APPLICATION NUMBER: US/09/188,579B
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 114
; SEQ ID NO 87
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of N-terminal RNA triphosphatase
; OTHER INFORMATION: domain of the capping enzyme.
US-09-188-579-87

Query Match 58.3%; Score 35; DB 3; Length 173;
Best Local Similarity 85.7%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CIVHKMK 10
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Db 82 CIVHKMK 88

RESULT 2
US-09-315-444-87
; Sequence 87, Application US/09315444A
; Patent No. 6232070
; GENERAL INFORMATION:
; APPLICANT: Shuman, Stewart
; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
; FILE REFERENCE: D6185CIP
; CURRENT APPLICATION NUMBER: US/09/315,444A
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 09/188,579
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 87
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of N-terminal RNA triphosphatase
; OTHER INFORMATION: domain of the capping enzyme.

US-09-315-444-87

Query Match 58.3%; Score 35; DB 4; Length 173;
Best Local Similarity 85.7%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CIVHKMK 10
|| ||||
Db 82 CIYHKMK 88

RESULT 3

US-08-948-564-12
; Sequence 12, Application US/08948564
; Patent No. 6121512
; GENERAL INFORMATION:
; APPLICANT: Siminsky, Balazs
; APPLICANT: Dewey, Ralph E.
; APPLICANT: Corbin, Frederick T.
; TITLE OF INVENTION: No. 6121512el Cytochrome P-450 Constructs and
; METHODS OF PRODUCING HERBICIDE-RESISTANT TRANSGENIC PLANTS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Virginia C. Bennett
; STREET: PO Box 37428
; CITY: Raleigh
; STATE: No. 6121512th Carolina
; COUNTRY: USA
; ZIP: 27627
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,564
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Virginia C.
; REGISTRATION NUMBER: 37,092
; REFERENCE/DOCKET NUMBER: 5051-409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-854-1400
; TELEFAX: 919-854-1401
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 516 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-948-564-12

Query Match 56.7%; Score 34; DB 3; Length 516;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKCIVH 7
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Db 126 KKCIVH 132

RESULT 4

US-08-742-621-3
; Sequence 3, Application US/08742621
; Patent No. 5856129
; GENERAL INFORMATION:
; APPLICANT: HILLMAN, JENNIFER L.
; APPLICANT: COLEMAN, ROGER
; TITLE OF INVENTION: NOVEL HUMAN PURINOCEPTOR
; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,621
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0147 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 399 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 166438
US-08-742-621-3

Query Match 55.0%; Score 33; DB 2; Length 399;
Best Local Similarity 71.4%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KTCIVHK 8
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Db 215 KTCIVHK 221

RESULT 5

US-08-750-134A-11
; Sequence 11, Application US/08750134A
; Patent No. 5985603
; GENERAL INFORMATION:
; APPLICANT: VALERA, SOLEDAD
; APPLICANT: BUELL, GARY
; TITLE OF INVENTION: P2X RECEPTORS (PURINOCEPTOR FAMILY)
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,134A
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:

NAME: CRAWFORD, ARTHUR C.
 REGISTRATION NUMBER: 25,327
 REFERENCE/DOCKET NUMBER: 1430-116
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4006
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 399 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-750-134A-11

Query Match 55.0%; Score 33; DB 2; Length 399;
 Best Local Similarity 71.4%; Pred. No. 3e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KTCIVHK 8
 |||: ||
 Db 215 KTCLEPHK 221

RESULT 6
 US-09-363-745-11
 Sequence 11, Application US/09363745
 Patent No. 6194162
 GENERAL INFORMATION:
 APPLICANT: VALERA, SOLEDAD
 APPLICANT: BUELL, GARY
 TITLE OF INVENTION: P2x RECEPTORS (PURINOCEPTOR FAMILY)
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHVE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/363,745
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/750,134
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: CRAWFORD, ARTHUR C.
 REGISTRATION NUMBER: 25,327
 REFERENCE/DOCKET NUMBER: 1430-116
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4006
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 399 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-363-745-11

Query Match 55.0%; Score 33; DB 4; Length 399;
 Best Local Similarity 71.4%; Pred. No. 3e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KTCIVHK 8

Db 215 KTCLEPHK 221
 |||: ||

RESULT 7
 US-09-106-075A-88
 Sequence 88, Application US/09106075A
 Patent No. 6316250
 GENERAL INFORMATION:
 APPLICANT: Hjelle MD, Brian
 APPLICANT: Jenison, Steve
 TITLE OF INVENTION: Molecular Clones Producing Recombinant DNA Antigens of
 FILE REFERENCE: 10312-8UL, Hjelle et al. (210312.0009)
 CURRENT APPLICATION NUMBER: US/09/106,075A
 CURRENT FILING DATE: 1998-06-29
 PRIOR APPLICATION NUMBER: 08/210,762
 PRIOR FILING DATE: 1994-03-22
 PRIOR APPLICATION NUMBER: 08/141,035
 PRIOR FILING DATE: 1993-10-26
 PRIOR APPLICATION NUMBER: 08/120,096
 PRIOR FILING DATE: 1993-09-13
 PRIOR APPLICATION NUMBER: 08/111,519
 PRIOR FILING DATE: 1993-08-25
 NUMBER OF SEQ ID NOS: 90
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 88
 LENGTH: 410
 TYPE: PRT
 ORGANISM: Four Corners hantavirus
 US-09-106-075A-88

Query Match 55.0%; Score 33; DB 4; Length 410;
 Best Local Similarity 55.6%; Pred. No. 3.1e+02;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCIVHKMK 11
 |||: |||:
 Db 376 TCLVKNKVK 384

RESULT 8
 US-09-004-838-41
 Sequence 41, Application US/09004838
 Patent No. 6350933
 GENERAL INFORMATION:
 APPLICANT: Michelmore, Richard W.
 APPLICANT: Shen, Kathy
 APPLICANT: Meyers, Blake
 TITLE OF INVENTION: Procedures and Materials for
 NUMBER OF SEQUENCES: 140
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/004,838
 FILING DATE: 09-JAN-1998
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/781,734
 FILING DATE: 10-JAN-1997
 ATTORNEY/AGENT INFORMATION:

```

; NAME: Einhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 023070-078810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 479 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..479
; OTHER INFORMATION: /note= "RLG2A protein"
;
US-09-004-838-41

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Query Match 55.0%; Score 33; DB 4; Length 479;
Best Local Similarity 50.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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QY 2 KTCIVHKMK 11
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Db 2 KTTMHRLKK 11

```

```

RESULT 9
US-09-004-838-117
; Sequence 117, Application US/09004838
; Patent No. 6350933
; GENERAL INFORMATION:
; APPLICANT: Michelmore, Richard W.
; APPLICANT: Shen, Kathy
; APPLICANT: Meyers, Blake
; TITLE OF INVENTION: Procedures and Materials for
; TITLE OF INVENTION: Conferring Pest Resistance in Plants
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/004,838
; FILING DATE: 09-JAN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/781,734
; FILING DATE: 10-JAN-1997
; NAME: Einhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 023070-078810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 483 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein

```

```

; FEATURE:
; NAME/KEY: -
; LOCATION: 1..483
; OTHER INFORMATION: /note= "RG2N deduced sequence"
;
US-09-004-838-117

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Query Match 55.0%; Score 33; DB 4; Length 483;
Best Local Similarity 50.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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```

QY 2 KTCIVHKMK 11
   ||::||
Db 3 KTTMHRLKK 12

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RESULT 10
US-08-454-455-4
; Sequence 4, Application US/08454455
; Patent No. 5635601
; GENERAL INFORMATION:
; APPLICANT: Moyle, Matthew
; APPLICANT: McLean, John W.
; TITLE OF INVENTION: NOVEL BETA INTEGRIN SUBUNIT
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 720 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,455
; FILING DATE: 30-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/193989
; FILING DATE: 09-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/004142
; FILING DATE: 13-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/670607
; FILING DATE: 14-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: P0699C2D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 768 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-454-455-4

```

```

Query Match 55.0%; Score 33; DB 1; Length 768;
Best Local Similarity 71.4%; Pred. No. 5.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 4 CIVHKMK 10
   ||::||
Db 531 CLCHKMK 537

```


RESULT 11
US-08-657-641-7
; Sequence 7, Application US/08657641
; Patent No. 5945277
; GENERAL INFORMATION:
; APPLICANT: Nichol, Stuart T.
; APPLICANT: Spiropoulos, Christina F.
; APPLICANT: Ksiazek, Thomas G.
; APPLICANT: Rollin, Pierre E.
; TITLE OF INVENTION: NUCLEIC ACIDS OF A NOVEL HANTAVIRUS
; TITLE OF INVENTION: AND
; TITLE OF INVENTION: REAGENTS FOR DETECTION AND PREVENTION OF INFECTION
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Suite 1200, The Candler Building
; STREET: 127 Peachtree Street, NE
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/657,641
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,591
; FILING DATE: 07-OCT-1993
; APPLICATION NUMBER: US 1414,074
; FILING DATE: 24-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Perryman, David G.
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414,089
; TELEPHONE: 404-688-0770
; TELEFAX: 404-688-9880
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1140 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Hantavirus
; STRAIN: New
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: M Segment
; UNITS: 1140 AA
US-08-657-641-7

Query Match 55.0%; Score 33; DB 2; Length 1140;
Best Local Similarity 55.6%; Pred. No. 7.4e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCIVHKMKK 11
||:|:|:
Db 408 TCLVKNVQK 416

RESULT 12
PCT-US94-07233-7
; Sequence 7, Application PC/TUS9407233

; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: NUCLEIC ACIDS OF A NOVEL HANTAVIRUS AND REAGENTS FOR DETECT
; NUMBER OF SEQUENCES: 12
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07233
; FILING DATE: 24-JUN-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/084,724
; FILING DATE: 24-JUN-1993
; APPLICATION NUMBER: US 08/591,133
; FILING DATE: 07-OCT-1993
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1140 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Polypeptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Hantavirus
; STRAIN: New
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: M Segment
; UNITS: 1140 AA
PCT-US94-07233-7

Query Match 55.0%; Score 33; DB 5; Length 1140;
Best Local Similarity 55.6%; Pred. No. 7.4e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCIVHKMKK 11
||:|:|:
Db 408 TCLVKNVQK 416

RESULT 13
US-09-004-838-22
; Sequence 22, Application US/09004838
; Patent No. 6350933
; GENERAL INFORMATION:
; APPLICANT: Michelmore, Richard W.
; APPLICANT: Shen, Kathy
; APPLICANT: Meyers, Blake
; TITLE OF INVENTION: Procedures and Materials for
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/004,838
; FILING DATE: 09-JAN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/781,734

```
; FILING DATE: 10-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Einhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 023070-078810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1366 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..1366
; OTHER INFORMATION: /note= "RLG2A amino acids"
US-09-004-838-22

Query Match 55.0%; Score 33; DB 4; Length 1366;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 KTCIVHKMKK 11
Db 185 KTTMHRLKK 194

RESULT 14
US-09-004-838-88
; Sequence 88, Application US/09004838
; Patent No. 6350933
; GENERAL INFORMATION:
; APPLICANT: Michelmore, Richard W.
; APPLICANT: Shen, Kathy
; APPLICANT: Meyers, Blake
; TITLE OF INVENTION: Procedures and Materials for
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/004,838
; FILING DATE: 09-JAN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/781,734
; FILING DATE: 10-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Einhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 023070-078810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1890 amino acids
; TYPE: amino acid
; STRANDEDNESS:
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..1890
; OTHER INFORMATION: /note= "RG2A deduced sequence"
US-09-004-838-88

Query Match 55.0%; Score 33; DB 4; Length 1890;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 KTCIVHKMKK 11
Db 185 KTTMHRLKK 194

RESULT 15
US-09-345-468-21
; Sequence 21, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevail, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-345-468-21

Query Match 53.3%; Score 32; DB 4; Length 27;
Best Local Similarity 40.0%; Pred. No. 43;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKTICIVHKMK 10
Db 6 RKKCLQHRMR 15

Search completed: September 4, 2002, 16:46:08
Job time: 329 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2002, 16:59:20 ; Search time 704.77 Seconds
(without alignments)
5.494 Million cell updates/sec

Title: US-09-821-726-4
Perfect score: 60
Sequence: 1 KKTCTIVHKMKK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

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3:	/cgn2_6/ptodata/2/paa/US07_COMB.pcp.*
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5:	/cgn2_6/ptodata/2/paa/US0801_COMB.pcp.*
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9:	/cgn2_6/ptodata/2/paa/US0805_COMB.pcp.*
10:	/cgn2_6/ptodata/2/paa/US0806_COMB.pcp.*
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12:	/cgn2_6/ptodata/2/paa/US0808_COMB.pcp.*
13:	/cgn2_6/ptodata/2/paa/US0809_COMB.pcp.*
14:	/cgn2_6/ptodata/2/paa/US090_COMB.pcp.*
15:	/cgn2_6/ptodata/2/paa/US091_COMB.pcp.*
16:	/cgn2_6/ptodata/2/paa/US092_COMB.pcp.*
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23:	/cgn2_6/ptodata/2/paa/US099_COMB.pcp.*
24:	/cgn2_6/ptodata/2/paa/US100_COMB.pcp.*
25:	/cgn2_6/ptodata/2/paa/US101_COMB.pcp.*
26:	/cgn2_6/ptodata/2/paa/US060_COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	60	100.0	11	22	US-09-821-726-4		Sequence 4, Appli
2	60	100.0	42	22	US-09-821-726-6		Sequence 6, Appli
3	60	100.0	185	22	US-09-821-726-13		Sequence 13, Appli
4	56	93.3	185	22	US-09-821-726-18		Sequence 18, Appli
5	55	91.7	150	13	US-08-906-708-24		Sequence 24, Appli
6	55	91.7	182	20	US-09-684-524-212		Sequence 212, App
7	55	91.7	182	24	US-10-050-704-212		Sequence 212, App

8	55	91.7	185	1	PCT-US98-16318-18	Sequence 18, Appl
9	55	91.7	185	15	US-09-130-189-18	Sequence 18, Appl
10	55	91.7	185	20	US-09-684-524-105	Sequence 105, App
11	55	91.7	185	21	US-09-709-238-211	Sequence 211, App
12	55	91.7	185	21	US-09-746-783-146	Sequence 146, App
13	55	91.7	185	23	US-09-941-992-211	Sequence 211, App
14	55	91.7	185	23	US-09-989-279-211	Sequence 211, App
15	55	91.7	185	23	US-09-989-293A-211	Sequence 211, App
16	55	91.7	185	23	US-09-989-721-211	Sequence 211, App
17	55	91.7	185	23	US-09-989-722-211	Sequence 211, App
18	55	91.7	185	23	US-09-989-723-211	Sequence 211, App
19	55	91.7	185	23	US-09-989-724-211	Sequence 211, App
20	55	91.7	185	23	US-09-989-725-211	Sequence 211, App
21	55	91.7	185	23	US-09-989-726-211	Sequence 211, App
22	55	91.7	185	23	US-09-989-727-211	Sequence 211, App
23	55	91.7	185	23	US-09-989-728-211	Sequence 211, App
24	55	91.7	185	23	US-09-989-729A-211	Sequence 211, App
25	55	91.7	185	23	US-09-989-730-211	Sequence 211, App
26	55	91.7	185	23	US-09-989-731-211	Sequence 211, App
27	55	91.7	185	23	US-09-989-732-211	Sequence 211, App
28	55	91.7	185	23	US-09-989-734-211	Sequence 211, App
29	55	91.7	185	23	US-09-989-735-211	Sequence 211, App
30	55	91.7	185	23	US-09-989-862-211	Sequence 211, App
31	55	91.7	185	23	US-09-990-427-211	Sequence 211, App
32	55	91.7	185	23	US-09-990-436-211	Sequence 211, App
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34	55	91.7	185	23	US-09-990-438-211	Sequence 211, App
35	55	91.7	185	23	US-09-990-439-211	Sequence 211, App
36	55	91.7	185	23	US-09-990-440-211	Sequence 211, App
37	55	91.7	185	23	US-09-990-441-211	Sequence 211, App
38	55	91.7	185	23	US-09-990-442-211	Sequence 211, App
39	55	91.7	185	23	US-09-990-443-211	Sequence 211, App
40	55	91.7	185	23	US-09-990-444-211	Sequence 211, App
41	55	91.7	185	23	US-09-990-456-211	Sequence 211, App
42	55	91.7	185	23	US-09-990-562-211	Sequence 211, App
43	55	91.7	185	23	US-09-990-711-211	Sequence 211, App
44	55	91.7	185	23	US-09-990-726-211	Sequence 211, App
45	55	91.7	185	23	US-09-991-073-211	Sequence 211, App

ALIGNMENTS

```

RESULT      1
US-09-821-726-4
; Sequence 4, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOWBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIV
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-821-726-4

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Query Match	100.0%	Score 60;	DB 22;	Length 11;
Best Local Similarity	100.0%;	Pred. No. 0.0011;		
Matches 11;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	KKTCIVHKMKK	11	
Db	1	KKTCIVHKMKK	11	

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RESULT 2
US-09-821-726-6
; Sequence 6, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-821-726-6

Query Match          100.0%; Score 60; DB 22; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKTClVHKMKK 11
Db 1 KKTClVHKMKK 11

RESULT 3
US-09-821-726-13
; Sequence 13, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-821-726-13

Query Match          100.0%; Score 60; DB 22; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKTClVHKMKK 11
Db 78 KKTClVHKMKK 88

RESULT 4
US-09-821-726-18
; Sequence 18, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Porcine sp.
US-09-821-726-18

Query Match          93.3%; Score 56; DB 22; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.095;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKTClVHKMKK 11
Db 78 KKTClVHKMKK 88

RESULT 5
US-08-906-708-24
; Sequence 24, Application US/08906708
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaValle, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; APPLICANT: Agostino, Michael J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING THEM
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,708
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: P-41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-906-708-24

Query Match          91.7%; Score 55; DB 13; Length 150;
Best Local Similarity 90.9%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTClVHKMKK 11
Db 78 KKTClVHKMKK 88

RESULT 6
```

US-09-684-524-212
; Sequence 212, Application US/09684524
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/09/684,524
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 212
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US98-16318-212

Query Match 91.7%; Score 55; DB 20; Length 182;
Best Local Similarity 90.9%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 11
Db 78 KKTCTIVHKMK 88

RESULT 7
US-10-050-704-212
; Sequence 212, Application US/10050704
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/10/050,704
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 09/684,524
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 212
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-704-212

Query Match 91.7%; Score 55; DB 24; Length 182;
Best Local Similarity 90.9%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 11
Db 78 KKTCTIVHKMK 88

RESULT 8
PCT-US98-16318-18
; Sequence 18, Application PC/TUS9816318
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.

; APPLICANT: LaVallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steinhinger II, Robert J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI6051A
; CURRENT APPLICATION NUMBER: PCT/US98/16318
; CURRENT FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US98-16318-18

Query Match 91.7%; Score 55; DB 1; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 11
Db 78 KKTCTIVHKMK 88

RESULT 9
US-09-130-189-18
; Sequence 18, Application US/09130189
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steinhinger II, Robert J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI6051A
; CURRENT APPLICATION NUMBER: US/09/130,189
; CURRENT FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-130-189-18

Query Match 91.7%; Score 55; DB 15; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 11
Db 78 KKTCTIVHKMK 88

RESULT 10
US-09-684-524-105
; Sequence 105, Application US/09684524
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1

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; CURRENT APPLICATION NUMBER: US/09/684,524
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-684-524-105

Query Match          91.7%; Score 55; DB 20; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMK 11
Db 78 KKTCTVHKMK 88

RESULT 11
US-09-709-238-211
; Sequence 211, Application US/09709238
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Chen, Jian
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Yuan, Jean
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding the Same
; FILE REFERENCE: P2730R1C1
; CURRENT APPLICATION NUMBER: US/09/709,238
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 60/087,607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: US 60/087,609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: US 60/087,759
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: US 60/087,827
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: US 60/088,021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: US 60/088,025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: US 60/088,028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: US 60/088,029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: US 60/088,030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: US 60/088,033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: US 60/088,326
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/088,167
; PRIOR FILING DATE: 1988-06-05
; PRIOR APPLICATION NUMBER: US 60/088,202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/088,212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/088,217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/088,217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/088,655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: US 60/088,722
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,730
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,740
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,741
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,742
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,810
; PRIOR FILING DATE: 1998-06-10
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; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,825
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: US 60/088,861
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; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: US 60/088,876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: US 60/089,090
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: US 60/089,105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: US 60/089,440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: US 60/089,512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: US 60/089,514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: US 60/089,532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/089,538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/089,598
; PRIOR FILING DATE: 1998-06-17
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; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/089,600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/089,653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/089,801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: US 60/089,907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: US 60/089,908
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: US 60/089,947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 60/089,948
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 60/089,952
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 60/090,246
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: US 60/090,252
; PRIOR FILING DATE: 1998-06-22
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;; PRIOR APPLICATION NUMBER: US 60/090,254
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: US 60/090,355
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: US 60/090,429
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: US 60/090,431
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;; PRIOR APPLICATION NUMBER: US 60/090,435
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: US 60/090,349
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: US 60/090,444
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: US 60/090,445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: US 60/090,461
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: US 60/090,472
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: US 60/090,535
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: US 60/090,538
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: US 60/090,540
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;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: US 60/090,676
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: US 60/090,678
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: US 60/090,688
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: US 60/090,690
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: US 60/090,691
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: US 60/090,694
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: US 60/090,695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: US 60/090,696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: US 60/090,862
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: US 60/090,863
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: US 60/091,358
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: US 60/091,360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: US 60/091,478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: US 60/091,486
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: US 60/091,519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: US 60/091,544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: US 60/091,626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: US 60/091,628
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: US 60/091,633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: US 60/091,646
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: US 60/091,673
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: US 60/091,978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: US 60/091,982

;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: US 60/092,182
;; PRIOR FILING DATE: 1998-07-09
;; PRIOR APPLICATION NUMBER: US 60/092,472
;; PRIOR FILING DATE: 1998-07-10
;; PRIOR APPLICATION NUMBER: US 60/093,339
;; PRIOR FILING DATE: 1998-07-20
;; PRIOR APPLICATION NUMBER: US 60/094,651
;; PRIOR FILING DATE: 1998-07-30

Query Match 91.7%; Score 55; DB 21; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KKTCTIVHKMK 11
|||||||
Db 78 KKTCTIVHKMK 88

RESULT 12
US-09-746-783-146
; Sequence 146, Application US/09746783
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; McCoy, John M.
; Lavallie, Edward R.
; Racie, Lisa A.
; Treacy, Maurice
; Spaulding, Vikki
; Agostino, Michael J.
; Howes, Steven H.
; Fechtel, Kim
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; ENCODING THEM
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/746,783
; FILING DATE: 21-Dec-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Milasincic, Debra J.
; REGISTRATION NUMBER: 46,931
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 146:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 146:
US-09-746-783-146

Query Match 91.7%; Score 55; DB 21; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KKTCTIVHKMK 11

Db 78 KKTCIVHKMK 88

RESULT 13

US-09-941-992-211

Sequence 211, Application US/09941992

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730PIC1

CURRENT APPLICATION NUMBER: US/09/941,992

CURRENT FILING DATE: 2001-08-28

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/084600

PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/087106

PRIOR FILING DATE: 1998-05-28

PRIOR APPLICATION NUMBER: 60/087607

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087609

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087759

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087827

PRIOR FILING DATE: 1998-06-03

PRIOR APPLICATION NUMBER: 60/088021

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088025

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088026

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088028

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088029

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088030

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088033

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088326

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088167

PRIOR FILING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: 60/088202

PRIOR FILING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: 60/088212

PRIOR FILING DATE: 1998-06-05

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PRIOR FILING DATE: 1998-06-22

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PRIOR APPLICATION NUMBER: 60/090254

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; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472

Query Match 91.7%; Score 55; DB 23; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMK 11

Db 78 KKTCTVHKMK 88

RESULT 14

US-09-989-279-211

; Sequence 211, Application US/09989279

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1G56
; CURRENT APPLICATION NUMBER: US/09/989,279
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1997-10-17
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 ; PRIOR APPLICATION NUMBER: 60/092472

Query Match 91.7%; Score 55; DB 23; Length 185;
 Best Local Similarity 90.9%; Pred. No. 0.14;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHRMKNK 11
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 Db 78 KKTCTVHRMKNK 88

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 ; Sequence 211, Application US/0989293A
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
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APPLICANT: Gurney, Austin L.
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APPLICANT: Napier, Mary A.
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC66
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
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Thu Sep 5 11:23:39 2002

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; PRIOR FILING DATE: 1998-06-24
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472

Query Match 91.7%; Score 55; DB 23; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KKTCTVHKMK 11
Db 78 KKTCTVHKMK 88

Search completed: September 4, 2002, 16:59:20
Job time: 1041 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 17:04:23 ; Search time 166.13 Seconds
(without alignments)
16.284 Million cell updates/sec

Title: US-09-821-726-4
Perfect score: 60
Sequence: 1 KKTCTIVHKMKK 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 763338 seqs, 245939087 residues

Total number of hits satisfying chosen parameters: 763338

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
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2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pcp.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pcp.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pcp.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pcp.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pcp.*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	91.7	185	5	US-09-991-150-211
2	55	91.7	185	5	US-09-720-533-49
3	55	91.7	185	6	US-10-119-480-148
4	55	91.7	185	6	US-10-216-159A-148
5	55	91.7	185	6	US-10-216-162-148
6	55	91.7	185	6	US-10-216-163-148
7	55	91.7	185	6	US-10-216-164-148
8	55	91.7	185	6	US-10-216-165-148
9	55	91.7	185	6	US-10-216-166-148
10	55	91.7	185	6	US-10-216-167-148
11	55	91.7	185	6	US-10-216-168-148
12	55	91.7	185	6	US-10-216-160-148
13	55	91.7	185	6	US-10-218-849-148
14	55	91.7	185	6	US-10-218-930-148
15	55	91.7	185	6	US-10-219-003-148
16	55	91.7	185	6	US-10-218-612-148
17	55	91.7	185	6	US-10-218-956-148
18	55	91.7	185	6	US-10-219-010-148
19	55	91.7	185	6	US-10-218-765-148
20	55	91.7	185	6	US-10-218-784-148
21	55	91.7	185	6	US-10-219-061-148
22	55	91.7	185	6	US-10-219-062-148
23	55	91.7	185	6	US-10-219-063-148
24	55	91.7	185	6	US-10-219-064-148
25	55	91.7	185	6	US-10-219-065-148
26	55	91.7	185	6	US-10-219-066-148

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27 55 91.7 185 6 US-10-219-070-148 Sequence 148, App
28 55 91.7 185 6 US-10-219-071-148 Sequence 148, App
29 55 91.7 185 6 US-10-219-072-148 Sequence 148, App
30 55 91.7 185 6 US-10-219-073-148 Sequence 148, App
31 55 91.7 185 6 US-10-219-074-148 Sequence 148, App
32 55 91.7 185 6 US-10-219-075-148 Sequence 148, App
33 55 91.7 185 6 US-10-219-077-148 Sequence 148, App
34 55 91.7 185 6 US-10-219-077-148 Sequence 148, App
35 55 91.7 185 6 US-10-219-464-148 Sequence 148, App
36 55 91.7 185 6 US-10-219-465-148 Sequence 148, App
37 55 91.7 185 6 US-10-219-466-148 Sequence 148, App
38 55 91.7 185 6 US-10-219-467-148 Sequence 148, App
39 55 91.7 185 6 US-10-219-470-148 Sequence 148, App
40 55 91.7 185 6 US-10-219-471-148 Sequence 148, App
41 55 91.7 185 6 US-10-219-474-148 Sequence 148, App
42 55 91.7 185 6 US-10-219-475-148 Sequence 148, App
43 55 91.7 185 6 US-10-219-476-148 Sequence 148, App
44 55 91.7 185 6 US-10-219-478-148 Sequence 148, App
45 55 91.7 185 6 US-10-219-479-148 Sequence 148, App
46 55 91.7 185 6 US-10-219-480-148 Sequence 148, App

```

ALIGNMENTS

```

RESULT 1
US-09-991-150-211
; Sequence 211, Application US/09991150
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavina, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC48
; CURRENT APPLICATION NUMBER: US/09/991,150
; CURRENT FILING DATE: 2001-11-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 532
; SEQ ID NO 211
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-991-150-211

```

Query Match 91.7%; Score 55; DB 5; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMKK 11

Db 78 KKTCTIVHKMKK 88

RESULT 2
US-09-720-533-49
; Sequence 49, Application US/09720533
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: LAL, Preeti
; APPLICANT: TANG, Y. Tom
; APPLICANT: GORGONE, Gina A.
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AKERBLOM, Ingrid E.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: YUE, Henry
; APPLICANT: PATTERSON, Chandra
; APPLICANT: REDDY, Roopa
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: BANDMAN, Olga
; TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
; FILE REFERENCE: PF-0541 PCT
; CURRENT APPLICATION NUMBER: US/09/720,533
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/090,762; 60/094,983; 60/102,686; 60/112,129
; PRIOR FILING DATE: 1998-06-26; 1998-07-31; 1998-10-01; 1998-12-11
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PERL Program
; SEQ ID NO 49
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte Clone No: 2593853
US-09-720-533-49

Query Match 91.7%; Score 55; DB 5; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMKK 11
|||||||
Db 78 KKTCTVHKMKK 88

RESULT 3
US-10-119-480-148
; Sequence 148, Application US/10119480
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C1
; CURRENT APPLICATION NUMBER: US/10/119,480
; CURRENT FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 246
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-119-480-148

Query Match 91.7%; Score 55; DB 6; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMKK 11
|||||||
Db 78 KKTCTVHKMKK 88

RESULT 4
US-10-216-159A-148
; Sequence 148, Application US/10216159A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C6
; CURRENT APPLICATION NUMBER: US/10/216,159A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-159A-148

Query Match 91.7%; Score 55; DB 6; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMKK 11
|||||||
Db 78 KKTCTVHKMKK 88

RESULT 5
US-10-216-162-148
; Sequence 148, Application US/10216162
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC2
; CURRENT APPLICATION NUMBER: US/10/216,162
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-162-148

Query Match 91.7%; Score 55; DB 6; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMK 11
| | | | | | | |
Db 78 KKTCTVHKMK 88

RESULT 6
US-10-216-163-148
; Sequence 148, Application US/10216163
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC3
; CURRENT APPLICATION NUMBER: US/10/216,163

; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-163-148

Query Match 91.7%; Score 55; DB 6; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMK 11
| | | | | | | |
Db 78 KKTCTVHKMK 88

RESULT 7
US-10-216-164-148
; Sequence 148, Application US/10216164
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC5
; CURRENT APPLICATION NUMBER: US/10/216,164
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079656
 ; PRIOR FILING DATE: 1998-03-26
 ; PRIOR APPLICATION NUMBER: 60/079728
 ; PRIOR FILING DATE: 1998-03-27
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 148
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-216-164-148

Query Match 91.7%; Score 55; DB 6; Length 185;
 Best Local Similarity 90.9%; Pred. No. 0.075;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMKK 11
 |||||
 Db 78 KKTCTVHKMKK 88

RESULT 8
 US-10-216-165-148
 ; Sequence 148, Application US/10216165
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530PIC7
 ; CURRENT APPLICATION NUMBER: US/10/216,165
 ; CURRENT FILING DATE: 2002-08-09
 ; PRIOR APPLICATION NUMBER: 10/119,480
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/062287
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063549
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/064103
 ; PRIOR FILING DATE: 1997-10-31
 ; PRIOR APPLICATION NUMBER: 60/069873
 ; PRIOR FILING DATE: 1997-12-17
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079656
 ; PRIOR FILING DATE: 1998-03-26
 ; PRIOR APPLICATION NUMBER: 60/079728
 ; PRIOR FILING DATE: 1998-03-27
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 148
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-216-165-148

Query Match 91.7%; Score 55; DB 6; Length 185;
 Best Local Similarity 90.9%; Pred. No. 0.075;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMKK 11
 |||||
 Db 78 KKTCTVHKMKK 88

RESULT 9
 US-10-216-166-148
 ; Sequence 148, Application US/10216166
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530PIC9
 ; CURRENT APPLICATION NUMBER: US/10/216,166
 ; CURRENT FILING DATE: 2002-08-09
 ; PRIOR APPLICATION NUMBER: 10/119,480
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/062287
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063549
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/064103
 ; PRIOR FILING DATE: 1997-10-31
 ; PRIOR APPLICATION NUMBER: 60/069873
 ; PRIOR FILING DATE: 1997-12-17
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079656
 ; PRIOR FILING DATE: 1998-03-26
 ; PRIOR APPLICATION NUMBER: 60/079728
 ; PRIOR FILING DATE: 1998-03-27
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 148
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-216-166-148

Query Match 91.7%; Score 55; DB 6; Length 185;
 Best Local Similarity 90.9%; Pred. No. 0.075;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMKK 11
 |||||
 Db 78 KKTCTVHKMKK 88

RESULT 10
 US-10-216-167-148
 ; Sequence 148, Application US/10216167
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc

; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC4
; CURRENT APPLICATION NUMBER: US/10/216,167
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-167-148

Query Match 91.7%; Score 55; DB 6; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 11
Db 78 KKTCTIVHKMK 88

RESULT 11
US-10-216-168-148
; Sequence 148, Application US/10216168
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC10
; CURRENT APPLICATION NUMBER: US/10/216,168
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480

; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-168-148

Query Match 91.7%; Score 55; DB 6; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 11
Db 78 KKTCTIVHKMK 88

RESULT 12
US-10-216-160-148
; Sequence 148, Application US/10216160
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC8
; CURRENT APPLICATION NUMBER: US/10/216,160
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; Remaining Prior Application data removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-160-148

Query Match 91.7%; Score 55; DB 6; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 11
Db 78 KKTCTIVHKMK 88

RESULT 13

US-10-218-849-148
; Sequence 148, Application US/10218849
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC11
; CURRENT APPLICATION NUMBER: US/10/218,849
; CURRENT FILING DATE: 2002-08-12
; -Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-849-148

Query Match 91.7%; Score 55; DB 6; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMKK 11
| | | | | | | | | |
Db 78 KKTCTIVHKMKK 88

RESULT 14

US-10-218-930-148
; Sequence 148, Application US/10218930
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC13
; CURRENT APPLICATION NUMBER: US/10/218,930
; CURRENT FILING DATE: 2002-08-12
; -Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-930-148

Query Match 91.7%; Score 55; DB 6; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMKK 11
| | | | | | | | | |
Db 78 KKTCTIVHKMKK 88

RESULT 15

US-10-219-003-148
; Sequence 148, Application US/10219003
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC12
; CURRENT APPLICATION NUMBER: US/10/219,003
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089905
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25

; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095318
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095916
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/096146
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: 60/096791
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/097986
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/098544
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099811
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100038
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101786
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101922
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/106178
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/106248
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 60/106464
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/106905
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 60/108787
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/108801
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/108849
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 60/112422
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113296
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621

; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/115558
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115565
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115733
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/119549
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/123618
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/125259
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 60/125775
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/126773
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: 60/127887
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/130232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131022
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: 60/131270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131445
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 60/134287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/140650
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/140723
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/146222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146963
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/149320
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835
; PRIOR FILING DATE: 1999-12-07

Query Match 91.7%; Score 55; DB 6; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMKK 11
Db 78 KKTCTIVHKMKK 88

Search completed: September 4, 2002, 17:04:23

Job time: 1154 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:47:31 ; Search time 75.48 Seconds
(without alignments)
14.003 Million cell updates/sec

Title: US-09-821-726-4
Perfect score: 60
Sequence: 1 KKTCTIVHKMKK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PTR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	65.0	320	T28379	ORF MSV218 hypothe
2	38	63.3	82	D64699	hypotheical prote
3	38	63.3	86	G71819	hypotheical prote
4	38	63.3	245	H97025	phospholipase C re
5	38	63.3	553	T19894	hypotheical prote
6	37	61.7	389	D96738	hypotheical prote
7	36	60.0	222	T26213	hypotheical prote
8	36	60.0	266	D71675	hypotheical prote
9	36	60.0	399	AC1601	hypotheical prote
10	36	60.0	598	F69792	hypotheical prote
11	36	60.0	671	T10755	kinesin-related pr
12	36	60.0	935	T19011	hypotheical prote
13	36	60.0	2484	T26216	hypotheical prote
14	36	60.0	2607	T26215	hypotheical prote
15	35	58.3	150	F59108	hypotheical prote
16	35	58.3	207	T05289	hypotheical prote
17	35	58.3	247	T40461	very hypotheical
18	35	58.3	283	G96810	unknown protein T1
19	35	58.3	324	G84610	hypotheical prote
20	35	58.3	327	F84610	hypotheical prote
21	35	58.3	329	A55221	dextranase inhibito
22	35	58.3	350	T34557	hypotheical prote
23	35	58.3	389	T25116	hypotheical prote
24	35	58.3	585	T18885	hypotheical prote
25	35	58.3	636	G96717	hypotheical prote
26	35	58.3	738	D86345	hypotheical prote
27	35	58.3	1326	B56395	secretory phosphol
28	35	58.3	1465	A56395	secretory phosphol
29	34	56.7	104	T39020	hypotheical prote

30	34	56.7	133	2	S28187	interleukin-4 - pi
31	34	56.7	162	2	PN0533	ribonuclease (EC 3
32	34	56.7	223	2	AB1541	ABC transporters,
33	34	56.7	257	2	A25394	SURF-2 protein - m
34	34	56.7	300	2	A81418	pseudouridylylate sy
35	34	56.7	303	2	S44455	transcription fact
36	34	56.7	329	2	T04244	hypotheical prote
37	34	56.7	361	2	T26610	hypotheical prote
38	34	56.7	373	2	D87790	protein B0207.7 [1
39	34	56.7	406	2	D69878	pantothenate metab
40	34	56.7	452	2	S78481	retinoic acid rece
41	34	56.7	457	2	S39713	probable aldehyde
42	34	56.7	458	2	S06123	retinoic acid rece
43	34	56.7	516	2	T05940	cytochrome P450 83
44	34	56.7	525	2	T47409	hypotheical prote
45	34	56.7	595	2	T49384	related to NR1 pr

ALIGNMENTS

RESULT 1

T28379
ORF MSV218 hypotheical protein - Melanoplus sanguinipes entomopoxvirus
C:Species: Melanoplus sanguinipes entomopoxvirus
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T28379
R:Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A:Reference number: 220484; MUID:99102612
A:Accession: T28379
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-320 <AFO>
A:Cross-references: EMBL:AF063866; NID:g4049647; PIDN:AAC97747.1; PID:g4049787
C:Genetics:
A:Note: MSV218

Query Match 65.0%; Score 39; DB 2; Length 320;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHK 8
DB 26 KKVCIHKK 33

RESULT 2

D64699
hypotheical protein HPI436 - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C:Accession: D64699
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKee
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467
A:Accession: D64699
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-82 <TOM>
A:Cross-references: GB:AE000644; GB:AE000511; NID:g314609; PIDN:AAD08488.1; PID:g231

Query Match 63.3%; Score 38; DB 2; Length 82;
Best Local Similarity 54.5%; Pred. No. 7;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMKK 11
 : | : : | | |
 Db 66 QKACLLHKDKK 76

RESULT 3
 T19819
 hypothetical protein jhp1329 - Helicobacter pylori (strain J99)
 C:Species: Helicobacter pylori
 A:Variety: strain J99
 C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
 R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
 Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
 Nature 397, 176-180, 1999
 A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
 A:Reference number: A71800; MUID:99120557
 A:Accession: G71819
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-86 <ARN>
 A:Cross-references: GB:AE001556; GB:AE001439; NID:g4155938; PIDN:AAD06905.1; PID:g415593
 A:Experimental source: strain J99
 C:Genetics:
 A:Gene: jhp1329

Query Match 63.3%; Score 38; DB 2; Length 86;
 Best Local Similarity 54.5%; Pred. No. 7.3;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMKK 11
 : | : : | | |
 Db 70 QKACLLHKDKK 80

RESULT 4
 H97025
 phospholipase C related protein [imported] - Clostridium acetobutylicum
 C:Species: Clostridium acetobutylicum
 C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 A:Accession: H97025
 R:Molling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
 J. Bacteriol. 183, 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: H97025
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-245 <KUR>
 A:Cross-references: GB:AE001437; PIDN:AAK78995.1; PID:gl5023929; GSPDB:GN00168
 A:Experimental source: Clostridium acetobutylicum ATCC824
 C:Genetics:
 A:Gene: CAC1019

Query Match 63.3%; Score 38; DB 2; Length 245;
 Best Local Similarity 75.0%; Pred. No. 17;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHK 8
 : | : : | | |
 Db 29 KTTCTIIHK 36

RESULT 5
 T19894
 hypothetical protein C41G7.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 A:Accession: T19894
 R:Steward, C.

submitted to the EMBL Data Library, October 1996
 A:Reference number: Z19192
 A:Accession: T19894
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-553 <WIL>
 A:Cross-references: EMBL:Z81048; PIDN:CAB02840.1; GSPDB:GN00019; CESP:C41G7.3
 A:Experimental source: clone C41G7
 C:Genetics:
 A:Gene: CESP:C41G7.3
 A:Map position: 1
 A:Introns: 25/1; 81/2; 106/3; 157/1; 179/3; 245/3; 368/1; 389/3; 423/3; 517/3

Query Match 63.3%; Score 38; DB 2; Length 553;
 Best Local Similarity 60.0%; Pred. No. 34;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 KTCIVHKMKK 11
 : | : : | | |
 Db 235 KTCVVERIKQ 244

RESULT 6
 D96738
 hypothetical protein F14023.1 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: D96738
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
 Chin, C.W.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marzia
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719
 A:Accession: D96738
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-389 <STO>
 A:Cross-references: GB:AE005173; NID:g7239515; PIDN:AAF43241.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F14023.1
 A:Map position: 1

Query Match 61.7%; Score 37; DB 2; Length 389;
 Best Local Similarity 70.0%; Pred. No. 39;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 10
 : | : : | | |
 Db 234 KVTCLSHKFK 243

RESULT 7
 T26213
 hypothetical protein W06A7.3b - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T26213
 R:Ainscough, R.
 submitted to the EMBL Data Library, August 1996
 A:Reference number: Z20173
 A:Accession: T26213
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-222 <WIL>
 A:Cross-references: EMBL:Z78066; PIDN:CAB01523.1; GSPDB:GN00023; CESP:W06A7.3b

A:Experimental source: clone W06A7

C:Genetics:

A:Gene: CESP:W06A7.3b

A:Map position: 5

A:Introns: 27/1; 77/2; 201/2

Query Match 60.0%; Score 36; DB 2; Length 222;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCIVHKMK 11

||| :||

Db 122 TCANKLKK 130

RESULT 8

D71675

hypothetical protein RP689 - Rickettsia prowazekii

C:Species: Rickettsia prowazekii

C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000

C:Accession: D71675

R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichert-Ponten, T.; Alsmark, U.

Nature 396, 133-140, 1998

A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.

A:Reference number: A71630; MUID:99039499

A:Accession: D71675

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-266 <AND>

A:Cross-references: GB:AJ235272; GB:AJ235269; NID:g3861033; PIDN:CAAL15136.1; PID:e134297

A:Experimental source: strain Madrid E

C:Genetics:

A:Gene: RP689

Query Match 60.0%; Score 36; DB 2; Length 266;
Best Local Similarity 64.3%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

QY 1 KKTC----IVHKMK 10

|||||

Db 135 KKTCLDFIVHKMK 148

RESULT 9

AC1601

hypothetical protein lin1348 [imported] - Listeria innocua (strain Cl1p11262)

C:Species: Listeria innocua

C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001

C:Accession: AC1601

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker

; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma

ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A:Title: Comparative genomics of Listeria species

A:Reference number: AB1077; MUID:21337279; PMID:11679669

A:Accession: AC1601

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-399 <GLA>

A:Cross-references: GB:AL592022; PIDN:CAC96579.1; PID:gl6413821; GSPDB:GN00178

A:Experimental source: strain Cl1p11262

C:Genetics:

A:Gene: lin1348

Query Match 60.0%; Score 36; DB 2; Length 399;
Best Local Similarity 54.5%; Pred. No. 61;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKTCIVHKMK 11

||| :||

Db 374 KKTSLHEFK 384

RESULT 10

F69792

hypothetical protein yeeB - Bacillus subtilis

C:Species: Bacillus subtilis

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 28-Jul-2000

C:Accession: F69792

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;

A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M

Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Paro, V.; Pohl, T.M.; Portete

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida

A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili

A:Reference number: A69580; MUID:98044033

A:Accession: F69792

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-598 <KUN>

A:Cross-references: GB:299107; GB:AL009126; NID:g2632866; PIDN:CAB12497.1; PID:e11826

A:Experimental source: strain 168

C:Genetics:

A:Gene: yeeB

A:Gene: yeeB

C:Superfamily: Bacillus subtilis hypothetical protein yeeB

Query Match 60.0%; Score 36; DB 2; Length 598;
Best Local Similarity 66.7%; Pred. No. 85;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KTCIVHKMK 10

||| :||

Db 466 KTCIKHKK 474

RESULT 11

T10755

kinesin-related protein 2 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 29-Sep-1999

C:Accession: T10755

R:Sperry, A.O.

submitted to the EMBL Data Library, January 1998

A:Reference number: Z17121

A:Accession: T10755

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-671 <SPE>

A:Cross-references: EMBL:U44979; NID:g2772515; PID:g2772516

A:Experimental source: strain Sprague-Dawley, testes

C:Genetics:

A:Gene: KRP2

C:Superfamily: kinesin-related protein KIF2; kinesin motor domain homology

F:205-542/Domain: kinesin motor domain homology <KMT>

Query Match 60.0%; Score 36; DB 2; Length 671;
Best Local Similarity 54.5%; Pred. No. 93;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCIVHKMK 11

Db 136 RKSCIVKEMK 146
:|||||:|:|

RESULT 12

T19011

hypothetical protein C06C6.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T19011

R:McMurray, A.

submitted to the EMBL Data Library, March 1997

A:Reference number: Z19059

A:Accession: T19011

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-935 <WIL>

A:Cross-references: EMBL:Z93374; PTDN:CAB07557.1; GSPDB:GN00023; CESP:C06C6.7

A:Experimental source: clone C06C6

C:Genetics:

A:Gene: CESP:C06C6.7

A:Map position: 5

A:Introns: 28/1; 55/1; 80/1; 801/2; 865/2

Query Match

Best Local Similarity 60.0%; Score 36; DB 2; Length 935;

Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 KTCIVHKMKK 11

:|||||:|:|

Db 825 QSCIVHKLKR 834

RESULT 13

T26216

hypothetical protein W06A7.3c - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T26216

R:Ainscough, R.

submitted to the EMBL Data Library, August 1996

A:Reference number: Z20173

A:Accession: T26216

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-2484 <WIL>

A:Cross-references: EMBL:Z78066; PTDN:CAB51467.1; GSPDB:GN00023; CESP:W06A7.3c

A:Experimental source: clone W06A7

C:Genetics:

A:Gene: CESP:W06A7.3c

A:Map position: 5

A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2

Query Match

Best Local Similarity 60.0%; Score 36; DB 2; Length 2484;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCIVHKMKK 11

|||||:|:|

Db 2384 TCIAKLLKK 2392

RESULT 14

T26215

hypothetical protein W06A7.3a - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T26215

R:Ainscough, R.

submitted to the EMBL Data Library, August 1996

A:Reference number: Z20173

A:Accession: T26215
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-2607 <WIL>
A:Cross-references: EMBL:Z78066; PTDN:CAB01522.2; GSPDB:GN00023; CESP:W06A7.3a
A:Experimental source: clone W06A7
C:Genetics:
A:Gene: CESP:W06A7.3a
A:Map position: 5
A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2; 2586/2

Query Match

Best Local Similarity 60.0%; Score 36; DB 2; Length 2607;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCIVHKMKK 11

|||||:|:|

Db 2507 TCIAKLLKK 2515

RESULT 15

F59108

hypothetical protein pX01-143 - Bacillus anthracis virulence plasmid pX01

C:Species: Bacillus anthracis

C>Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 11-May-2000

C:Accession: F59108

R:Okinkaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koeh

J. Bacteriol. 181, 6509-6515, 1999

A:Title: Sequence and organization of pX01, the large Bacillus anthracis plasmid harb

A:Reference number: A59091; MUID:99445483

A:Accession: F59108

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-150 <OKI>

A:Cross-references: GB:AF065404; NID:g4894216; PIDN:AAD32446.1; PID:g4894358

A:Experimental source: strain Sterne

C:Genetics:

A:Gene: pX01-143

A:Genome: plasmid

Query Match

Best Local Similarity 58.3%; Score 35; DB 2; Length 150;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMKK 11

|:|:|:|

Db 77 KGACMLHKKK 87

Search completed: September 4, 2002, 16:47:33

Job time: 369 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 17:05:05 ; Search time 34.18 Seconds
(without alignments)
12.461 Million cell updates/sec

Title: US-09-821-726-4
Perfect score: 60
Sequence: 1 KKTCTIVHKMK 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	55	91.7	1	Q9ns71 homo sapien
2	48	80.0	1	Q9cr36 mus musculu
3	36	60.0	1	Q9zcn4 rickettsia
4	36	60.0	1	KRP2_RAT
5	36	60.0	1	MCAK_CRIGR
6	35	58.3	1	YCXA_EUGGR
7	35	58.3	1	MCE1_CAEEL
8	34	56.7	1	YD7D_SCHPO
9	34	56.7	1	IL4_PIG
10	34	56.7	1	SUR2_MOUSE
11	34	56.7	1	TFH3_HUMAN
12	34	56.7	1	DHA2_BACSU
13	34	56.7	1	RRA_NOTVI
14	34	56.7	1	ALB2_SALSA
15	34	56.7	1	KPCL_HUMAN
16	34	56.7	1	KPCL_MOUSE
17	34	56.7	1	KPCL_RAT
18	34	56.7	1	KPCE_RABIT
19	34	56.7	1	KPCE_HUMAN
20	34	56.7	1	KPCE_MOUSE
21	34	56.7	1	KPCE_RAT
22	34	56.7	1	KPC2_APLCA
23	34	56.7	1	OPPE_MYCGE
24	33	55.0	1	TRBG_ECOLI
25	33	55.0	1	ALL1_LEPDS
26	33	55.0	1	YE12_HAEIN
27	33	55.0	1	Y599_METJA
28	33	55.0	1	IOD2_FUNHE
29	33	55.0	1	CHEB_THENA
30	33	55.0	1	CHEB_RHIME
31	33	55.0	1	CHEB_AGR75
32	33	55.0	1	P2X1_HUMAN
33	33	55.0	1	C71F_ARATH

34 33 55.0 603 1 UVRC_CHLPN Q9z6w6 chlamydia p
35 33 55.0 768 1 ITB8_RABIT P26013 oryctolagus
36 33 55.0 844 1 MCEL_VACCC P20979 vaccinia vi
37 33 55.0 844 1 MCEL_VACCC P04298 vaccinia vi
38 33 55.0 844 1 MCEL_VACCC P33057 variola vir
39 32 53.3 90 1 VGE_BPPHX P03639 bacterioph
40 32 53.3 91 1 RACC_ECOLI P15033 escherichia
41 32 53.3 141 1 ALL2_TYRPU O02380 tyrophagus
42 32 53.3 343 1 TRA3_CORDI P35879 corynebacte
43 32 53.3 400 1 Y4PO_RHIME P80011 rhizobium m
44 32 53.3 400 1 Y4PO_RHIME P55620 rhizobium s
45 32 53.3 438 1 YZ32_METJA Q60289 methanococc

ALIGNMENTS

RESULT 1
CLIP_HUMAN
ID CLIP_HUMAN STANDARD; PRT; 199 AA.
AC Q9NS71;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE CALL protein.
GN CALL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RX MEDLINE=20296773; PubMed=10835488;
RA Yoshikawa Y., Mukai H., Hino F., Asada K., Kato I.;
RT "Isolation of two novel genes, down-regulated in gastric cancer."
RL Jpn. J. Cancer Res. 91:459-463(2000).
CC -!- TISSUE SPECIFICITY: Expressed in stomach. No expression is
CC detected in cancer tissue or gastric cancer cell lines.
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CC -----
CC EMBL; AB039886; BAA92433.1; -.
DR MIN: 606402; -.
SQ SEQUENCE 199 AA; 21999 MW; C099B8B9A1338D7A CRC64;

Query Match 91.7%; Score 55; DB 1; Length 199;
Best Local Similarity 90.9%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KKTCTIVHKMK 11
| | | | | | | | | |
Db 92 KKTCTIVHKMK 102

RESULT 2
CLIP_MOUSE
ID CLIP_MOUSE STANDARD; PRT; 184 AA.
AC Q9CR36; Q9D7K7; Q9CTZ5;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE CALL protein homolog.
GN CALL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Stomach, and Tongue;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staibli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
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 DR EMBL; AK008990; BAB26010.1; -;
 DR EMBL; AK008622; BAB25784.1; -;
 DR EMBL; AK008641; BAB25801.1; -;
 DR EMBL; AK008647; BAB25803.1; -;
 DR EMBL; AK008722; BAB25856.1; -;
 DR EMBL; AK008745; BAB25856.1; -;
 DR EMBL; AK008933; BAB25872.1; -;
 DR EMBL; AK008933; BAB25975.1; -;
 DR EMBL; AK008956; BAB25988.1; -;
 DR EMBL; AK009145; BAB26103.1; -;
 DR EMBL; AK019050; BAB31525.1; -;
 FT CONFLICT 113 113 P -> L (IN REF. 1; BAB26103).
 SQ SEQUENCE 184 AA; 20134 MW; 288982F0404FFA8B CRC64;
 Query Match 80.0%; Score 48; DB 1; Length 184;
 Best Local Similarity 72.7%; Pred. NO. 0.06;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KKTICIVHKMK 11
 DB 78 KKSCIVHRMKN 88
 RESULT 3
 ID Y689_RICPR STANDARD; PRT; 266 AA.
 AC Q9ZCN4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein RP689.
 GN RP689.
 OS Rickettsia prowazekii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsia.
 OX NCBI_TaxID=782;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=MADRID E;
 RX MEDLINE=99039499; PubMed=9823893;
 RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
 RA Slicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
 RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
 RT "The genome sequence of Rickettsia prowazekii and the origin of
 RT mitochondria.";
 RL Nature 396:133-140(1998).
 CC -1- SIMILARITY: STRONG, TO R.PROWAZEKII RP688. SOME TO H.INFLUENZAE
 CC LICD.
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 CC -----
 DR EMBL; AJ235272; CAAL5126.1; -;
 DR Hypothetical protein; Transmembrane; Complete proteome.
 KW TRANSMEM 13 33 POTENTIAL.
 FT SEQUENCE 266 AA; 31400 MW; 0624B3F66EDE9FE5 CRC64;
 SQ
 Query Match 60.0%; Score 36; DB 1; Length 266;
 Best Local Similarity 64.3%; Pred. NO. 13;
 Matches 9; Conservative 0; Mismatches 1; Indels 4; Gaps 1;
 QY 1 KKTICIVHKMK 10
 DB 135 KKTCLDIFIVHKEK 148
 RESULT 4
 KRP2_RAT STANDARD; PRT; 671 AA.
 ID KRP2_RAT
 AC Q62909;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Kinesin-related protein 2.
 GN KRP2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Testis;
 RX MEDLINE=96228687; PubMed=8688559;
 RA Sperry A.O., Zhao L.-P.;
 RT "Kinesin-related proteins in the mammalian testes: candidate motors
 RT for meiosis and morphogenesis.";
 RL Mol. Biol. Cell 7:289-305(1996).
 RN [2]
 RP REVISIONS.
 RA Sperry A.O.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MOTOR PROTEIN, ACTIVE IN MEIOSIS.
 CC -1- TISSUE SPECIFICITY: TESTIS. LOCALIZED TO THE TESTIS.
 CC CELLS OF THE SEMINIFEROUS EPITHELIA IN THE TESTIS.
 CC -1- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. MCAK/KIF2
 CC SUBFAMILY.
 CC -----
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DR EMBL; U44979; AAC53528.1; -.
DR HSSP; P17119; 3KAR.
DR InterPro; IPR001752; kinesin.
DR Pfam; PF00225; kinesin; 2.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.
KW Motor protein; Microtubules; ATP-binding; Coiled coil; Meiosis.
FT DOMAIN 1 198 GLOBULAR (POTENTIAL).
FT DOMAIN 199 540 KINESIN-MOTOR (BY SIMILARITY).
FT DOMAIN 541 671 COILED COIL (POTENTIAL).
FT NP_BIND 294 301 ATP (POTENTIAL).
SQ SEQUENCE 671 AA; 75661 MW; F2B54598C78D8DE CRC64;

Query Match 60.0%; Score 36; DB 1; Length 671;
Best Local Similarity 54.5%; Pred. No. 31;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 11
   :|:|:|:|:|
DB 136 RKSCIVKEMEK 146

RESULT 5
MCAC_CRIGR
ID MCAC_CRIGR STANDARD; PRT; 718 AA.
AC P70096;
DT 01-NOV-1997 (Rel. 35, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Mitotic centromere-associated kinesin (MCAC) (Kinesin-like protein 6).
GN KNSL6.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95122643; PubMed=7822426;
RA Wordeman L., Mitchison T.J.;
RT "Identification and partial characterization of mitotic centromere-
RT associated kinesin, a kinesin-related protein that associates with
RT centromeres during mitosis."
RL J. Cell Biol. 128:95-105(1995).
RN [2]
RP REVISIONS.
RA Wordeman L.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PRESENT THROUGHOUT THE CELL CYCLE, ASSOCIATES WITH
CC CENTROMERES AT EARLY PROPHASE, AND REMAINS ASSOCIATED WITH THE
CC CENTROMERE UNTIL AFTER TELOPHASE.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
CC -!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. MCAC/KIF2
CC SUBFAMILY.
CC -----
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CC -----
DR EMBL; U11790; AAB17358.2; -.
DR HSSP; P17119; 3KAR.
DR InterPro; IPR001752; kinesin.
DR Pfam; PF00225; kinesin; 2.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.

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DR PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
KW Motor protein; Microtubules; ATP-binding; Coiled coil;
KW Nuclear protein.
FT DOMAIN 1 246 GLOBULAR (POTENTIAL).
FT DOMAIN 247 612 KINESIN-MOTOR (BY SIMILARITY).
FT DOMAIN 613 651 COILED COIL (POTENTIAL).
FT DOMAIN 689 716 COILED COIL (POTENTIAL).
FT NP_BIND 342 349 ATP (POTENTIAL).
FT DOMAIN 409 412 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
SQ SEQUENCE 718 AA; 80918 MW; 16ABD8BC66AD11B2 CRC64;

Query Match 60.0%; Score 36; DB 1; Length 718;
Best Local Similarity 54.5%; Pred. No. 33;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 11
   :|:|:|:|:|
DB 184 RKSCIVKEMEK 194

RESULT 6
YCCA_EUGGR
ID YCCA_EUGGR STANDARD; PRT; 350 AA.
AC P31561;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 40.9 kDa protein in 16S rRNA 3'region (ORF350).
OS Euglena gracilis.
OC Chloroplast.
OC Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.
OX NCBI_TaxID=3039;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z;
RX MEDLINE=93347989; PubMed=8346031;
RA Hallick R.B., Hong L., Drager R.G., Favreau M.R., Monfort A.,
RA Orsat B., Spielmann A., Stutz E.;
RT "Complete sequence of Euglena gracilis chloroplast DNA."
RL Nucleic Acids Res. 21:3537-3544(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Z;
RA Schlunegger B., Stutz E.;
RT "The Euglena gracilis chloroplast genome: structural features of a
RT DNA region possibly carrying the single origin of DNA replication."
RL Curr. Genet. 8:629-634(1984).
RN [3]
RP SEQUENCE FROM N.A.
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CC -----
DR EMBL; Z11874; -. NOT_ANNOTATED_CDS.
DR EMBL; X70810; CAA50140.1; -.
DR PIR; S34557; S34557.
DR PIR; S36933; S36933.
KW Chloroplast; Hypothetical protein.
SQ SEQUENCE 350 AA; 40861 MW; 1ACA7EC540FF51 CRC64;

Query Match 58.3%; Score 35; DB 1; Length 350;
Best Local Similarity 55.6%; Pred. No. 26;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 9
   :|:|:|:|:|
DB 342 KKKCLLHKI 350

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RESULT 7
MCEL_CABEL
ID MCEL_CABEL STANDARD; PRT; 573 AA.
AC Q17607; 002558;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE mRNA capping enzyme [Includes: Polynucleotide 5'-triphosphatase
DE (EC 3.1.3.33) (mRNA 5'-triphosphatase) (TPase); mRNA
DE guanylyltransferase (EC 2.7.7.50) (GTP--RNA guanylyltransferase)
DE (Gtase)].
DE CEL-1 OR C03D6.3.
GN Caenorhabditis elegans.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Shuman S., Ho C.K.;
RT "Identification of mRNA capping enzyme from C.elegans.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Burton J.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RN CHARACTERIZATION, AND MUTAGENESIS OF CYS-124.
RX MEDLINE-97344078; PubMed-9200605;
RA Takagi T., Moore C.R., Diehn F., Buratowski S.;
RT "An RNA 5'-triphosphatase related to the protein tyrosine
RT phosphatases.";
RL Cell 89:867-873(1997).
CC -!- FUNCTION: BIFUNCTIONAL mRNA CAPPING ENZYME EXHIBITING RNA 5'-
CC TRIPHOSPHATASE ACTIVITY IN THE N-TERMINAL PART AND MRNA
CC GUANYLYLTRANSFERASE ACTIVITY IN THE C-TERMINAL PART. CATALYZES THE
CC FIRST TWO STEPS OF CAP FORMATION: BY REMOVING THE GAMMA-PHOSPHATE
CC FROM THE 5'-TRIPHOSPHATE END OF NASCENT MRNA TO YIELD A
CC DIPOSPHATE END, AND BY TRANSFERRING THE GMP MOIETY OF GTP TO THE
CC 5'-DIPOSPHATE TERMINUS.
CC -!- CATALYTIC ACTIVITY: 5'-phosphopolynucleotide + H(2)O =
CC polynucleotide + phosphate.
CC -!- CATALYTIC ACTIVITY: GTP + (5')pp-pur-mRNA = diphosphate +
CC G(5')ppp-pur-mRNA.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- INDUCTION: INHIBITED BY MAGNESIUM.
CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE NON-RECEPTOR
CC CLASS OF THE PROTEIN-TYROSINE PHOSPHATASE FAMILY.
CC -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE EUKARYOTIC
CC GTASE FAMILY.
CC -----
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CC -----
EMBL; AF003925; AAB61344.1; -.
DR EMBL; 275525; CAA99765.1; ALT_INIT.
DR WormPep; C03D6.3; CE15578.
DR InterPro; IPR000340; DS_phosphatase.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR001339; mRNA_cap_enzyme.
DR Pfam; PF01331; mRNA_cap_enzyme; 1.
DR SMART; SM00012; PTPC_DSPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR mRNA processing; mRNA capping; Transferase; Nucleotidyltransferase;
KW Hydrolase; Multifunctional enzyme; Nuclear protein.

Query Match 58.3%; Score 35; DB 1; Length 573;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CIVHKMK 10
DB 82 CIVHKMK 88
II IIII

RESULT 8
YSTD_SCHPO STANDARD; PRT; 104 AA.
AC O14218;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Hypothetical 11.7 kDa protein C6B12.13 in chromosome I.
GN SPAC6B12.13.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=972;
RA Gentles S., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO YEAST YFR003C.
CC -----
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CC -----
EMBL; Z98531; CAB11073.1; -.
DR Hypothetical protein.
KW Hypothetical protein.
FT DOMAIN 78
SQ SEQUENCE 104 AA; 11659 MW; E4753ACFB8302D00 CRC64;

Query Match 56.7%; Score 34; DB 1; Length 104;
Best Local Similarity 54.5%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 KKCTIVHKMKK 11
DB 64 KVCCIFHKQK 74
II IIII

RESULT 9
IL4_PIG STANDARD; PRT; 133 AA.
AC Q04745; Q29054;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-4 precursor (IL-4) (B-cell stimulatory factor 1) (BSF-1)
DE (Lymphocyte stimulatory factor 1).
GN IL4.
OS Sus scrofa (Pig).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP MEDLINE=93144350; PubMed=8424960;
RX Bailey M., Perry A.C.F., Bland P.W., Stokes C.R., Hall L.;
RT "Nucleotide and deduced amino acid sequence of porcine Interleukin 4
RT cDNA derived from lamina propria lymphocytes.";
RL Biochim. Biophys. Acta 1171:328-330(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhou Y., Murtaugh M.P.;
RL Submitted (MAR-1993) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: IL-4 PARTICIPATES IN AT LEAST SEVERAL B-CELL ACTIVATION
CC PROCESSES AS WELL AS OF OTHER CELL TYPES. IT IS A COSTIMULATOR OF
CC DNA-SYNTHESIS. IT INDUCES THE EXPRESSION OF CLASS II MHC MOLECULES
CC ON RESTING B-CELLS. IT ENHANCES BOTH SECRETION AND CELL SURFACE
CC EXPRESSION OF IGE AND IGGL. IT ALSO REGULATES THE EXPRESSION OF
CC THE LOW AFFINITY FC RECEPTOR FOR IGE (CD23) ON BOTH LYMPHOCYTES
CC AND MONOCYTES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-4 / IL-13 FAMILY.
CC -----
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CC -----
DR EMBL; X68330; CAA48407.1; -;
DR EMBL; L12991; AAA31055.1; -;
DR PIR; S28187; S28187.
DR HSP; P05112; ILL.
DR InterPro; IPR002354; Interleukin_4.
DR InterPro; IPR001325; Interleukin_4_13.
DR Pfam; PF00727; IL4; 1.
DR ProDom; PD004070; Interleukin_4.
DR SMART; SM00190; IL4_13; 1.
DR PROSITE; PS00838; INTERLEUKIN_4_13; 1.
KW Cytokine; Glycoprotein; B-cell activation; Growth factor; Signal.
FT SIGNAL 1 24
FT CHAIN 25 133 BY SIMILARITY.
FT DISULFID 27 133 BY SIMILARITY.
FT DISULFID 48 85 BY SIMILARITY.
FT DISULFID 70 105 BY SIMILARITY.
FT CARBOHYD 62 62 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 53 54 VT -> GD (IN REF. 2).
FT CONFLICT 64 64 T -> R (IN REF. 2).
SQ SEQUENCE 133 AA; 15023 MW; 333033EF515D084F CRC64;

Query Match 56.7%; Score 34; DB 1; Length 133;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCIVHKMK 11
DB 104 TCSVHEAK 112
11111111

RESULT 10
SUR2_MOUSE
ID SUR2_MOUSE STANDARD; PRT; 257 AA.
AC P09926;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Surfeit locus protein 2 (Surf-2).
GN SURF2 OR SURF-2.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87089816; PubMed=3025660;
RA Williams T.J., Fried M.;
RT "The WES-1 murine enhancer element is closely associated with the
RT heterogeneous 5' ends of two divergent transcription units.";
RL Mol. Cell. Biol. 6:4558-4569(1986).
RN [2]
RP -!- SIMILARITY: BELONGS TO THE SURF2 FAMILY.
CC -----
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CC -----
DR EMBL; M14689; AAA40154.1; -;
DR PIR; A25394; A25394.
DR MGD; MGI:98444; Surf2.
SQ SEQUENCE 257 AA; 30355 MW; 9DF3F3FF19F2BC5 CRC64;

Query Match 56.7%; Score 34; DB 1; Length 257;
Best Local Similarity 62.5%; Pred. No. 30;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 CIVHKMK 11
DB 127 CLLHKRK 134
11111111

RESULT 11
TFH3_HUMAN
ID TFH3_HUMAN STANDARD; PRT; 303 AA.
AC Q13889;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE TFIIH basal transcription factor complex p34 subunit (Basic
DE transcription factor 234 kDa subunit) (BTF2-p34) (General
DE transcription factor IIH polypeptide 3).
GN GTF2H3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 57-68; 78-97; 107-112; 127-132
RP AND 239-251.
RX MEDLINE=94252326; PubMed=8194529;
RA Humbert S., van Vuuren H.A., Lutz Y., Hoeijmakers J.H.J., Egly J.-M.,
RA Moncollin V.;
RT "p44 and p34 subunits of the BTF2/TFIIH transcription factor have
RT homologues with SSLI, a yeast protein involved in DNA repair.";
RL EMBO J. 13:2393-2398(1994).
CC -!- FUNCTION: Component of the core-TFIIH basal transcription factor
CC involved in nucleotide excision repair (NER) of DNA and, when
CC complexed to CAK, in RNA transcription by RNA polymerase II.
CC Anchors XPB.
CC -!- SUBUNIT: One of the six subunits forming the core-TFIIH basal
CC transcription factor.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: CONTAINS 1 C4-TYPE ZINC FINGER.
CC -----
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CC -----
 DR EMBL; Z30093; CAA82909.1; -
 DR TRANSFAC; T02188; -
 DR MIM; 601750; -
 KW Transcription regulation; DNA repair; Nuclear protein; Zinc-finger.
 FT ZN_FING 268 285 C4-TYPE.
 SQ SEQUENCE 303 AA; 33893 MW; BIDD95EE876D3F9E CRC64;

Query Match 56.7%; Score 34; DB 1; Length 303;
 Best Local Similarity 45.5%; Pred. No. 35;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KKTCTVHKMK 11
 | | : | : |
 Db 139 KALCYTHRMNK 149

RESULT 12
 ID DHA2_BACSU STANDARD; PRT; 457 AA.
 AC P39616;
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable aldehyde dehydrogenase YMDH (EC 1.2.1.3).
 GN YMDH OR IPA-58R.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=95020337; PubMed=7934828;
 RA Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W.,
 RA Hullo M.F., Ionescu M., Lubochinsky B., Marcellino L., Moszer I.,
 RA Presecan E., Santana M., Schneider E., Schweizer J., Vertes A.,
 RA Rapoport G., Danchin A.;
 RT "Bacillus subtilis genome project: cloning and sequencing of the 97
 kb region from 325 degrees to 333 degrees.";
 RL Mol. Microbiol. 10:371-384(1993).
 CC -1- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid + NADH.
 CC -1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.

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CC EMBL; X73124; CAA51614.1; -
 DR EMBL; Z99123; CAB15822.1; -
 DR PIR; S39713; S39713.
 DR HSSP; P11883; IAD3.
 DR Subtilist; BG10604; ywdH.
 DR InterPro; IPR002086; Aldehyde_dehydr.
 DR Pfam; PF00171; algedh; 1.
 DR PROSITE; PS00070; ALDEHYDE_DEHYDR_GLU; 1.
 DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
 KW Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
 FT ACT_SITE 211 211 BY SIMILARITY.
 FT ACT_SITE 245 245 BY SIMILARITY.
 SQ SEQUENCE 457 AA; 50765 MW; C238D9FD07DFB92A CRC64;

Query Match 56.7%; Score 34; DB 1; Length 457;
 Best Local Similarity 75.0%; Pred. No. 51;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKTCTVHK 8
 | | : | : |
 Db 215 KSPCTVHK 222

RESULT 13
 ID RRA_NOTVI STANDARD; PRT; 458 AA.
 AC P18514; Q91155;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Retinoic acid receptor alpha (RAR-alpha).
 GN RARA OR NR1B1.
 OS Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
 OC Notophthalmus.
 OX NCBI_TaxID=8316;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA-1).
 RX MEDLINE=90015190; PubMed=2552324;
 RA Ragsdale C.W. Jr., Petkovich M., Gates P.B., Chambon P., Brookes J.P.;
 RT "Identification of a novel retinoic acid receptor in regenerative
 RT tissues of the newt.";
 RL Nature 341:654-657(1989).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA-2).
 RX MEDLINE=93087213; PubMed=1333589;
 RA Ragsdale C.W., Gates P.B., Brookes J.P.;
 RT "Identification and expression pattern of a second isoform of the newt
 RT alpha retinoic acid receptor.";
 RL Nucleic Acids Res. 20:5851-5851(1992).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR RETINOIC ACID. THIS METABOLITE
 CC HAS PROFOUND EFFECTS ON VERTEBRATE DEVELOPMENT. RETINOIC ACID IS
 CC A MORPHOGEN AND IS A POWERFUL TERATOGEN. THIS RECEPTOR CONTROLS
 CC CELLS FUNCTIONS BY DIRECTLY REGULATING GENE EXPRESSION.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-1 (SHOWN HERE) AND ALPHA-
 CC 2; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 CC NR1 SUBFAMILY.

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CC EMBL; X17585; CAA35602.1; -
 DR EMBL; Z14254; CAA78621.1; -
 DR PIR; S06123; S06123.
 DR HSSP; P10826; 1HRA.
 DR InterPro; IPR000536; Hormone_rec_lig.
 DR InterPro; IPR001723; Steroidhormone_receptor.
 DR InterPro; IPR001628; zf-C4.
 DR Pfam; PF00104; hormone_rec; 1.
 DR Pfam; PF00105; zf-C4; 1.
 DR PRINTS; PR00398; STRDHORMONER.
 DR PRINTS; PR00047; STROIDFINGER.
 DR SMART; SM00430; HOLT; 1.
 DR SMART; SM00399; znf_C4; 1.
 DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
 KW PROSITE; Transcription regulation; DNA-binding; Nuclear protein;
 KW Zinc-finger; Multigene family; Alternative splicing.
 FT DOMAIN 1 86 MODULATING.
 FT DNA_BIND 87 152 NUCLEAR RECEPTOR-TYPE.

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FT ZN_FING 87 107 C4-TYPE.
FT ZN_FING 123 147 C4-TYPE.
FT ZN_FING 153 199 HINGE.
FT ZN_FING 200 419 LIGAND-BINDING.
FT VARSPLIC 1 59 MASNGSGCPSSGGHMGVVPVHYAFFFPMLGLSPGSLA
FT GIPHPLPYSAYSTPSPAT -> MYDSVEVSSPSPYIMIDFY
FT SONRACLMDKGLGHPVPGSPIRNPHWSSSSHS (IN
FT ISOFORM ALPHA-2).
FT SEQUENCE 458 AA; 50637 MW; B4370822FBAADB54 CRC64;

Query Match 56.7%; Score 34; DB 1; Length 458;
Best Local Similarity 50.0%; Pred. No. 51;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 KTCIVHKMK 11
DB 127 KTCIINKVTR 136
|||||:|:|

RESULT 14
ALB2_SALSA STANDARD; PRT; 608 AA.
ID ALB2_SALSA
AC Q03156;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Serum albumin 2 precursor.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93013056; PubMed=1398147;
RA Byrnes L., Gannon F.;
RT "Sequence analysis of a second cDNA encoding Atlantic salmon (Salmo
RT salar) serum albumin."
RL Gene 120:319-320(1992).
CC
CC -!- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
CC BINDING CAPACITY FOR WATER, CA++, NA+, K+, FATTY ACIDS, HORMONES,
CC BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
CC COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: PLASMA.
CC -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE ALB/APP/VDB FAMILY.
CC
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CC
CC EMBL; X60776; CAA43187.1; .
CC PIR; A46757; AB0N52.
CC InterPro; IPR000264; Serum_albumin.
CC Pfam; PF00273; transport_prot; 3.
CC PRINTS; PR00802; SERUMALBUMIN.
CC ProDom; PD002486; Serum_albumin; 1.
CC SMART; SM00103; ALBUMIN; 3.
CC PROSITE; PS00212; ALBUMIN; 2.
KW Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal.
FT SIGNAL 1 14 POTENTIAL.
FT PROPEP 15 18
FT CHAIN 19 608 SERUM ALBUMIN 2.
FT REPEAT 22 194 1.
FT REPEAT 215 390 2.
FT REPEAT 411 591 3.

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FT DISULFID 26 72 POTENTIAL.
FT DISULFID 71 80 BY SIMILARITY.
FT DISULFID 93 108 BY SIMILARITY.
FT DISULFID 107 118 BY SIMILARITY.
FT DISULFID 142 187 BY SIMILARITY.
FT DISULFID 186 195 BY SIMILARITY.
FT DISULFID 218 264 BY SIMILARITY.
FT DISULFID 263 271 BY SIMILARITY.
FT DISULFID 283 299 BY SIMILARITY.
FT DISULFID 298 309 BY SIMILARITY.
FT DISULFID 336 381 BY SIMILARITY.
FT DISULFID 380 389 BY SIMILARITY.
FT DISULFID 414 460 BY SIMILARITY.
FT DISULFID 459 471 BY SIMILARITY.
FT DISULFID 484 500 BY SIMILARITY.
FT DISULFID 499 510 BY SIMILARITY.
FT DISULFID 537 582 BY SIMILARITY.
FT DISULFID 581 590 BY SIMILARITY.
FT CARBOHYD 501 501 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 608 AA; 67058 MW; C168DD349F4E16C5 CRC64;

Query Match 56.7%; Score 34; DB 1; Length 608;
Best Local Similarity 75.0%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKTICIVHK 8
DB 215 KSLCIVHK 222
|||||

RESULT 15
KPCIL_HUMAN STANDARD; PRT; 682 AA.
ID KPCIL_HUMAN
AC P24723;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein kinase C, eta type (EC 2.7.1.-) (PKC-eta) (PKC-L).
GN PKCH OR PKCL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=91094824; PubMed=1986216;
RA Bacher N., Zisman Y., Berent E., Livneh E.;
RT "Isolation and characterization of PKC-L, a new member of the protein
RT kinase C-related gene family specifically expressed in lung, skin,
RT and heart."
RL Mol. Cell. Biol. 11:126-133(1991).
RN [2]
RP REVISIONS.
RX MEDLINE=92186874; PubMed=1545821;
RA Bacher N., Zisman Y., Berent E., Livneh E.;
RL Mol. Cell. Biol. 12:1404-1404(1992).
CC -!- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- TISSUE SPECIFICITY: MOST ABUNDANT IN LUNG TISSUE, LESS IN HEART
CC AND SKIN TISSUE.
CC -!- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
CC BINDING DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC
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CC EMBL; M55284; AAA60100.1; -.
DR PIR; A39666; A39666.
DR HSSP; P28867; IPTQ.
DR MIM; 605437; -.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000719; Euk_kinase.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE-bind; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.
FT DOMAIN 12 112 C2 DOMAIN.
FT DOMAIN 171 221 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 245 294 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 354 613 PROTEIN KINASE.
FT NP_BIND 360 368 ATP (BY SIMILARITY).
FT BINDING 383 383 ATP (BY SIMILARITY).
FT ACT_SITE 478 478 BY SIMILARITY.
SQ SEQUENCE 682 AA; 77563 MW; 13D4EAB01F3B5AB8 CRC64;

Query Match 56.7%; Score 34; DB 1; Length 682;
Best Local Similarity 83.3%; Pred. No. 74;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCIVHK 8

Db 206 TCVVK 211

Search completed: September 4, 2002, 17:05:06
Job time: 1132 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 17:01:35 ; Search time 124.34 seconds
(without alignments)
15.304 Million cell updates/sec

Title: US-09-821-726-4

Perfect score: 60

Sequence: 1 KKTCTVHKMK 11

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	42	70.0	478	5 Q9U4M7	Q9U4M7 Leishmania
2	41	68.3	971	5 Q9V6Y6	Q9V6Y6 drosophila
3	41	68.3	1261	5 Q95TJ2	Q95TJ2 drosophila
4	40	66.7	1138	12 Q55345	Q55345 hu39694 vir
5	40	66.7	1386	8 Q9XMS2	Q9XMS2 tetrahymena
6	39	65.0	320	12 Q9VVM4	Q9VVM4 melanoplus
7	38	63.3	82	16 Q25977	Q25977 helicobacte
8	38	63.3	86	16 Q9ZJ10	Q9ZJ10 helicobacte
9	38	63.3	245	16 Q937K0	Q937K0 clostridium
10	38	63.3	553	5 Q93367	Q93367 caenorhabdi
11	37	61.7	389	10 Q9M9I0	Q9M9I0 arabidopsis
12	37	61.7	610	5 Q9VC31	Q9VC31 drosophila
13	37	61.7	655	10 Q9C9I9	Q9C9I9 arabidopsis
14	37	61.7	1247	5 Q9GV23	Q9GV23 sarcophaga
15	36	60.0	173	6 Q95L17	Q95L17 felis silve
16	36	60.0	174	6 Q9GMZ9	Q9GMZ9 felis silve

17	36	60.0	198	16 Q992F2	Q992F2 streptococc
18	36	60.0	222	5 Q23188	Q23188 caenorhabdi
19	36	60.0	292	6 Q9GMZ8	Q9GMZ8 felis silve
20	36	60.0	292	6 Q02758	Q02758 felis silve
21	36	60.0	378	10 Q9MAD5	Q9MAD5 arabidopsis
22	36	60.0	399	16 Q92C43	Q92C43 listeria in
23	36	60.0	464	5 Q9V8D8	Q9V8D8 drosophila
24	36	60.0	598	16 Q34469	Q34469 bacillus su
25	36	60.0	721	11 Q922S8	Q922S8 mus musculu
26	36	60.0	762	10 Q943W8	Q943W8 oryza sativ
27	36	60.0	935	5 Q62033	Q62033 caenorhabdi
28	36	60.0	2484	5 Q9U347	Q9U347 caenorhabdi
29	36	60.0	2607	5 Q23187	Q23187 caenorhabdi
30	36	60.0	3901	5 Q9N533	Q9N533 caenorhabdi
31	36	58.3	143	5 Q965E2	Q965E2 psoroptes o
32	35	58.3	150	2 Q9X398	Q9X398 bacillus an
33	35	58.3	161	5 Q9V5U5	Q9V5U5 drosophila
34	35	58.3	207	10 Q65691	Q65691 arabidopsis
35	35	58.3	235	6 Q9TQ88	Q9TQ88 canis famil
36	35	58.3	235	6 Q9N0T0	Q9N0T0 canis famil
37	35	58.3	247	3 Q94357	Q94357 schizosacch
38	35	58.3	283	10 Q9C9R7	Q9C9R7 arabidopsis
39	35	58.3	304	6 Q9TQX1	Q9TQX1 canis famil
40	35	58.3	324	10 Q9SID9	Q9SID9 arabidopsis
41	35	58.3	327	10 Q9SIE0	Q9SIE0 arabidopsis
42	35	58.3	330	2 Q55228	Q55228 streptococc
43	35	58.3	334	12 Q06314	Q06314 hepatitis c
44	35	58.3	346	5 Q9U262	Q9U262 caenorhabdi
45	35	58.3	389	5 Q44147	Q44147 caenorhabdi

ALIGNMENTS

RESULT 1

ID Q9U4M7 PRELIMINARY; PRT; 478 AA.
AC Q9U4M7;
DC 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE 7138.4.
GN 7138.4.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Ravel C., Dubessay P., Blaineau C., Lignon M.-F., Bastien P.,
RA Dedet J.-P., Pages M.;
RT "Leishmania major chromosome 5 complete sequence."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF163772; AAF14644.1; -
SQ SEQUENCE 478 AA; 55256 MW; 768A24D0C62A7CB7 CRC64;

Query Match 70.0%; Score 42; DB 5; Length 478;
Best Local Similarity 70.0%; Pred. No. 3.1;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KKTCTVHKMK 10
|| || || ||
Db 264 KQCTIHHMK 273

RESULT 2

ID Q9V6Y6 PRELIMINARY; PRT; 971 AA.
AC Q9V6Y6;
DC 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

Query Match	68.3%;	Score 41;	DB 5;	Length 971;	
Best Local Similarity	63.6%;	Pred. NO. 9.1;			
Matches	7;	Conservative	2;	Mismatches	0;
				Indels	0;
				Gaps	0;
QY	1	KKTCIVHKMKK	11		
Db	942	KTTCVAVHKIKQ	952		
RESULT	3				
Q95TJ2		PRELIMINARY;		PRT;	1261 AA.
ID	Q95TJ2				
AC	Q95TJ2				
DT	01-DEC-2001	(TrEMBLrel. 19, Created)			
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)			
DT	01-DEC-2001	(TrEMBLrel. 19, Last annotation update)			
DE	ORF1386.				
Query Match	66.7%;	Score 40;	DB 12;	Length 1138;	
Best Local Similarity	66.7%;	Pred. NO. 17;			
Matches	6;	Conservative	3;	Mismatches	0;
				Indels	0;
				Gaps	0;
QY	3	TCIVHKMKK	11		
Db	407	TCLVHKVQK	415		
RESULT	5				
Q9XMS2		PRELIMINARY;		PRT;	1386 AA.
ID	Q9XMS2				
AC	Q9XMS2;				
DT	01-NOV-1999	(TrEMBLrel. 12, Created)			
DT	01-NOV-1999	(TrEMBLrel. 12, Last sequence update)			
DT	01-DEC-2001	(TrEMBLrel. 19, Last annotation update)			
DE	ORF1386.				

GN ORF1386.
 OS Tetrahymena pyriformis.
 OG Mitochondrion.
 OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
 OC Tetrahymenina; Tetrahymena.
 OX NCBI_TaxID=5908;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20181866; PubMed=10715208;
 RA Edqvist J., Burger G., Gray M.W.;
 RT "Expression of mitochondrial protein-coding genes in Tetrahymena
 pyriformis.";
 RL J. Mol. Biol. 297:381-393(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20181865; PubMed=10715207;
 RA Burger G., Zhu Y., Littlejohn T.G., Greenwood S.J., Schnare M.N.,
 RA Lang B.F., Gray M.W.;
 RT "Complete sequence of the mitochondrial genome of Tetrahymena
 pyriformis and comparison with Paramecium aurelia mitochondrial DNA.";
 RL J. Mol. Biol. 297:365-380(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Burger G.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF160864; AAD41942.1; -;
 KW Mitochondrion.
 SQ SEQUENCE .1386 AA; 171837 MW; 310DBA7FECB6913A CRC64;

Query Match 66.7%; Score 40; DB 8; Length 1386;
 Best Local Similarity 77.8%; Pred. No. 20;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KKTCTVHKM 9
 ||||| ||
 DB 382 KKTCTVHKM 390

RESULT 6

Q9YVM4 PRELIMINARY; PRT; 320 AA.
 AC Q9YVM4
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DE ORF MSV218 HYPOTHETICAL PROTEIN.
 GN MSV218.
 OS Melanoplus sanguinipes entomopoxvirus (MSEPV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
 OX NCBI_TaxID=83191;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TUCSON;
 RX MEDLINE=99102612; PubMed=9847359;
 RA Afonso C.L., Tulman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L.;
 RT "The genome of Melanoplus sanguinipes entomopoxvirus.";
 RL J. Virol. 73:533-552(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TUCSON;
 RA Afonso C.L., Tulman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF063866; AAC97747.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 320 AA; 38982 MW; FCFBE193C5BA5F13 CRC64;

Query Match 65.0%; Score 39; DB 12; Length 320;
 Best Local Similarity 75.0%; Pred. No. 8.3;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KKTCTVHKM 8
 ||||| ||
 DB 26 KKTCTVHKM 33

RESULT 7

O25977 PRELIMINARY; PRT; 82 AA.
 AC O25977
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DE HYPOTHETICAL 9.6 KDA PROTEIN.
 GN HP1436.
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 OX NCBI_TaxID=210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=26695 / ATCC 700392;
 RX MEDLINE=97394467; PubMed=9252185;
 RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
 RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
 RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
 RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
 RA McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
 RA Berg D.E., Gocayne J.D., Otterback T.R., Peterson J.D., Kelley J.M.,
 RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Wattey L., Wallin E.,
 RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
 RA Venter J.C.;
 RT "The complete genome sequence of the gastric pathogen Helicobacter
 pylori.";
 RL Nature 388:539-547(1997).
 DR EMBL: AE000644; AAD08488.1; -;
 DR TIGR: HP1436; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 82 AA; 9599 MW; 7AF6FBAF6B6B15 CRC64;

Query Match 63.3%; Score 38; DB 16; Length 82;
 Best Local Similarity 54.5%; Pred. No. 3.9;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 KKTCTVHKMK 11
 :||::||| ||
 DB 66 QKACLLHKDKK 76

RESULT 8

O9ZJ10 PRELIMINARY; PRT; 86 AA.
 AC O9ZJ10
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DE PUTATIVE
 GN JHP1329.
 OS Helicobacter pylori J99 (Campylobacter pylori J99).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 OX NCBI_TaxID=85963;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99120557; PubMed=9923682;
 RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
 RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
 RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
 RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
 RA Trust T.J.;
 RT "Genomic sequence comparison of two unrelated isolates of the human
 gastric pathogen Helicobacter pylori.";
 RL Nature 397:176-180(1999).

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us-09-821-726-4.rspt

RT EMBL; AE001556; AAD06905.1; -;
 KW Complete proteome.
 SQ SEQUENCE 86 AA; 10034 MW; 41E8E9AA37BE084A CRC64;
 Query Match 63.3%; Score 38; DB 16; Length 86;
 Best Local Similarity 54.5%; Pred. No. 4;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

DR EMBL; AE001556; AAD06905.1; -;
 KW Complete proteome.
 SQ SEQUENCE 86 AA; 10034 MW; 41E8E9AA37BE084A CRC64;
 Query Match 63.3%; Score 38; DB 16; Length 86;
 Best Local Similarity 54.5%; Pred. No. 4;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKTICIVHKMKK 11
 :|:|:|:|:|
 Db 70 QKACLLHKDKK 80

QY 1 KKTICIVHKMKK 11
 :|:|:|:|:|
 Db 70 QKACLLHKDKK 80

RESULT 9
 Q97KA0 PRELIMINARY; PRT; 245 AA.
 AC Q97KA0; 2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
 DE PHOSPHOLIPASE C RELATED PROTEIN.
 GN CAC1019.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RA Noelling J., Breston G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 bacterium Clostridium acetobutylicum";
 RL J. Bacteriol. 183:4823-4838(2001).
 DR EMBL; AE007617; AAK78995.1; -;
 KW Complete proteome.
 SQ SEQUENCE 245 AA; 28890 MW; CF431EB9293762F2 CRC64;

QY 1 KKTICIVHK 8
 | | | | |
 Db 29 KTTCTIHK 36
 Query Match 63.3%; Score 38; DB 16; Length 245;
 Best Local Similarity 75.0%; Pred. No. 10;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 10
 Q93367 PRELIMINARY; PRT; 553 AA.
 AC Q93367;
 DT 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE C41G7.3 PROTEIN.
 GN C41G7.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Steward C.A.;
 RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RX SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;

QY 1 KKTICIVHK 8
 | | | | |
 Db 29 KTTCTIHK 36
 Query Match 63.3%; Score 38; DB 16; Length 245;
 Best Local Similarity 75.0%; Pred. No. 10;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query Match 61.7%; Score 37; DB 10; Length 389;
 Best Local Similarity 70.0%; Pred. No. 25;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 KKTICIVHKMK 10
 | | | | |
 Db 234 KVTCTSHKFK 243

Query Match 61.7%; Score 37; DB 10; Length 389;
 Best Local Similarity 70.0%; Pred. No. 25;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 KKTICIVHKMK 10
 | | | | |
 Db 234 KVTCTSHKFK 243

RESULT 12

RESULT 12

Q9VC31 Q9VC31 PRELIMINARY; PRT; 610 AA.
 AC Q9VC31;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE CGI3638 PROTEIN.
 GN CGI3638.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 [1]
 RN
 RP
 RQ
 RC
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang O., Chen L.X.,
 RA Brannon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Aghayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Moberly C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 CC -1- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
 DR EMBL; AE003749; AAF56345.1;
 DR HSP; P05713; 3RAB
 DR FlyBase; FBgn0039231; CGI3638.
 DR InterPro; IPR003579; Rab.
 DR InterPro; IPR001806; Ras_trnsmg.
 DR Pfam; PF00071; ras; 1.
 DR PRINTS; PR00449; RASTRNSFRMG.
 DR SMART; SM00175; RAB; 1.
 KW GTP-binding; Lipoprotein.
 RQ
 RQ SEQUENCE 610 AA; 69826 MW; DE8BCC9BB097EC79 CRC64;

Query Match 61.7%; Score 37; DB 5; Length 610;
 Best Local Similarity 85.7%; Pred. No. 37;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KTCIVHK 8

Db 418 KTCIVHR 424
 RESULT 13
 Q9C919
 ID Q9C919 PRELIMINARY; PRT; 655 AA.
 AC Q9C919;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE HYPOPHETICAL 72.4 KDA PROTEIN.
 GN F26A9.10.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 [1]
 RN
 RP
 RQ
 RC
 RC STRAIN=CV. COLUMBIA;
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
 RA Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
 RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
 RA "Arabidopsis thaliana chromosome 1 BAC F26A9 genomic sequence."
 RT Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC016163; AAG51826.1;
 DR HSSP; P24941; IHCL.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF000669; Pkinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding; Hypothetical protein; Transferase.
 RQ
 RQ SEQUENCE 655 AA; 72442 MW; EFC70BE1608A1F9F CRC64;

Query Match 61.7%; Score 37; DB 10; Length 655;
 Best Local Similarity 70.0%; Pred. No. 39;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KTCIVHKMK 10
 Db 500 KVICSHKFK 509

RESULT 14
 Q9GV23
 ID Q9GV23 PRELIMINARY; PRT; 1247 AA.
 AC Q9GV23;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE 210KDA PROTEIN (FRAGMENT).
 OS Sarcophaga peregrina (Flesh fly) (Boettcherisca peregrina).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Oestroidea; Sarcophagidae; Sarcophaga.
 OX NCBI_TaxID=7386;
 [1]
 RN
 RP
 RQ
 RC
 RC MEDLINE=20536508; PubMed=10965055;
 RA Fujii-Taira I., Tanaka Y., Homma K.J., Natori S.;
 RT "Hydrolysis and synthesis of substrate proteins for cathepsin L in the
 RL brain basement membranes of Sarcophaga during metamorphosis."
 DR J. Biochem. 128:539-542(2000).
 DR EMBL; AB041729; BAB16608.1;
 FT NON_TER 1
 RQ
 RQ SEQUENCE 1247 AA; 142521 MW; 12B097428B518959 CRC64;

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Query Match 61.7%; Score 37; DB 5; Length 1247;
Best Local Similarity 66.7%; Pred. No. 70;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 3 TCIVHKMKK 11
| | | | |
Db 1221 TCAVHKIKQ 1229

RESULT 15
Q95L17 PRELIMINARY; PRT; 173 AA.
AC Q95L17;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE CD80.
GN CD80.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21390213; PubMed=11498243;
RA Yang S., Sellins K.S., Powell T., Stoneman E., Sim G.K.;
RT "Novel transcripts encoding secreted forms of feline CD80 and CD86
costimulatory molecules.";
RL Vet. Immunol. Immunopathol. 81:15-21(2001).
DR EMBL; AY007703; AAC23341.1;
SQ SEQUENCE 173 AA; 19841 MW; A7AB46A71E5E97AC CRC64;

Query Match 60.0%; Score 36; DB 6; Length 173;
Best Local Similarity 54.5%; Pred. No. 19;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 1 KKTICIVHKMKK 11
| | | | |
Db 113 KYTCIIQKIEK 123

Search completed: September 4, 2002, 17:01:37
Job time: 1158 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:45:02 ; Search time 158.52 Seconds
(without alignments)
9.810 Million cell updates/sec

Title: US-09-821-726-3

Perfect score: 81

Sequence: 1 KKLQGGKGGPPPK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT: *
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6: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	185	20	AAW99667 Human secreted pro
2	81	100.0	185	21	AAW99667 Human PRO1005 prot
3	81	100.0	185	21	AAW99667 Human signal pept
4	81	100.0	185	21	AAW99667 Membrane-bound pro
5	81	100.0	185	22	AAW99667 Human PRO1005 (UNQ
6	81	100.0	185	22	AAW99667 Human PRO1005 prot
7	81	100.0	186	21	AAW99667 Human secreted pro
8	81	100.0	194	19	AAW99667 Cancer associated
9	81	100.0	194	20	AAW99667 Human ovarian tumo
10	52	64.2	103	21	AAW99667 Human ORFX ORF812
11	52	64.2	163	22	AAW99667 Human polypeptide

12	52	64.2	279	22	AAU03592 Human DNA modifca
13	52	64.2	467	22	AAW94309 Human protein sequ
14	51	63.0	108	22	AAO04166 Human polypeptide
15	51	63.0	125	22	AAO11472 Human polypeptide
16	50.5	62.3	140	22	AAO08289 Human polypeptide
17	50	61.7	673	21	AAV58042 Escherichia coli D
18	49.5	61.1	147	22	AAO06887 Human polypeptide
19	49	60.5	84	22	AAO13411 Human polypeptide
20	49	60.5	115	22	AAO08183 Human polypeptide
21	49	60.5	120	22	AAO00652 Human polypeptide
22	49	60.5	855	22	AAO08748 Human protease pol
23	48	59.3	127	22	AAO05497 Human polypeptide
24	48	59.3	128	22	AAO03588 Human polypeptide
25	48	59.3	247	20	AAW89037 Polypeptide fragme
26	48	59.3	247	22	ABB51188 Human secreted pro
27	48	59.3	532	21	AAW42542 Human ORFX ORF2306
28	48	59.3	774	22	ABB64148 Drosophila melanog
29	48	59.3	2061	22	ABB71759 Drosophila melanog
30	47.5	58.6	109	22	AAO09868 Human polypeptide
31	47	58.0	71	22	AAU41527 Propionibacterium
32	47	58.0	102	22	AAO00839 Human polypeptide
33	47	58.0	1963	22	ABB62819 Drosophila melanog
34	46.5	57.4	127	22	AAO07630 Human polypeptide
35	46	56.8	99	22	AAO11475 Human polypeptide
36	46	56.8	114	22	AAO03173 Human polypeptide
37	46	56.8	125	22	AAO12870 Human polypeptide
38	46	56.8	133	22	AAO02140 Human polypeptide
39	46	56.8	135	22	AAO01562 Human polypeptide
40	46	56.8	141	22	AAO06613 Human polypeptide
41	46	56.8	356	22	ABG21039 Novel human diagno
42	46	56.8	498	22	ABG09968 Novel human diagno
43	46	56.8	560	22	ABG21040 Novel human diagno
44	46	56.8	1194	22	ABB59646 Drosophila melanog
45	45.5	56.2	584	20	AAV34934 Chlamydia pneumoni

ALIGNMENTS

RESULT 1

AAW99667

ID AAW99667 standard; Protein: 185 AA.

AC AAW99667;

XX

XX

XX

DT 07-JUN-1999 (first entry)

XX

XX

DE Human secreted protein clone ej90_5 protein.

XX

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XX

XX New polynucleotides encoding secreted human proteins - derived from
PT fetal kidney, adult testes, adult brain, adult heart, adult placenta
PT or adult retina cDNA libraries
XX
PS Claim 34; Page 98-99; 107pp; English.
XX
CC The present sequence represents a human secreted protein. The secreted
CC protein can have activities such as: nutritional activity, cytokine and
CC cell proliferation/differentiation activity, immune stimulating activity,
CC (cancer) or suppressing activity, haematopoiesis regulating activity,
CC tissue growth activity, activin/inhibin activity, chemotactic/
CC chemokinetic activity, haemostatic and thrombolytic activity, receptor/
CC ligand activity, anti-inflammatory activity, cadherin/tumour invasion
CC suppressor activity, and tumour inhibition activity. The secreted
CC protein polynucleotides and proteins are predicted to have biological
CC activities which would make them suitable for treating, preventing or
CC ameliorating medical conditions in humans and animals. The
CC polynucleotides are also stated to be useful for gene therapy.
XX
SQ Sequence 185 AA;

Query Match 100.0%; Score 81; DB 20; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQKGKGGGPPPK 14
| | | | | | | | | | | | | | | |
DB 104 kklqkgpggpppk 117

RESULT 2
ID AAB24067 standard; Protein; 185 AA.
XX
AC AAB24067;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human PRO1005 protein sequence SEQ ID NO:34.
XX
KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
KW proliferation; tumorigenesis; identification; cancer; cytostatic;
KW immunosuppressant; antineoplastic; immunosuppressive;
KW immunostimulant; antineoplastic; leukaemia; lymphoid malignancy;
KW neuronal disorder; glial disorder; astrocytal disorder; angiogenic;
KW hypothalamic disorder; glandular disorder; macrophagal disorder;
KW epithelial disorder; stromal disorder; blastocoele disorder;
KW inflammatory disorder; immunologic disorder.
XX
OS Homo sapiens.
XX
PN WO200053755-A2.
XX
XX 14-SEP-2000.
XX
XX 06-JAN-2000; 2000WO-US00376.
XX
XX 08-MAR-1999; 99WO-US05028.
XX
XX 02-JUN-1999; 99WO-US12252.
XX
XX 23-JUN-1999; 99US-0141037.
XX
XX 07-JUL-1999; 99US-0143048.
XX
XX 26-JUL-1999; 99US-0145698.
XX
XX 30-NOV-1999; 99WO-US28313.
XX
XX 20-DEC-1999; 99WO-US30911.
XX
XX 05-JAN-2000; 2000WO-US00219.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
XX Watanabe CK, Wood WI;
XX

DR WPI; 2000-572270/53.
XX N-PSDB; AAC58377.
XX
PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
PT treatment, diagnosis and prevention of cancer -
XX
XX Claim 61; Fig 22; 286pp; English.
XX
XX The present invention describes an isolated antibody that binds to
CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,
CC PRO639, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,
CC PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1133, PRO1182, PRO1184,
CC PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094,
CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell
CC growth. The PRO polypeptides and nucleotides are useful in the
CC treatment, diagnosis and prevention of cancer. The antibodies and other
CC anti-tumour compounds may be used to treat various conditions, including
CC those characterised by overexpression and/or activation of the amplified
CC PRO genes. Exemplary conditions or disorders to be treated with such
CC antibodies and other compounds include benign or malignant tumours
CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,
CC colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic,
CC carcinomas, sarcomas, glioblastomas, and various head and neck tumours),
CC leukaemias and lymphoid malignancies, and other disorders such as neuronal,
CC glial, astrocytal, hypothalamic and other glandular, macrophagal,
CC epithelial, stromal and blastocoele disorders, and inflammatory,
CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR
CC primers and hybridisation probes used in the isolation of the human PRO
CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human
CC PRO polynucleotide and protein sequences given in the exemplification of
CC the present invention.
XX
XX Sequence 185 AA;

Query Match 100.0%; Score 81; DB 21; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQKGKGGGPPPK 14
| | | | | | | | | | | | | | | |
DB 104 kklqkgpggpppk 117

RESULT 3
AAAY87272
ID AAY87272 standard; Protein; 185 AA.
XX
AC AAY87272;
XX
XX 11-MAY-2000 (first entry)
XX
XX Human signal peptide containing protein HSPP-49 SEQ ID NO:49.
XX
XX Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
XX inflammation; cardiovascular disease; anticancer; anti-inflammatory;
XX antimicrobial; neurotropic; neuroprotective; cardiovascular; hepatotropic;
XX antiasthmatic; gene therapy; cell proliferation; neurological disorder;
XX reproductive disorder; developmental disorder; arteriosclerosis;
XX cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
XX asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
XX Parkinson's disease; Huntington's diseases; ovulatory defect;
XX muscular dystrophy.
XX
XX Homo sapiens.
XX
XX WO200000610-A2.
XX
XX 06-JAN-2000.
XX
XX 25-JUN-1999; 99WO-US14484.
XX
XX 26-JUN-1998; 98US-0090762.
XX

PR 31-JUL-1998; 98US-0094983.
 PR 01-OCT-1998; 98US-0102686.
 PR 11-DEC-1998; 98US-0112129.
 XX
 PA (INCYTE) INCYTE PHARM INC.
 XX
 PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
 PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
 PI Bandman O;
 XX
 DR WPI: 2000-160673/14.
 DR N-PSDB; AA298157.
 XX
 PT New human signal peptide-containing proteins useful in treatment,
 PT prevention and diagnosis of e.g. cancer, inflammation and
 PT cardiovascular disease
 XX
 PS Claim 1; Page 193-194; 327pp; English.
 XX
 CC AA298109 to AA298242 encode AA298724 to AA298737 which represent the
 CC human signal peptide-containing proteins HSPp-1 to HSPp-134. HSPps have
 CC anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,
 CC neuroprotective, cardiovascular and antiasthmatic activities, and can
 CC be used in gene therapy. HSPps can be used to treat or prevent disorders
 CC associated with decreased activity or function of HSPp. Antagonists of
 CC HSPp are used to treat or prevent disorders associated with increased
 CC activity or function of HSPp. Such diseases include cell proliferation
 CC (including cancer), inflammation, cardiovascular, neurological,
 CC reproductive or developmental disorders, (e.g. arteriosclerosis,
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
 CC asthma, Crohn's disease, microbial or other infections, congestive or
 CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPp
 CC nucleic acids can be used for the recombinant production of HSPp, for
 CC detecting HSPp in standard hybridisation and amplification assays (for
 CC diagnosis and monitoring), in gene therapy, as antisense,
 CC triplex-forming or ribozyme therapeutics, for detecting related sequences
 CC or genetic variations, and for chromosomal mapping. HSPp are also used to
 CC raise specific antibodies (Ab) and to screen for agonists and
 CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
 CC monitor, HSPp-related diseases (in usual immunoassays), as therapeutic
 CC antagonists, in competitive drug screens, and for purification of HSPp
 CC from natural sources.
 XX
 SQ Sequence 185 AA;

Query Match 100.0%; Score 81; DB 21; Length 185;
 Best Local Similarity 100.0%; Pred. No. 0.0029;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLGKGGPGPPPK 14
 |||||
 Db 104 kklgkkgpgpppk 117

RESULT 4
 AA298686
 ID AA298686 standard; protein; 185 AA.
 XX
 AC AA298686;
 XX
 DT 05-APR-2000 (first entry)
 XX
 DE Membrane-bound protein PR01005.
 XX
 KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
 KW pharmaceutical; receptor immunoadhesin; gene mapping.
 XX
 OS Homo sapiens.
 XX
 PN W09963088-A2.
 XX

PD 09-DEC-1999.
 XX
 PF 02-JUN-1999; 99WO-US12252.
 XX
 PR 02-JUN-1998; 98US-0087607.
 PR 02-JUN-1998; 98US-0087609.
 PR 02-JUN-1998; 98US-0087759.
 PR 03-JUN-1998; 98US-0087827.
 PR 04-JUN-1998; 98US-0088021.
 PR 04-JUN-1998; 98US-0088025.
 PR 04-JUN-1998; 98US-0088028.
 PR 04-JUN-1998; 98US-0088029.
 PR 04-JUN-1998; 98US-0088030.
 PR 04-JUN-1998; 98US-0088033.
 PR 04-JUN-1998; 98US-0088326.
 PR 05-JUN-1998; 98US-0088167.
 PR 05-JUN-1998; 98US-0088202.
 PR 05-JUN-1998; 98US-0088212.
 PR 05-JUN-1998; 98US-0088217.
 PR 05-JUN-1998; 98US-0088655.
 PR 10-JUN-1998; 98US-0088722.
 PR 10-JUN-1998; 98US-0088730.
 PR 10-JUN-1998; 98US-0088734.
 PR 10-JUN-1998; 98US-0088738.
 PR 10-JUN-1998; 98US-0088740.
 PR 10-JUN-1998; 98US-0088741.
 PR 10-JUN-1998; 98US-0088742.
 PR 10-JUN-1998; 98US-0088810.
 PR 10-JUN-1998; 98US-0088811.
 PR 10-JUN-1998; 98US-0088824.
 PR 10-JUN-1998; 98US-0088825.
 PR 10-JUN-1998; 98US-0088826.
 PR 11-JUN-1998; 98US-0088858.
 PR 11-JUN-1998; 98US-0088861.
 PR 11-JUN-1998; 98US-0088863.
 PR 11-JUN-1998; 98US-0088876.
 PR 12-JUN-1998; 98US-0089090.
 PR 12-JUN-1998; 98US-0089105.
 PR 16-JUN-1998; 98US-0089440.
 PR 16-JUN-1998; 98US-0089512.
 PR 16-JUN-1998; 98US-0089514.
 PR 17-JUN-1998; 98US-0089532.
 PR 17-JUN-1998; 98US-0089538.
 PR 17-JUN-1998; 98US-0089598.
 PR 17-JUN-1998; 98US-0089599.
 PR 17-JUN-1998; 98US-0089600.
 PR 17-JUN-1998; 98US-0089653.
 PR 18-JUN-1998; 98US-0089801.
 PR 18-JUN-1998; 98US-0089907.
 PR 18-JUN-1998; 98US-0089908.
 PR 19-JUN-1998; 98US-0089947.
 PR 19-JUN-1998; 98US-0089948.
 PR 19-JUN-1998; 98US-0089952.
 PR 22-JUN-1998; 98US-0090246.
 PR 22-JUN-1998; 98US-0090252.
 PR 22-JUN-1998; 98US-0090254.
 PR 23-JUN-1998; 98US-0090349.
 PR 23-JUN-1998; 98US-0090355.
 PR 24-JUN-1998; 98US-0090429.
 PR 24-JUN-1998; 98US-0090431.
 PR 24-JUN-1998; 98US-0090435.
 PR 24-JUN-1998; 98US-0090444.
 PR 24-JUN-1998; 98US-0090445.
 PR 24-JUN-1998; 98US-0090461.
 PR 24-JUN-1998; 98US-0090472.
 PR 24-JUN-1998; 98US-0090535.
 PR 24-JUN-1998; 98US-0090538.
 PR 24-JUN-1998; 98US-0090540.
 PR 24-JUN-1998; 98US-0090557.
 PR 25-JUN-1998; 98US-0090676.
 PR 25-JUN-1998; 98US-0090678.
 PR 25-JUN-1998; 98US-0090688.
 PR 25-JUN-1998; 98US-0090690.

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PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 07-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 99US-0115565.
PR
PR (GETH ) GENENTECH INC.
XX Baker K, Chen J, Goddard A, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX
```

WPI; 2000-072883/06.
N-PSDB; AA265023.
Membrane-bound proteins and related nucleotide sequences -
claim 12; Fig 139; 822pp; English.
The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor-immunoconjugates, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques.

DR WPI; 2000-072883/06.
DR N-PSDB; AA265023.
XX Membrane-bound proteins and related nucleotide sequences -
PT claim 12; Fig 139; 822pp; English.
PS The invention provides membrane-bound PRO polypeptides and
XX polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoconjugates, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC will also be useful for the preparation of PRO polypeptides, especially
CC by recombinant techniques.
XX
SQ Sequence 185 AA;

Query Match 100.0%; Score 81; DB 21; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLOGKGGGPPPK 14
Db 104 kklgkgpggpppk 117
|||||
kklgkgpggpppk 117

RESULT 5
AAB65209
ID AAB65209 standard; Protein; 185 AA.
XX
AC AAB65209;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO1005 (UNQ489) protein sequence SEQ ID NO:211.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic;
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay.
XX
OS Homo sapiens.
XX
PN WO2000073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US08439.
XX
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 17-AUG-1999; 99US-0149396.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 08-OCT-1999; 99US-0158663.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;
 XX
 DR WPI: 2001-032160/04.
 DR N-PSDB; AAF44169.
 XX
 PT PRO polynucleotides used to produce polypeptides used to target
 PT bioactive molecules such as toxins, radiolabels or antibodies, to
 PT specific cells, to cause targeted cell death -
 XX
 PS Claim 12; Fig 139; 935pp; English.
 XX
 CC The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
 CC can be used for targeted delivery of bioactive molecules, such as
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC and DNA. They may also be used to produce transgenic animals which are
 CC used to develop and screen therapeutically useful reagents. The PRO
 CC nucleotide and protein sequence can be used for tissue typing and in
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
 CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 XX
 SQ Sequence 185 AA;
 XX
 Query Match 100.0%; Score 81; DB 22; Length 185;
 Best Local Similarity 100.0%; Pred. No. 0.0029;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KKLOGKGGGPPPK 14
 Db 104 kklqgkpggpppk 117
 XX
 RESULT 6
 AAB50957
 ID AAB50957 standard; Protein; 185 AA.
 XX
 AC AAB50957;
 XX
 DT 21-MAR-2001 (first entry)
 XX
 DE Human PRO1005 protein.
 XX
 KW Human; PRO; cytostatic; nootropic; neuroprotective; respiratory general;
 KW antiinflammatory; angiogenic; immunosuppressive; immunostimulant;
 KW PRO agonist; cancer; inflammatory disorder; immunological disorder.
 XX
 OS Homo sapiens.
 XX
 XX WO200073348-A2.
 PN
 PD 07-DEC-2000.
 XX
 PF 30-MAY-2000; 2000WO-US14941.

XX
 PR 02-JUN-1999; 99WO-US12352.
 PR 22-JUN-1999; 99US-0140650.
 PR 23-JUN-1999; 99US-0141037.
 PR 20-JUL-1999; 99US-0144758.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30999.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 02-MAR-2000; 2000WO-US04342.
 PR 03-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000US-0187202.
 PR 15-MAR-2000; 2000WO-US06319.
 PR 30-MAR-2000; 2000WO-US06884.
 PR 17-MAY-2000; 2000WO-US08439.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
 PI Shelton DL, Smith V, Watanabe CK, Wood WI;
 XX
 DR WPI: 2001-016509/02.
 DR N-PSDB; AAC91559.
 XX
 PT Twenty eight nucleic acids encoding PRO polypeptides which are useful
 PT for treating various tumors, e.g. breast cancer, and other
 PT inflammatory, angiogenic and immunological disorders -
 XX
 PS Claim 31; Fig 14; 188pp; English.
 XX
 CC The present sequence is one of twenty eight novel PRO polypeptides. The
 CC PRO polypeptides and their agonists, including antibodies, peptides, and
 CC small molecule agonists, may be used to treat various tumours, e.g.,
 CC cancers such as breast cancer, ovarian cancer, renal cancer, colorectal
 CC cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,
 CC central nervous system cancer, melanoma or leukaemia. They are also
 CC useful for treating other disorders such as neuronal, glial, astrocytal,
 CC hypothalamic and other glandular, macrophagal, epithelial, stromal and
 CC blastocoelec disorders, and inflammatory, angiogenic and immunological
 CC disorders.
 XX
 SQ Sequence 185 AA;

Query Match 100.0%; Score 81; DB 22; Length 185;
 Best Local Similarity 100.0%; Pred. No. 0.0029;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KKLOGKGGGPPPK 14
 Db 104 kklqgkpggpppk 117
 XX
 RESULT 7
 AAB38329
 ID AAB38329 standard; Protein; 186 AA.
 XX
 AC AAB38329;
 XX
 DT 31-JAN-2001 (first entry)
 XX
 DE Human secreted protein encoded by gene 9 clone HNSAD53.
 XX
 KW Immunosuppressive; antiarthritic; antirheumatic; antiproliferative;
 KW cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective;

KW nootropic; antibacterial; virucide; fungicide; ophthalmological; human;
 KW vulnery; gene therapy; infection; secreted protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200061623-A1.
 XX
 PD 19-OCT-2000.
 XX
 PF 06-APR-2000; 2000WO-US08979.
 XX
 PR 09-APR-1999; 99US-0128693.
 PR 26-APR-1999; 99US-0130991.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Ruben SM, Ni J, Komatsoulis GA, Rosen CA, Soppet DR, Shi Y;
 PI Lafleur DW, Olsen HS, Ebner R, Florence KA, Moore PA, Birse CE;
 PI Young PE;
 XX
 DR WPI; 2000-647418/62.
 XX
 XX New nucleic acid molecules encoding 62 human secreted proteins for
 PT diagnosing, preventing, treating or ameliorating medical conditions and
 PT used as food additives or preservatives -
 XX
 PS Claim 11; Page 598; 716pp; English.
 XX
 CC Sequences AAB38321-B38396 represent the amino acid sequences of 62
 CC human secreted proteins encoded by the genes AAC69512-C69587. The genes
 CC and proteins are useful for preventing, ameliorating or treating medical
 CC conditions e.g. by protein or gene therapy. The genes are isolated from
 CC a range of human tissues disclosed in the specification. The nucleic
 CC acids, proteins, antibodies and (ant)agonists are useful in the
 CC diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.
 CC rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms
 CC of the breast or liver; (c) cardiovascular disorders e.g. cardiac
 CC arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e)
 CC angiogenesis; (f) nervous system disorders e.g. Alzheimer's disease; (g)
 CC infections caused by bacteria, viruses and fungi; and (h) ocular
 CC disorders e.g. corneal infection. The polypeptides can also be used to
 CC aid wound healing and epithelial cell proliferation, to prevent skin
 CC aging due to sunburn, to maintain organs before transplantation, for
 CC supporting cell culture of primary tissues, to regenerate tissues and in
 CC chemotaxis.
 XX
 SQ Sequence 186 AA;
 Query Match 100.0%; Score 81; DB 21; Length 186;
 Best Local Similarity 100.0%; Pred. No. 0.0029;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLOGKGGGPPPK 14
 Db 104 KKlqgkpgpgppk 117
 RESULT 8
 AAW69974
 ID AAW69974 standard; Protein: 194 AA.
 XX
 AC AAW69974;
 XX
 DT 16-NOV-1998 (first entry)
 XX
 DE Cancer associated protein.
 XX
 KW Cancer; PCR; Northern blotting; ribonuclease protection assay;
 KW diagnosis; metastatic cancer.
 XX
 OS Synthetic.
 XX

PN WO9837187-A1.
 XX
 PD 27-AUG-1998.
 XX
 PF 18-FEB-1998; 98WO-JP00667.
 XX
 PR 21-FEB-1997; 97JP-0052508.
 XX
 PA (TAKI) TAKARA SHUZO CO LTD.
 XX
 PI Asada K, Hino F, Kato I, Mukai H, Yoshikawa Y;
 XX
 DR WPI; 1998-467552/40.
 XX
 XX Detection of cancer cells in tissue samples - by changes in mRNA
 PT expression compared to normal tissue of specific cancer-associated
 PT gene sequences
 XX
 PS Claim 14; Page 64-65; 92pp; Japanese.
 XX
 CC The cancer associated proteins AAW69974-W69976 where used in the method
 CC of the invention to detect cancer cells in tissue samples or biological
 CC fluids. They are detected by monitoring the change in mRNA expression
 CC as compared to normal tissue of one or more cancer-associated genes
 CC whose cDNA stringently hybridises to cancer associated gene nucleic acid
 CC fragments. The change in expression may be an increase or a decrease
 CC compared to normal tissue. The mRNA expression may be determined by
 CC PCR, Northern blotting or ribonuclease protection assay, or by
 CC determining the change in the amount of protein encoded by the gene(s) as
 CC compared to normal tissue, for example by using a labelled antibody
 CC recognising the protein. Detection of cancer cells for cancer diagnosis,
 CC including detection of metastatic cancer cells in tissues other than the
 CC primary tumour site.
 XX
 SQ Sequence 194 AA;
 Query Match 100.0%; Score 81; DB 19; Length 194;
 Best Local Similarity 100.0%; Pred. No. 0.003;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLOGKGGGPPPK 14
 Db 113 KKlqgkpgpgppk 126
 RESULT 9
 AAY76591
 ID AAY76591 standard; Protein: 194 AA.
 XX
 AC AAY76591;
 XX
 DT 10-APR-2000 (first entry)
 XX
 DE Human ovarian tumor EST fragment encoded protein 87.
 XX
 KW Expressed sequence tag; EST; human; ovarian tumor; anticancer;
 KW gene therapy; treatment.
 XX
 OS Homo sapiens.
 XX
 PN DE19817557-A1.
 XX
 PD 21-OCT-1999.
 XX
 PF 09-APR-1998; 98DE-1017557.
 XX
 PR 09-APR-1998; 98DE-1017557.
 XX
 PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
 XX
 PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pillarsky C, Dahl E;
 XX

DR WPI; 1999-591920/51.
 DR N-PSDB; AAZ77487.
 XX
 PT New nucleic acid sequences expressed in ovarian, and some other, cancer
 PT tissues, and derived polypeptides, for treatment of ovarian cancer and
 PT identification of therapeutic agents -
 XX
 PS Claim 25; Page 279; 310pp; German.
 XX
 CC This invention describes novel nucleic acid (cDNA) sequences (A) which
 CC have anticancer activity and are highly expressed in ovarian tumor
 CC tissue (and some also in testis and breast cancer tissue). The products
 CC of the invention can be used for gene therapy. (A) are used (i) for
 CC recombinant expression of polypeptides (B) and (ii) to isolate complete
 CC genes. (B) are used (i) to identify agents suitable for treatment of
 CC ovarian cancer; (ii) directly for treating this form of cancer
 CC (including expression from gene therapy vectors) and (iii) for generation
 CC of specific antibodies. (A) are identified by assembling ESTs (expressed
 CC sequence tags) from a particular tissue type before comparison of
 CC expression patterns. This allows a significantly longer fragment of the
 CC gene to be revealed, so should reduce the number of failures associated
 CC with the fact that ESTs from different libraries may represent different
 CC parts of the same unknown gene, distorting the estimated frequency of
 CC occurrence in a particular tissue. AAY76505-Y76638 represent protein
 CC fragments encoded by the human ovarian tumor cDNA library derived EST
 CC fragments represented in AAZ77450-277572.
 XX
 CC Sequence 194 AA;

Query Match 100.0%; Score 81; DB 20; Length 194;
 Best Local Similarity 100.0%; Pred. No. 0.003;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLGKGGPGGPPK 14
 |||||
 Db 113 kklqgpgpgppk 126

RESULT 10
 AAB41048
 ID AAB41048 standard; Protein; 103 AA.
 AC AAB41048;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Human ORFX ORF812 polypeptide sequence SEQ ID NO:1624.
 XX
 KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
 KW vulnary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antinflammatory;
 KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
 KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antinflammatory disease; coagulation;
 KW thrombosis; contraceptive.
 XX
 OS Homo sapiens.
 XX
 PN WO200058473-A2.
 XX
 PD 05-OCT-2000.
 XX
 PF 31-MAR-2000; 2000WO-US08621.
 XX
 PF 31-MAR-1999; 99US-0127607.
 PR

PR 02-APR-1999; 99US-0127636.
 PR 05-APR-1999; 99US-0127728.
 PR 30-MAR-2000; 2000US-0540763.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 XX Shimkets RA, Leach M;
 XX
 PI WPI; 2000-602362/57.
 XX
 DR N-PSDB; AAC75257.
 XX
 CC Novel nucleic acids and peptides derived from open reading frame X,
 CC useful for treating e.g. cancers, proliferative disorders,
 CC neurodegenerative disorders and cardiovascular disease -
 PT
 PT Claim 11; Page 1306; 5507pp; English.
 PS
 CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
 CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
 CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
 CC antithyroid; and antianemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.
 XX
 CC Sequence 103 AA;

Query Match 64.2%; Score 52; DB 21; Length 103;
 Best Local Similarity 64.3%; Pred. No. 9.8;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 KKLGKGGPGGPPK 14
 :| ||||| |
 Db 61 rkssgkpgnprk 74

RESULT 11
 AA001151
 ID AA001151 standard; Protein; 163 AA.
 XX
 AC AA001151;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 15043.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200164835-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 26-FEB-2001; 2001WO-US04927.

DR WPI; 2001-318749/34.
 XX
 PT Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX
 PS Claim 8; SEQ ID 14777; 2537pp + CD ROM; English.
 XX
 CC The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 XX
 SQ Sequence 467 AA;

Query Match 64.2%; Score 52; DB 22; Length 467;
 Best Local Similarity 64.3%; Pred. No. 36;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KKLOGKGGGPPPK 14
 :| ||||| |
 Db 213 rkssgkgpgnprk 226

RESULT 14
 AA004166
 ID AA004166 standard; Protein; 108 AA.

XX AA004166;

DT 06-NOV-2001 (first entry)

XX Human polypeptide SEQ ID NO 18058.

DE Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

XX Homo sapiens.

XX WO200164835-A2.

XX 07-SEP-2001.

XX 26-FEB-2001; 2001WO-US04927.

XX 28-FEB-2000; 2000US-0515126.

PR 18-MAY-2000; 2000US-0577409.

XX (HYSE-) HYSEQ INC.

PA Tang YT, Liu C, Drmanac RT;

XX

DR WPI; 2001-514838/56.
 DR N-PSDB; AA184097.

XX Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -

XX Claim 20; SEQ ID NO 18058; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AA179941-AA193841) and
 CC the encoded proteins (AA000010-AA013910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.

CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 108 AA;

Query Match 63.0%; Score 51; DB 22; Length 108;
 Best Local Similarity 80.0%; Pred. No. 14;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QGKGGGPPPP 13
 :| ||||| |
 Db 56 rgggpggpppp 65

RESULT 15

AA011472
 ID AA011472 standard; Protein; 125 AA.

XX AA011472;

DT 06-NOV-2001 (first entry)

XX Human polypeptide SEQ ID NO 25364.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

XX Homo sapiens.

XX WO200164835-A2.

XX 07-SEP-2001.

XX 26-FEB-2001; 2001WO-US04927.

XX 28-FEB-2000; 2000US-0515126.

PR 18-MAY-2000; 2000US-0577409.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-514838/56.

DR N-PSDB; AA191403.

XX Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -

XX PS Claim 20; SEQ ID NO 25364; 1399pp + Sequence Listing; English.
XX CC
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 125 AA;

Query Match 63.0%; Score 51; DB 22; Length 125;
Best Local Similarity 81.8%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 LOGKGPGGPPP 13
Db ||| | |||||
58 lqgpgnggppp 68

Search completed: September 4, 2002, 16:45:03
Job time: 379 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:46:06 ; Search time 57.74 Seconds
(without alignments)
5.922 Million cell updates/sec

Title: US-09-821-726-3
Perfect score: 81
Sequence: 1 KKLQGGPGGPPPK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	50	61.7	673	4	US-09-078-347A-2
2	49	60.5	855	4	US-09-813-819-2
3	49	60.5	855	4	US-09-920-048-2
4	45	55.6	402	2	US-08-709-979A-3
5	45	55.6	402	3	US-08-709-974A-1
6	45	55.6	402	3	US-08-709-974A-5
7	45	55.6	415	2	US-08-833-642A-5
8	45	55.6	415	3	US-08-709-974A-4
9	45	55.6	415	4	US-09-069-632-1
10	45	55.6	435	1	US-08-361-920-27
11	45	55.6	435	1	US-08-479-939-27
12	45	55.6	435	1	US-08-483-432-27
13	45	55.6	435	1	US-09-069-632-3
14	45	55.6	752	4	US-09-817-180-2
15	45	55.6	822	4	US-09-817-180-4
16	44	54.3	18	3	US-08-630-916A-9
17	44	54.3	218	1	US-08-247-946A-3
18	44	54.3	218	5	PCT-US95-06420-3
19	44	54.3	1205	1	US-07-908-245-2
20	44	54.3	1205	2	US-08-319-866-10
21	44	54.3	1205	4	US-09-123-708-6
22	44	54.3	1205	4	US-09-123-624-6
23	43	53.1	265	2	US-08-484-905-119
24	43	53.1	265	3	US-08-481-585B-119
25	43	53.1	265	4	US-08-370-476-119
26	43	53.1	298	2	US-08-207-481-39
27	43	53.1	298	5	PCT-US95-02689-41

28	43	53.1	311	2	US-08-318-837-9	Sequence 9, Appli
29	42	51.9	118	1	US-08-393-985-14	Sequence 14, Appl
30	42	51.9	298	3	US-08-767-942A-25	Sequence 25, Appl
31	41	50.6	107	3	US-08-478-097A-19	Sequence 19, Appl
32	41	50.6	124	1	US-08-455-559-11	Sequence 11, Appl
33	41	50.6	124	4	US-09-145-060-11	Sequence 11, Appl
34	41	50.6	124	5	PCT-US94-00657-11	Sequence 11, Appl
35	41	50.6	147	4	US-09-347-833-10	Sequence 10, Appl
36	41	50.6	437	2	US-08-935-450-8	Sequence 8, Appli
37	41	50.6	629	3	US-08-464-258B-6	Sequence 6, Appli
38	41	50.6	3025	6	5223423-3	Patent No. 5223423
39	40	49.4	112	2	US-08-301-915-3	Sequence 3, Appli
40	40	49.4	112	3	US-08-524-694A-3	Sequence 3, Appli
41	40	49.4	112	5	PCT-US93-04301-3	Sequence 3, Appli
42	40	49.4	133	1	US-07-917-722-3	Sequence 3, Appli
43	40	49.4	256	2	US-08-727-688-33	Sequence 33, Appl
44	40	49.4	269	2	US-07-857-224B-14	Sequence 14, Appl
45	40	49.4	269	2	US-07-857-224B-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-078-347A-2
; Sequence 2, Application US/09078347A
; Patent No. 6132968
; GENERAL INFORMATION:
; APPLICANT: Le, Xiao-Chun
; APPLICANT: Weinfield, Michael
; APPLICANT: Xing, James Z.
; TITLE OF INVENTION: Methods for Quantitating Low Level
; TITLE OF INVENTION: Modifications of Nucleotide Sequences
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/078,347A
; FILING DATE: 13-MAY-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Carroll, Peter G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: UALB-03283
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-078-347A-2

Query Match 61.7%; Score 50; DB 4; Length 673;
Best Local Similarity 72.7%; Pred. No. 30;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LOGKGGGPPPK 13
| : ||| |||

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DB 313 LSGRGPGEPPP 323
RESULT 2
US-09-813-819-2
; Sequence 2, Application US/09813819
; Patent No. 6294368
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001177
; CURRENT APPLICATION NUMBER: US/09/813,819
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Human
US-09-813-819-2
Query Match 60.5%; Score 49; DB 4; Length 855;
Best Local Similarity 61.5%; Pred. No. 49;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 KKLGKGGGGPPP 13
|:|:|:|:|:|
DB 797 KRLQSQGPAKPPP 809
RESULT 3
US-09-920-048-2
; Sequence 2, Application US/09920048
; Patent No. 6344352
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001177DIV
; CURRENT APPLICATION NUMBER: US/09/920,048
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/813,819
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Human
US-09-920-048-2
Query Match 60.5%; Score 49; DB 4; Length 855;
Best Local Similarity 61.5%; Pred. No. 49;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 KKLGKGGGGPPP 13
|:|:|:|:|:|
DB 797 KRLQSQGPAKPPP 809
RESULT 4
US-08-709-979A-3
; Sequence 3, Application US/08709979A
; Patent No. 5912157
; GENERAL INFORMATION:
; APPLICANT: Claus von der Osten
; APPLICANT: Martin Sch lein
; TITLE OF INVENTION: No. 5912157el Alkaline Cellulases
```

```
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5912157o No. 5912157disk of No. 5912157th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,979A
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4160.404-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-709-979A-3
Query Match 55.6%; Score 45; DB 2; Length 402;
Best Local Similarity 47.4%; Pred. No. 82;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;
QY 2 KLQKGGPGG-----PPPK 14
|:|:|:|:|:|
DB 42 RAEGLGPGCGDGNPPPK 60
RESULT 5
US-08-709-974A-1
; Sequence 1, Application US/08709974A
; Patent No. 6117664
; GENERAL INFORMATION:
; APPLICANT: Sch lein, Martin
; APPLICANT: Rosholm, Peter
; APPLICANT: Nielsen, Jack Bech
; APPLICANT: Hansen, Svend Aage
; APPLICANT: von der Osten, Claus
; TITLE OF INVENTION: No. 6117664el Alkaline Cellulases
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6117664o No. 6117664disk of No. 6117664th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,974A
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta
```

REGISTRATION NUMBER: 35,127Y
REFERENCE/DOCKET NUMBER: 4160.414-US
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-709-974A-1

Query Match 55.6%; Score 45; DB 3; Length 402;
Best Local Similarity 47.4%; Pred. No. 82;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 KLOGKPGG-----PPPK 14
: : | | | |
Db 42 RAELGPGGCGDGNPPPK 60

RESULT 6
US-08-709-974A-5
; Sequence 5, Application US/08709974A
; Patent No. 6117664
; GENERAL INFORMATION:
; APPLICANT: Sch lein, Martin
; APPLICANT: Rosholm, Peter
; APPLICANT: Nielsen, Jack Bech
; APPLICANT: Hansen, Svend Aage
; APPLICANT: von der Osten,Claus
; TITLE OF INVENTION: No. 6117664el Alkaline Cellulases
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6117664o No. 6117664disk of No. 6117664th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,974A
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta
; REGISTRATION NUMBER: 35,127Y
; REFERENCE/DOCKET NUMBER: 4160.414-US
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-709-974A-5

Query Match 55.6%; Score 45; DB 3; Length 402;
Best Local Similarity 47.4%; Pred. No. 82;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 KLOGKPGG-----PPPK 14
: : | | | |
Db 42 RAELGPGGCGDGNPPPK 60

RESULT 7
US-08-833-642A-5
; Sequence 5, Application US/08833642A
; Patent No. 5883066
; GENERAL INFORMATION:
; APPLICANT: Ivan M. A. J. Herbols et al.
; TITLE OF INVENTION: Liquid Detergent Compositions
; TITLE OF INVENTION: Containing Cellulase and Amine
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jackie Ann Zurcher
; ADDRESSEE: Dinsmore & Shohl LLP
; STREET: 255 E. Fifth Street
; STREET: 1900 Chemed Center
; CITY: Cincinnati
; STATE: Ohio
; COUNTRY: USA
; ZIP: 45202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,642A
; FILING DATE: April 8, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Zurcher, J. A.
; REGISTRATION NUMBER: P42,251
; REFERENCE/DOCKET NUMBER: CM551C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (513) 977-8377
; TELEFAX: (513) 977-8141
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-833-642A-5

Query Match 55.6%; Score 45; DB 2; Length 415;
Best Local Similarity 47.4%; Pred. No. 84;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 KLOGKPGG-----PPPK 14
: : | | | |
Db 42 RAELGPGGCGDGNPPPK 60

RESULT 8
US-08-709-974A-4
; Sequence 4, Application US/08709974A
; Patent No. 6117664
; GENERAL INFORMATION:
; APPLICANT: Sch lein, Martin
; APPLICANT: Rosholm, Peter
; APPLICANT: Nielsen, Jack Bech
; APPLICANT: Hansen, Svend Aage
; APPLICANT: von der Osten,Claus
; TITLE OF INVENTION: No. 6117664el Alkaline Cellulases
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6117664o No. 6117664disk of No. 6117664th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York

COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,974A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 4160.414-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-709-974A-4

Query Match 55.6%; Score 45; DB 3; Length 415;
Best Local Similarity 47.4%; Pred. No. 84;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 KLOGKPGG-----PPPK 14
Db 42 RAELGPGGCGDGNPPPK 60

RESULT 9
US-09-069-632-1
Sequence 1, Application US/09069632
Patent No. 6261828
GENERAL INFORMATION:
APPLICANT: Lund, Henrik
TITLE OF INVENTION: A Process For Combined Desizing
TITLE OF INVENTION: And Stone-Washing of Dyed Denim
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6261828o No. 6261828disk of No. 6261828th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,632
FILING DATE: 29-APR-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK96/00469
FILING DATE: 15-NOV-1996
APPLICATION NUMBER: 1278/95
FILING DATE: 15-NOV-1995
NAME: Gregg, Valeta
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 4588.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123

TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-069-632-1

Query Match 55.6%; Score 45; DB 4; Length 415;
Best Local Similarity 47.4%; Pred. No. 84;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 KLOGKPGG-----PPPK 14
Db 42 RAELGPGGCGDGNPPPK 60

RESULT 10
US-08-361-920-27
Sequence 27, Application US/08361920
Patent No. 5457046
GENERAL INFORMATION:
APPLICANT: Woeldike, Helle F.
APPLICANT: Hagen, Frederick
APPLICANT: Hjort, Carsten M.
APPLICANT: Sved, Hastrup
TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
TITLE OF INVENTION: or Hemicellulose
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5457046o No. 5457046disk of No. 5457046th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,920
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/940,860
FILING DATE: 28-OCT-1992
APPLICATION NUMBER: DK 1158/90
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK91/00124
FILING DATE: 08-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3435.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-361-920-27

Query Match 55.6%; Score 45; DB 1; Length 435;

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Best Local Similarity 47.4%; Pred. No. 88;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 KLOGKPGG-----PPPK 14
Db 62 RAEGLGPGCGDGNPPPK 80

RESULT 11
US-08-479-939-27
; Sequence 27, Application US/08479939
; Patent No. 5686593
; GENERAL INFORMATION:
; APPLICANT: Woeldike, Helle F.
; APPLICANT: Hagen, Frederick
; APPLICANT: Hjort, Carsten M.
; APPLICANT: Sven, Hastrup
; TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
; TITLE OF INVENTION: or Hemicellulose
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 56865930 No. 5686593disk of No. 5686593th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,939
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,920
; FILING DATE:
; APPLICATION NUMBER: US 07/940,860
; FILING DATE: 28-OCT-1992
; APPLICATION NUMBER: DK 1158/90
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK91/00124
; FILING DATE: 08-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3435.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-867-0298
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-479-939-27

Query Match 55.6%; Score 45; DB 1; Length 435;
Best Local Similarity 47.4%; Pred. No. 88;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 KLOGKPGG-----PPPK 14
Db 62 RAEGLGPGCGDGNPPPK 80

RESULT 12
US-08-483-432-27
; Sequence 27, Application US/08483432
; Patent No. 5763254
; GENERAL INFORMATION:
; APPLICANT: Woeldike, Helle F.
; APPLICANT: Hagen, Frederick
; APPLICANT: Hjort, Carsten M.
; APPLICANT: Sven, Hastrup
; TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
; TITLE OF INVENTION: or Hemicellulose
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 57632540 No. 5763254disk of No. 5763254th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,432
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,920
; FILING DATE:
; APPLICATION NUMBER: US 07/940,860
; FILING DATE: 28-OCT-1992
; APPLICATION NUMBER: DK 1158/90
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK91/00124
; FILING DATE: 08-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3435.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-867-0298
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-432-27

Query Match 55.6%; Score 45; DB 1; Length 435;
Best Local Similarity 47.4%; Pred. No. 88;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 KLOGKPGG-----PPPK 14
Db 62 RAEGLGPGCGDGNPPPK 80

RESULT 13
US-09-069-632-3
; Sequence 3, Application US/09069632
; Patent No. 6261828
; GENERAL INFORMATION:
; APPLICANT: Lund, Henrik
; TITLE OF INVENTION: A Process For Combined Desizing
; TITLE OF INVENTION: And Stone-Washing of Dyed Denim
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 62618280 No. 6261828th America, Inc.
; STREET: 405 Lexington Avenue
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; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,632
; FILING DATE: 29-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK96/00469
; FILING DATE: 15-NOV-1996
; APPLICATION NUMBER: 1278/95
; FILING DATE: 15-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta
; REGISTRATION NUMBER: 35,127
; REFERENCE/DOCKET NUMBER: 4588,204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-069-632-3

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Query Match 55.6%; Score 45; DB 4; Length 435;
Best Local Similarity 47.4%; Pred. No. 88;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 KLOGKGGG-----PPPK 14
DB 62 RAELGPGGGGDMGNPPPK 80

RESULT 14
US-09-817-180-2
; Sequence 2, Application US/09817180
; Patent No. 6340584
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183
; CURRENT APPLICATION NUMBER: US/09/817,180
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 752
; TYPE: PRT
; ORGANISM: Human
; US-09-817-180-2

Query Match 55.6%; Score 45; DB 4; Length 822;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KLOGKGGGPPPP 13
DB 387 KLEHLGPGGPPPP 398

Search completed: September 4, 2002, 16:46:07
Job time: 328 sec

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; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
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; FILING DATE: 29-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK96/00469
; FILING DATE: 15-NOV-1996
; APPLICATION NUMBER: 1278/95
; FILING DATE: 15-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta
; REGISTRATION NUMBER: 35,127
; REFERENCE/DOCKET NUMBER: 4588,204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-069-632-3

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Query Match 55.6%; Score 45; DB 4; Length 752;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KLOGKGGGPPPP 13
DB 387 KLEHLGPGGPPPP 398

Search completed: September 4, 2002, 16:46:07
Job time: 328 sec

GenCore version 4.5
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OM protein - protein search, using sw model
Run on: September 4, 2002, 16:59:19 ; Search time 704.77 Seconds
(without alignments)
6.992 Million cell updates/sec

Title: US-09-821-726-3
Perfect score: 81
Sequence: 1 KKLQKGGGPPPK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues 3502263
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	81	100.0	21	22	US-09-821-726-8
4	81	100.0	25	22	US-09-821-726-10
5	81	100.0	42	22	US-09-821-726-6
6	81	100.0	150	13	US-08-906-708-24
7	81	100.0	182	20	US-09-684-524-212
					Sequence 212, App
					Sequence 3, Appli
					Sequence 7, Appli
					Sequence 8, Appli
					Sequence 10, Appli
					Sequence 6, Appli
					Sequence 24, Appli
					Sequence 212, App

8	81	100.0	182	24	US-10-050-704-212	Sequence 212, App
9	81	100.0	185	1	PCT-US98-16318-18	Sequence 18, Appl
10	81	100.0	185	15	US-09-130-189-18	Sequence 18, Appl
11	81	100.0	185	20	US-09-684-524-105	Sequence 105, App
12	81	100.0	185	21	US-09-709-238-211	Sequence 211, App
13	81	100.0	185	21	US-09-746-783-146	Sequence 146, App
14	81	100.0	185	22	US-09-821-726-13	Sequence 13, Appl
15	81	100.0	185	22	US-09-821-726-18	Sequence 18, Appl
16	81	100.0	185	23	US-09-941-992-211	Sequence 211, App
17	81	100.0	185	23	US-09-989-279-211	Sequence 211, App
18	81	100.0	185	23	US-09-989-293A-211	Sequence 211, App
19	81	100.0	185	23	US-09-989-722-211	Sequence 211, App
20	81	100.0	185	23	US-09-989-723-211	Sequence 211, App
21	81	100.0	185	23	US-09-989-724-211	Sequence 211, App
22	81	100.0	185	23	US-09-989-725-211	Sequence 211, App
23	81	100.0	185	23	US-09-989-726-211	Sequence 211, App
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25	81	100.0	185	23	US-09-989-728-211	Sequence 211, App
26	81	100.0	185	23	US-09-989-729A-211	Sequence 211, App
27	81	100.0	185	23	US-09-989-730-211	Sequence 211, App
28	81	100.0	185	23	US-09-989-731-211	Sequence 211, App
29	81	100.0	185	23	US-09-989-732-211	Sequence 211, App
30	81	100.0	185	23	US-09-989-734-211	Sequence 211, App
31	81	100.0	185	23	US-09-989-735-211	Sequence 211, App
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34	81	100.0	185	23	US-09-990-436-211	Sequence 211, App
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44	81	100.0	185	23	US-09-990-562-211	Sequence 211, App
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ALIGNMENTS

RESULT 1
US-09-821-726-3
; Sequence 3, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-821-726-3

Query Match 100.0%; Score 81; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQKGGGPPPK 14
DB 1 KKLQKGGGPPPK 14

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RESULT 2
US-09-821-726-7
; Sequence 7, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-821-726-7

Query Match      100.0%; Score 81; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQKGPGGPPPK 14
Db 1 KKLQKGPGGPPPK 14
|||||

RESULT 3
US-09-821-726-8
; Sequence 8, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-821-726-8

Query Match      100.0%; Score 81; DB 22; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQKGPGGPPPK 14
Db 8 KKLQKGPGGPPPK 21
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RESULT 4
US-09-821-726-10
; Sequence 10, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-821-726-10

Query Match      100.0%; Score 81; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQKGPGGPPPK 14
Db 8 KKLQKGPGGPPPK 21
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RESULT 5
US-09-821-726-6
; Sequence 6, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-821-726-6

Query Match      100.0%; Score 81; DB 22; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQKGPGGPPPK 14
Db 27 KKLQKGPGGPPPK 40
|||||

RESULT 6
US-08-906-708-24
; Sequence 24, Application US/08906708
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: MCCOY, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki J.
; APPLICANT: Agostino, Michael J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,708
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: P-41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-906-708-24

Query Match 100.0%; Score 81; DB 13; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQKGGPGGPPPK 14
Db 104 KKLQKGGPGGPPPK 117

RESULT 7
US-09-684-524-212
; Sequence 212, Application US/09684524
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/09/684,524
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 212
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-684-524-212

Query Match 100.0%; Score 81; DB 20; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQKGGPGGPPPK 14
Db 104 KKLQKGGPGGPPPK 117

RESULT 8
US-10-050-704-212
; Sequence 212, Application US/10050704
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/10/050,704
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 09/684,524
; PRIOR FILING DATE: 2000-10-10

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; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 212
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-050-704-212

Query Match 100.0%; Score 81; DB 24; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQKGGPGGPPPK 14
Db 104 KKLQKGGPGGPPPK 117

RESULT 9
PCT-US98-16318-18
; Sequence 18, Application PC/TUS9816318
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI6051A
; CURRENT APPLICATION NUMBER: PCT/US98/16318
; CURRENT FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US98-16318-18

Query Match 100.0%; Score 81; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQKGGPGGPPPK 14
Db 104 KKLQKGGPGGPPPK 117

RESULT 10
US-09-130-189-18
; Sequence 18, Application US/09130189
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.

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; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: G16051A
; CURRENT APPLICATION NUMBER: US/09/130,189
; CURRENT FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-130-189-18

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Query Match      100.0%; Score 81; DB 15; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLQKGGPGPPPK 14
Db 104 KKLQKGGPGPPPK 117

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RESULT 11

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US-09-684-524-105
; Sequence 105, Application US/09684524
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/09/684,524
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-684-524-105

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Query Match      100.0%; Score 81; DB 20; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLQKGGPGPPPK 14
Db 104 KKLQKGGPGPPPK 117

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RESULT 12

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US-09-709-238-211
; Sequence 211, Application US/09709238
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Chen, Jian
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Yuan, Jean
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding the Same
; FILE REFERENCE: P2730R1C1
; CURRENT APPLICATION NUMBER: US/09/709,238
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US99/12252

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; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 60/087,607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: US 60/087,609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: US 60/087,759
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: US 60/087,827
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: US 60/088,021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: US 60/088,025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: US 60/088,028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: US 60/088,029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: US 60/088,030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: US 60/088,033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: US 60/088,326
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/088,167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/088,202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/088,212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/088,217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/088,655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: US 60/088,722
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,730
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,740
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,741
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,742
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,811
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,825
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: US 60/088,861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: US 60/088,863
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: US 60/088,876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: US 60/089,090
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: US 60/089,105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: US 60/089,440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: US 60/089,512
; PRIOR FILING DATE: 1998-06-16

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us-09-821-726-3.rapm

Thu Sep 5 11:23:37 2002

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; PRIOR APPLICATION NUMBER: US 60/089,514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: US 60/089,532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/089,538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/089,598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/089,599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/089,600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/089,653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/089,801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: US 60/089,907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: US 60/089,908
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: US 60/089,947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 60/089,948
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 60/089,952
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 60/090,246
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: US 60/090,252
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: US 60/090,254
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: US 60/090,355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: US 60/090,429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: US 60/090,431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: US 60/090,435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: US 60/090,349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: US 60/090,444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: US 60/090,445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: US 60/090,461
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: US 60/090,472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: US 60/090,535
; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: US 60/090,540
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: US 60/090,676
; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,696
; PRIOR FILING DATE: 1998-06-25

; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,862
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,863
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/091,358
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: US 60/091,360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: US 60/091,478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,486
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: US 60/091,626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,628
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,646
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,673
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: US 60/091,982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: US 60/092,182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: US 60/092,472
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 60/093,339
; PRIOR FILING DATE: 1998-07-20
; PRIOR APPLICATION NUMBER: US 60/094,651
; PRIOR FILING DATE: 1998-07-30

Query Match 100.0%; Score 81; DB 21; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLOGKGGGPPPK 14
DB 104 KKLOGKGGGPPPK 117

RESULT 13
US-09-746-783-146
; Sequence 146, Application US/09746783
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; McCoy, John M.
; Lavallie, Edward R.
; Racie, Lisa A.
; Treacy, Maurice
; Spaulding, Vikki
; Agostino, Michael J.
; Howes, Steven H.
; Fechtel, Kim
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:

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;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/746,783
;; FILING DATE: 21-Dec-2000
;; CLASSIFICATION: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Milasincic, Debra J.
;; REGISTRATION NUMBER: 46,931
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 227-7400
;; TELEFAX: (617) 742-4214
;; INFORMATION FOR SEQ ID NO: 146:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 185 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 146:
US-09-746-783-146

Query Match 100.0%; Score 81; DB 21; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KKLOGKGGGPPPK 14
|||||
Db 104 KKLOGKGGGPPPK 117

RESULT 14
US-09-821-726-13
; Sequence 13, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-821-726-13

Query Match 100.0%; Score 81; DB 22; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KKLOGKGGGPPPK 14
|||||
Db 104 KKLOGKGGGPPPK 117

RESULT 15
US-09-821-726-18
; Sequence 18, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS

;; FILE REFERENCE: 21459/90913
;; CURRENT APPLICATION NUMBER: US/09/821,726
;; CURRENT FILING DATE: 2001-03-29
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 18
;; LENGTH: 185
;; TYPE: PRT
;; ORGANISM: Porcine sp.
US-09-821-726-18

Query Match 100.0%; Score 81; DB 22; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KKLOGKGGGPPPK 14
|||||
Db 104 KKLOGKGGGPPPK 117

Search completed: September 4, 2002, 16:59:20
Job time: 1041 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 17:04:23 ; Search time 166.13 Seconds
(without alignments)
20.726 Million cell updates/sec

Title: us-09-821-726-3

Perfect score: 81

Sequence: 1 KKLQKGPGGPPPK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 763338 seqs, 245939087 residues

Total number of hits satisfying chosen parameters: 763338

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA_New: *
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	185	5	US-09-991-150-211
2	81	100.0	185	5	US-09-720-533-49
3	81	100.0	185	6	US-10-119-480-148
4	81	100.0	185	6	US-10-216-159A-148
5	81	100.0	185	6	US-10-216-162-148
6	81	100.0	185	6	US-10-216-163-148
7	81	100.0	185	6	US-10-216-164-148
8	81	100.0	185	6	US-10-216-165-148
9	81	100.0	185	6	US-10-216-166-148
10	81	100.0	185	6	US-10-216-167-148
11	81	100.0	185	6	US-10-216-168-148
12	81	100.0	185	6	US-10-216-160-148
13	81	100.0	185	6	US-10-218-949-148
14	81	100.0	185	6	US-10-218-930-148
15	81	100.0	185	6	US-10-219-003-148
16	81	100.0	185	6	US-10-218-612-148
17	81	100.0	185	6	US-10-218-956-148
18	81	100.0	185	6	US-10-219-010-148
19	81	100.0	185	6	US-10-218-765-148
20	81	100.0	185	6	US-10-218-784-148
21	81	100.0	185	6	US-10-219-061-148
22	81	100.0	185	6	US-10-219-062-148
23	81	100.0	185	6	US-10-219-063-148
24	81	100.0	185	6	US-10-219-064-148
25	81	100.0	185	6	US-10-219-065-148
26	81	100.0	185	6	US-10-219-066-148

27 81 100.0 185 6 US-10-219-070-148 Sequence 148, App
28 81 100.0 185 6 US-10-219-071-148 Sequence 148, App
29 81 100.0 185 6 US-10-219-072-148 Sequence 148, App
30 81 100.0 185 6 US-10-219-073-148 Sequence 148, App
31 81 100.0 185 6 US-10-219-074-148 Sequence 148, App
32 81 100.0 185 6 US-10-219-075-148 Sequence 148, App
33 81 100.0 185 6 US-10-219-077-148 Sequence 148, App
34 81 100.0 185 6 US-10-219-464-148 Sequence 148, App
35 81 100.0 185 6 US-10-219-465-148 Sequence 148, App
36 81 100.0 185 6 US-10-219-466-148 Sequence 148, App
37 81 100.0 185 6 US-10-219-470-148 Sequence 148, App
38 81 100.0 185 6 US-10-219-471-148 Sequence 148, App
39 81 100.0 185 6 US-10-219-474-148 Sequence 148, App
40 81 100.0 185 6 US-10-219-475-148 Sequence 148, App
41 81 100.0 185 6 US-10-219-476-148 Sequence 148, App
42 81 100.0 185 6 US-10-219-478-148 Sequence 148, App
43 81 100.0 185 6 US-10-219-479-148 Sequence 148, App
44 81 100.0 185 6 US-10-219-480-148 Sequence 148, App
45 81 100.0 185 6 US-10-219-480-148 Sequence 148, App

ALIGNMENTS

RESULT 1

US-09-991-150-211

; Sequence 211, Application US/09991150

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zewin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730PIC48

; CURRENT APPLICATION NUMBER: US/09/991,150

; CURRENT FILING DATE: 2001-11-16

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 532

; SEQ ID NO 211

; LENGTH: 185

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-991-150-211

Query Match 100.0%; Score 81; DB 5; Length 185;

Best Local Similarity 100.0%; Pred. NO. 0.0031;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQKGPGGPPPK 14

DB 104 KKLQKGPGGPPPK 117

RESULT 2
US-09-720-533-49
; Sequence 49, Application US/09720533
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: LAL, Preeti
; APPLICANT: TANG, Y. Tom
; APPLICANT: GORGONE, Gina A.
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AKERBLOM, Ingrid E.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: YUE, Henry
; APPLICANT: PATTERSON, Chandra
; APPLICANT: REDDY, Roopa
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: BANDMAN, Olga
; TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
; FILE REFERENCE: PF-0541 PCT
; CURRENT APPLICATION NUMBER: US/09/720,533
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/090,762; 60/094,983; 60/102,686; 60/112,129
; PRIOR FILING DATE: 1998-06-26; 1998-07-31; 1998-10-01; 1998-12-11
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PERL Program
; SEQ ID NO 49
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte Clone No: 2593853
US-09-720-533-49

Query Match 100.0%; Score 81; DB 5; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLOGKGGGPPPK 14
|||||
Db 104 KKLOGKGGGPPPK 117

RESULT 3
US-10-119-480-148
; Sequence 148, Application US/10119480
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C1
; CURRENT APPLICATION NUMBER: US/10/119,480
; CURRENT FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 246
; Remaining Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-119-480-148

Query Match 100.0%; Score 81; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLOGKGGGPPPK 14
|||||
Db 104 KKLOGKGGGPPPK 117

RESULT 4
US-10-216-159A-148
; Sequence 148, Application US/10216159A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C6
; CURRENT APPLICATION NUMBER: US/10/216,159A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-159A-148

Query Match 100.0%; Score 81; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLOGKGGGPPPK 14
|||||
Db 104 KKLOGKGGGPPPK 117

RESULT 5
US-10-216-162-148
; Sequence 148, Application US/10216162
; GENERAL INFORMATION:

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; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC2
; CURRENT APPLICATION NUMBER: US/10/216,162
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC5
; CURRENT APPLICATION NUMBER: US/10/216,164
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-162-148

Query Match 100.0%; Score 81; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQKGGGPPPK 14
| | | | | | | | | | | | | | | |
Db 104 KKLQKGGGPPPK 117

RESULT 6
US-10-216-163-148
; Sequence 148, Application US/10216163
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC3
; CURRENT APPLICATION NUMBER: US/10/216,163

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; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-163-148

Query Match 100.0%; Score 81; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQKGGGPPPK 14
| | | | | | | | | | | | | | | |
Db 104 KKLQKGGGPPPK 117

RESULT 7
US-10-216-164-148
; Sequence 148, Application US/10216164
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC5
; CURRENT APPLICATION NUMBER: US/10/216,164
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20

```


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```

; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C4
; CURRENT APPLICATION NUMBER: US/10/216,167
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-167-148

Query Match 100.0%; Score 81; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 KKLQKGPGGPPK 14
Db 104 KKLQKGPGGPPK 117

RESULT 12
US-10-216-160-148
; Sequence 148, Application US/10216160
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C8
; CURRENT APPLICATION NUMBER: US/10/216,160
; CURRENT FILING DATE: 2002-08-09
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-160-148

Query Match 100.0%; Score 81; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 KKLQKGPGGPPK 14
Db 104 KKLQKGPGGPPK 117

RESULT 11
US-10-216-168-148
; Sequence 148, Application US/10216168
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C10
; CURRENT APPLICATION NUMBER: US/10/216,168
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480

```

RESULT 13
 US-10-218-849-148
 ; Sequence 148, Application US/10218849
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530P1C11
 ; CURRENT APPLICATION NUMBER: US/10/218,849
 ; CURRENT FILING DATE: 2002-08-12
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 148
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-218-849-148

Query Match 100.0%; Score 81; DB 6; Length 185;
 Best Local Similarity 100.0%; Pred. No. 0.0031;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLOGKGGGPPPK 14
 |||||

Db 104 KKLOGKGGGPPPK 117

RESULT 14
 US-10-218-930-148
 ; Sequence 148, Application US/10218930
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530P1C13
 ; CURRENT APPLICATION NUMBER: US/10/218,930
 ; CURRENT FILING DATE: 2002-08-12
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 148
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-218-930-148

Query Match 100.0%; Score 81; DB 6; Length 185;
 Best Local Similarity 100.0%; Pred. No. 0.0031;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLOGKGGGPPPK 14
 |||||

Db 104 KKLOGKGGGPPPK 117

RESULT 15
 US-10-219-003-148
 ; Sequence 148, Application US/10219003
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530P1C12
 ; CURRENT APPLICATION NUMBER: US/10/219,003
 ; CURRENT FILING DATE: 2002-08-12
 ; Prior Application Number: 10/119,480
 ; Prior Filing Date: 2002-04-09
 ; Prior Application Number: 60/059113
 ; Prior Filing Date: 1997-09-17
 ; Prior Application Number: 60/062287
 ; Prior Filing Date: 1997-10-17
 ; Prior Application Number: 60/063549
 ; Prior Filing Date: 1997-10-28
 ; Prior Application Number: 60/064103
 ; Prior Filing Date: 1997-10-31
 ; Prior Application Number: 60/069873
 ; Prior Filing Date: 1997-12-17
 ; Prior Application Number: 60/078910
 ; Prior Filing Date: 1998-03-20
 ; Prior Application Number: 60/079294
 ; Prior Filing Date: 1998-03-25
 ; Prior Application Number: 60/079656
 ; Prior Filing Date: 1998-03-26
 ; Prior Application Number: 60/079728
 ; Prior Filing Date: 1998-03-27
 ; Prior Application Number: 60/081819
 ; Prior Filing Date: 1998-04-15
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 ; Prior Application Number: 60/086392
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 ; Prior Filing Date: 1998-06-24
 ; Prior Application Number: 60/090691
 ; Prior Filing Date: 1998-06-25
 ; Prior Application Number: 60/090695
 ; Prior Filing Date: 1998-06-25

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PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/095302
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095318
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095916
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/096146
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PRIOR APPLICATION NUMBER: 60/099811
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099816
PRIOR FILING DATE: 1998-09-10
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PRIOR APPLICATION NUMBER: 60/101477
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PRIOR APPLICATION NUMBER: 60/101738
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PRIOR APPLICATION NUMBER: 60/101741
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101786
PRIOR FILING DATE: 1998-09-25
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PRIOR FILING DATE: 1998-11-17
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PRIOR APPLICATION NUMBER: 60/115558
PRIOR FILING DATE: 1999-01-12
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PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115733
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119549
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/123618
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/125259
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 60/125775
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PRIOR APPLICATION NUMBER: 60/131445
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PRIOR FILING DATE: 1999-05-14
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PRIOR APPLICATION NUMBER: 60/140723
PRIOR FILING DATE: 1999-06-22
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PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
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PRIOR FILING DATE: 1999-08-17
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PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/164418
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: 60/166361
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PRIOR APPLICATION NUMBER: 60/169445
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835
PRIOR FILING DATE: 1999-12-07

Query Match 100.0%; Score 81; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLOGKFGGPPK 14
Db 104 KKLOGKFGGPPK 117

Search completed: September 4, 2002, 17:04:23

Thu Sep 5 11:23:37 2002

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Page 8

Job time: 1154 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2002, 16:47:30 : Search time 75.48 Seconds
(without alignments)
17.823 Million cell updates/sec

Title: US-09-821-726-3

Perfect score: 81

Sequence: 1 KKLQKGGGPPPK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_71: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	74.1	1677	T14267	Xin protein, stage
2	50	61.7	673	BVEUCB	excinuclease ABC c
3	50	61.7	673	A93736	excision nuclease
4	50	61.7	673	B85586	DNA repair, excisi
5	50	61.7	673	AD0597	excision nuclease
6	47	58.0	22	C42856	hypothetical prote
7	47	58.0	669	D82739	excinuclease ABC s
8	46	56.8	377	E87022	probable conserved
9	46	56.8	426	A39695	transforming prote
10	46	56.8	551	S57447	HPBR11-7 protein -
11	46	56.8	561	T16148	hypothetical prote
12	46	56.8	830	T18860	hypothetical prote
13	46	56.8	1105	S40243	DNA-directed DNA p
14	46	56.8	1315	T32734	myosin-IA - Acanth
15	46	56.8	1357	T29265	hypothetical prote
16	45.5	56.2	579	D72092	conserved hypotet
17	45.5	56.2	579	C86532	CT082 hypotet
18	45	55.6	171	H96833	hypothetical prote
19	45	55.6	477	TVMVCS	protein-tyrosine k
20	45	55.6	609	TVMVGC	protein-tyrosine k
21	45	55.6	820	TVCTFF	protein-tyrosine k
22	45	55.6	822	TVHUFF	protein-tyrosine k
23	45	55.6	2715	T13049	eyelid - fruit fly
24	44	54.3	142	D32880	hypothetical prote
25	44	54.3	149	T31446	plastoquinol--plas
26	44	54.3	182	B86462	hypothetical prote
27	44	54.3	218	TVHURR	transforming prote
28	44	54.3	230	I56979	nitric-oxide synth
29	44	54.3	347	E97487	hypothetical prote

30	44	54.3	347	2	AF2705	ABC transporter, s
31	44	54.3	558	2	B81711	conserved hypotet
32	44	54.3	560	2	D71560	hypothetical prote
33	44	54.3	593	2	T43323	cell division cycl
34	44	54.3	670	2	A83255	excinuclease ABC s
35	44	54.3	706	2	D97303	ABC-type multidrug
36	44	54.3	996	2	A71080	hypothetical prote
37	44	54.3	1202	2	S71424	nitric-oxide synth
38	44	54.3	1203	1	A47501	nitric-oxide synth
39	44	54.3	1205	1	A38943	nitric-oxide synth
40	44	54.3	1464	2	S59856	collagen alpha 1(I
41	43.5	53.7	1049	1	CGBO7S	collagen alpha 1(I
42	43	53.1	140	2	S46351	vpx protein - simi
43	43	53.1	189	2	A86369	hypothetical prote
44	43	53.1	221	2	G72665	hypothetical prote
45	43	53.1	224	2	B72710	hypothetical prote

ALIGNMENTS

RESULT 1

T14267

Xin protein, stage early embryo - mouse

C:Species: Mus musculus (house mouse)

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T14267

R:Wang, D.Z.; Lin, J.J.C.

submitted to the EMBL Data Library, March 1998

A:Description: Involvement of a novel gene, Xin, in cardiac looping.

A:Reference number: Z17948

A:Accession: T14267

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-1677 <WAN>

A:Cross-references: EMBL:AF051945; NID:g2970645; PID:g2970645; PIDN:AAC06023.1

A:Experimental source: cardiac muscle; stage early embryo

Query Match 74.1%; Score 60; DB 2; Length 1677;

Best Local Similarity 81.8%; Pred. No. 1.9;

Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 4 QKGGGPPPK 14

Db 574 EGKGGPPPE 584

RESULT 2

BVEUCB

excinuclease ABC chain B - Escherichia coli

N:Alternate names: uvrB protein

N:Contains: excision endonuclease ABC (EC 3.1.-.-) chain B

C:Species: Escherichia coli

C>Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 19-Jan-2001

C:Accession: A93612; C64814; A23765; A24939

R:Backendorf, C.; Spink, H.; Barbeiro, A.P.; van de Putte, P.

Nucleic Acids Res. 14, 2877-2890, 1986

A:Title: Structure of the uvrB gene of Escherichia coli. Homology with other DNA repa

A:Reference number: A93613; MUID:86176773

A:Accession: A93613

A:Molecule type: DNA

A:Residues: 1-673 <BAC>

A:Cross-references: GB:X03722; NID:g43285; PIDN:CAA27357.1; PID:g43286

R:Arikan, E.; Kulkarni, M.S.; Thomas, D.C.; Sancar, A.

Nucleic Acids Res. 14, 2637-2650, 1986

A:Title: Sequences of the E. coli uvrB gene and protein.

A:Reference number: A93612; MUID:86176755

A:Accession: A93612

A:Molecule type: DNA

A:Residues: 1-476, 'R', 478-673 <ARI>

A:Cross-references: GB:X03678; GB:J01722; GB:J01723; GB:M24329; GB:V00374; GB:V00375;

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of *Escherichia coli* K-12.

A:Reference number: A64720; MUID:97426617

A:Accession: C64814

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-673 <BLAT>

A:CROSS-references: GB:AB000180; GB:U00096; NID:g1786988; PIDN:AAC73866.1; PID:g1786996;

A:Experimental source: strain K-12, substrain MG1655

C:Comment: uvrA, uvrB, and uvrC function together as excision nuclease.

C:Genetics:

A:Gene: uvrB

A:Map position: 18 min

C:Function:

A:Description: stimulates the ATPase activity of uvrA protein in the presence of UV-irradiation

C:Superfamily: excinuclease ABC chain B

C:Keywords: ATP; DNA repair; hydrolase; nucleotide binding; P-loop

F:39-46/Region: nucleotide-binding motif A (P-loop)

F:334-339/Region: nucleotide-binding motif B

F:338-341/Region: DEXH motif

Query Match 61.7%; Score 50; DB 1; Length 673;

Best Local Similarity 72.7%; Pred. No. 19;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LOGKGGGPPPP 13

| : : : : |

Db 313 LSGRGGGPPPP 323

RESULT 3

A99736

excision nuclease subunit B [imported] - *Escherichia coli* (strain O157:H7, substrain RIM)

C:Species: *Escherichia coli*

C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001

C:Accession: A99736

R:Hayashi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genomic islands

A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: A99736

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-673 <HAY>

A:CROSS-references: GB:BA000007; PIDN:BA034280.1; PID:g13360316; GSPDB:GN00154

A:Experimental source: strain O157:H7, substrain RIMD 050952

C:Genetics:

A:Gene: EC0857

C:Superfamily: excinuclease ABC chain B

Query Match 61.7%; Score 50; DB 2; Length 673;

Best Local Similarity 72.7%; Pred. No. 19;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LOGKGGGPPPP 13

| : : : : |

Db 313 LSGRGGGPPPP 323

RESULT 4

B85586

DNA repair, excision nuclease subunit B [imported] - *Escherichia coli* (strain O157:H7, s

C:Species: *Escherichia coli*

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C:Accession: B85586

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grothbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: B85586

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-673 <STO>

A:CROSS-references: GB:AE005174; NID:g12513768; PIDN:AAG55150.1; GSPDB:GN00145; UWGP:

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: uvrB

C:Superfamily: excinuclease ABC chain B

Query Match 61.7%; Score 50; DB 2; Length 673;

Best Local Similarity 72.7%; Pred. No. 19;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LOGKGGGPPPP 13

| : : : : |

Db 313 LSGRGGGPPPP 323

RESULT 5

AD0597

excision nuclease ABC chain B STY0831 [imported] - *Salmonella enterica* subsp. enteric

C:Species: *Salmonella enterica* subsp. enterica serovar Typhi

A:Note: this species has also been called *Salmonella typhi*

C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001

C:Accession: AD0597

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church

th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr

, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,

A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* se

A:Reference number: AB0502; PMID:11677608

A:Accession: AD0597

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-673 <PAR>

A:CROSS-references: GB:AL513382; PIDN:CAD05246.1; PID:g16502016; GSPDB:GN00176

C:Genetics:

A:Gene: STY0831

C:Superfamily: excinuclease ABC chain B

Query Match 61.7%; Score 50; DB 2; Length 673;

Best Local Similarity 72.7%; Pred. No. 19;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LOGKGGGPPPP 13

| : : : : |

Db 313 LSGRGGGPPPP 323

RESULT 6

C42856

hypothetical protein 3 EPF-region [Imported] - human (fragment)

C:Species: *Homo sapiens* (man)

C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000

C:Accession: C42856

R:Li, Z.; Diaz, L.A.; Haas, A.L.; Giudice, G.J.

J. Biol. Chem. 267, 15829-15835, 1992

A:Title: cDNA cloning of a novel human ubiquitin carrier protein. An antigenic domain

this human epidermal transcript.

A:Reference number: A42856; MUID:92348449

A:Accession: C42856

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-22 <LIU>

A:Experimental source: keratinocyte

A:Note: sequence extracted from NCBI backbone (NCBI:109895, NCBI:109899)

Thu' Sep 5 11:23:37 2002

Query Match 58.0%; Score 47; DB 2; Length 22;
Best Local Similarity 66.7%; Pred. No. 1.9;
Matches 8; Conservative 1; Mismatches 0; Gaps 0;
Qy 2 KLOGKGGPGPPP 13
I :||||| I
Db 6 KNAGRGPGGPAP 17

RESULT 7
D82739
excinuclease ABC subunit B XF0967 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000
C:Accession: D82739
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: D82739
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-669 <STM>
A:Cross-references: GB:AE003935; GB:AE003849; NID:g9105894; PIDN:AAF83777.1; GSPDB:GN001
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, P
as-Nelo, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranee, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshakho, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF0967
C:Superfamily: excinuclease ABC chain B

Query Match 58.0%; Score 47; DB 2; Length 669;
Best Local Similarity 61.5%; Pred. No. 50;
Matches 8; Conservative 1; Mismatches 0; Gaps 0;
Qy 1 KLOGKGGPGPPP 13
: ||| ||| |||
Db 311 RHLTGKAPGEP 323

RESULT 8
E87022
probable conserved membrane protein ML0907 [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: E87022
R:Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S
A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: E87022
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <STO>
A:Cross-references: GB:AL450380; NID:g13092977; PIDN:CAC31288.1; GSPDB:GN00147
C:Genetics:

A:Gene: ML0907

Query Match 56.8%; Score 46; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 GPGGPPP 13
|||||
Db 254 GPGGPPP 260

RESULT 9
A39695
transforming protein (N-myc) - common canary
C:Species: Serinus canaria (common canary)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 28-Feb-1997
C:Accession: A39695
R:Collum, R.G.; Clayton, D.F.; Alt, F.W.
Mol. Cell. Biol. 11, 1770-1776, 1991
A:Title: Structure and expression of canary myc family genes.
A:Reference number: A39695; MUID:91141534
A:Accession: A39695
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-426 <COL>
A:Cross-references: GB:M64251; GB:M64598
C:Superfamily: myc transforming protein; myc transforming protein homology
C:Keywords: DNA binding; leucine zipper; nucleus; phosphoprotein
F:11-426/Domain: myc transforming protein homology <MYC>
F:395-423/Region: leucine zipper motif

Query Match 56.8%; Score 46; DB 2; Length 426;
Best Local Similarity 61.5%; Pred. No. 45;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 1 KKLOGKGGPGPPP 13
: ||| ||| |||
Db 144 EKLNKTPAAPPP 156

RESULT 10
S57447
HPBRII-7 protein - human
N:Alternate names: HPBRII-4 protein
C:Species: Homo sapiens (man)
C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 24-Sep-1999
C:Accession: S57447; S57489
R:Fleischhauer, K.L.
submitted to the EMBL Data Library, June 1992
A:Reference number: S57447
A:Accession: S57447
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-351 <FLE>
A:Cross-references: EMBL:X67336; NID:g871300; PIDN:CAA47751.1; PID:g871301
A:Accession: S57489
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-551 <FL2>
A:Cross-references: EMBL:X67337; NID:g871298; PIDN:CAA47752.1; PID:g871299
C:Genetics:
A:Introns: 231/3
C:Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleopro
F:82-151/Domain: ribonucleoprotein repeat homology <RRM4>

Query Match 56.8%; Score 46; DB 2; Length 551;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 GPGGPPP 13

Db 222 GPGGPPP 228
|||||||

RESULT 11

T16148 hypothetical protein F25B5.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T16148

R:Taich, A.

submitted to the EMBL Data Library, March 1995

A:Description: The sequence of C. elegans cosmid F25B5.

A:Reference number: Z18458

A:Accession: T16148

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-561 <TAI>

A:Cross-references: EMBL:U23172; NID:q726388; PID:g726394; PIDN:AAC46528.1; CESP:F25B5.7

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:F25B5.7

A:Introns: 39/2; 157/3; 258/2; 290/2; 356/1; 531/1

Query Match 56.8%; Score 46; DB 2; Length 561;
Best Local Similarity 100.0%; Pred. No. 58;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GPGGPPP 13

|||||||

Db 409 GPGGPPP 415

RESULT 12

T18860

hypothetical protein C02C6.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C:Accession: T18860

R:Swinburne, J.

submitted to the EMBL Data Library, August 1996

A:Reference number: Z19032

A:Accession: T18860

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-830 <WIL>

A:Cross-references: EMBL:Z79596; PIDN:CAB01857.1; GSPDB:GN000028; CESP:C02C6.1

A:Experimental source: clone C02C6

C:Genetics:

A:Gene: CESP:C02C6.1

A:Map position: X

A:Introns: 56/2; 131/1; 333/2; 501/2; 593/2; 686/3; 815/2

C:Superfamily: human dynamin II; pleckstrin repeat homology

Query Match 56.8%; Score 46; DB 2; Length 830;
Best Local Similarity 100.0%; Pred. No. 84;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GPGGPPP 13

|||||||

Db 818 GPGGPPP 824

RESULT 13

S40243

DNA-directed DNA polymerase (EC 2.7.7.7) delta chain - mouse

C:Species: Mus musculus (house mouse)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S40243; JT0670

R:Cullmann, G.; Hindges, R.; Berchtold, M.W.; Huebscher, U.

submitted to the EMBL Data Library, March 1993

A:Reference number: S40243

A:Accession: S40243

A:Molecule type: mRNA

A:Residues: 1-1105 <CUL>

A:Cross-references: EMBL:Z21848; NID:q438133; PIDN:CAA79895.1; PID:g438134

R:Cullmann, G.; Hindges, R.; Berchtold, M.W.; Huebscher, U.

Gene 134, 191-200, 1993

A:Title: Cloning of a mouse cDNA encoding DNA polymerase delta: refinement of the hom

A:Reference number: JT0670; MUID:94085777

A:Accession: JT0670

A:Molecule type: DNA

A:Residues: 1-1111, 'G', 113, 'P', 115-1034, 'Y', 1036-1105 <CU2>

A:Cross-references: EMBL:Z21848

A>Note: the sequence translated from Z21848 is inconsistent with that from this sequ

C:Comment: Three DNA polymerases alpha, delta and epsilon chains are essential. This

C:Genetics:

A:Gene: poldelta

C:Superfamily: herpesvirus DNA-directed DNA polymerase

C:Keywords: DNA replication; heterodimer; nucleotidyltransferase

Query Match 56.8%; Score 46; DB 1; Length 1105;
Best Local Similarity 57.1%; Pred. No. 1.1e+02;

Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KKLOGKGGGPPPK 14

|||||||

Db 4 KRRQGGPGVPPKR 17

RESULT 14

T32734

myosin-IA - Acanthamoeba castellanii

C:Species: Acanthamoeba castellanii

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 08-Sep-2000

C:Accession: T32734

R:Lee, W.L.; Ostap, E.M.; Zot, H.G.; Pollard, T.D.

submitted to the EMBL Data Library, August 1998

A:Description: Hydrodynamic and ligand binding properties of Acanthamoeba myosin-IA G

A:Reference number: Z21216

A:Accession: T32734

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-1215 <LEE>

A:Cross-references: EMBL:AF085185; NID:g3599477; PID:g3599478; PIDN:AAC35357.1

A:Experimental source: strain Neff

C:Genetics:

A:Gene: MIA

A:Introns: 1/3; 41/3; 72/2; 103/2; 162/3; 184/1; 217/1; 296/1; 340/3; 390/3; 447/3; 5

C:Superfamily: protozoan myosin heavy chain IB; myosin motor domain homology; SH3 hom

F:14-674/Domain: myosin motor domain homology <MMO>

Query Match

Best Local Similarity 56.8%; Score 46; DB 2; Length 1215;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GPGGPPP 13

|||||||

Db 1075 GPGGPPP 1081

RESULT 15

T29265

hypothetical protein C01G8.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T29265

R:Du, Z.; Gattung, S.

submitted to the EMBL Data Library, November 1996

A:Description: The sequence of C. elegans cosmid C01G8.

A:Reference number: Z20597

A:Accession: T29265

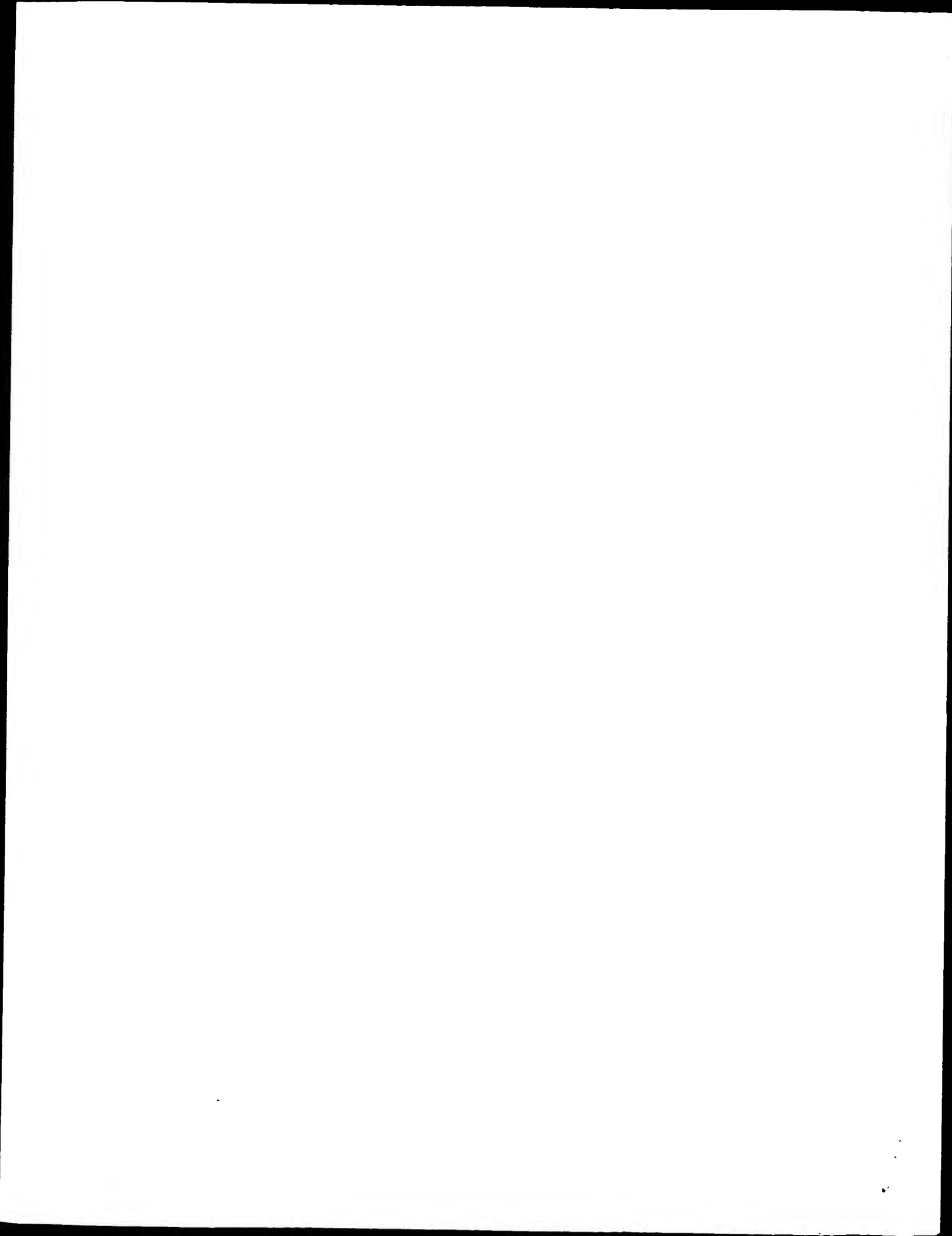
Thu Sep 5 11:23:37 2002

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1357 <DUZ>
A;Cross-references: EMBL:U80439; PIDN:AAB37645.1; GSPDB:GN00019; CESP:C01G8.7
A;Experimental source: strain Bristol N2; clone C01G8
C;Genetics:
A;Gene: CESP:C01G8.7
A;Map position: 1
A;Introns: 89/1; 488/1; 701/3; 1056/2; 1159/3; 1197/1; 1312/3

Query Match 56.8%; Score 46; DB 2; Length 1357;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 GPGGPPP 13
|||||
Db 153 GPGGPPP 159

Search completed: September 4, 2002, 16:47:31
Job time: 367 sec



Thú Sep 5 11:23:38 2002

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 17:05:04 ; Search time 34.18 Seconds
(without alignments)
15.859 Million cell updates/sec

Title: US-09-821-726-3

Perfect score: 81

Sequence: 1 KKLQKGGPGPPPK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	81	100.0	199	1 C11P_HUMAN	Q9ns71 homo sapien
2	59	72.8	184	1 C11P_MOUSE	Q9cr36 mus musculu
3	50	61.7	673	1 UVRB_ECOLI	P07025 escherichia
4	48	59.3	532	1 CG48_HUMAN	Q9y5j1 homo sapien
5	46	56.8	427	1 MYCN_SERCA	P26014 serinus can
6	46	56.8	830	1 DYNL_CAEEL	P39055 caenorhabdi
7	46	56.8	1103	1 DPOD_MESAU	P97283 mesocricetu
8	46	56.8	1105	1 DPOD_MOUSE	P52431 mus musculu
9	45	55.6	402	1 GUN1_HUMAN	P56680 humicola in
10	45	55.6	477	1 PES_FSVST	P00543 feline sarc
11	45	55.6	609	1 PES_FELCA	P00542 feline sarc
12	45	55.6	820	1 PES_HUMAN	P14238 felis silve
13	44	54.3	142	1 YPUB_KLEPN	P20732 homo sapien
14	44	54.3	218	1 RRAS_HUMAN	P20775 klebsiella
15	44	54.3	593	1 CC23_SCHPO	P10301 homo sapien
16	44	54.3	670	1 UVRB_PSEAE	P72174 pseudomonas
17	44	54.3	919	1 NOS3_RAT	Q62600 rattus norv
18	44	54.3	1048	1 AGO1_ARATH	Q04379 arabidopsis
19	44	54.3	1201	1 NOS3_MOUSE	P70313 mus musculu
20	44	54.3	1202	1 NOS3_HUMAN	P29474 homo sapien
21	44	54.3	1204	1 NOS3_BOVIN	P29473 bos taurus
22	44	54.3	1204	1 NOS3_PIG	Q28967 sus scrofa
23	44	54.3	1464	1 CA13_MOUSE	P08121 mus musculu
24	44	54.3	1049	1 CA13_BOVIN	P04258 bos taurus
25	43.5	53.7	233	1 HB2A_RAT	P06341 rattus norv
26	43	53.1	252	1 CRH1_BOVIN	P06341 rattus norv
27	43	53.1	252	1 HB2F_MOUSE	P06346 mus musculu
28	43	53.1	263	1 HB2B_MOUSE	P29826 rattus norv
29	43	53.1	263	1 HB2K_MOUSE	P06343 mus musculu
30	43	53.1	263	1 HB2S_MOUSE	P06344 mus musculu
31	43	53.1	263	1 HB2U_MOUSE	P14483 mus musculu
32	43	53.1	263	1 HB2A_MOUSE	
33	43	53.1	263	1 HB2A_MOUSE	

34 43 53.1 265 1 HB2D_MOUSE
35 43 53.1 265 1 HB2Q_MOUSE
36 43 53.1 268 1 HB2X_HUMAN
37 43 53.1 360 1 OC3A_HUMAN
38 43 53.1 379 1 Y671_CHIMU
39 43 53.1 423 1 TBX2_CAEEL
40 43 53.1 736 1 DVL2_MOUSE
41 43 53.1 860 1 ELS_MOUSE
42 43 53.1 864 1 ELS_RAT
43 43 53.1 886 1 SM6B_MOUSE
44 43 53.1 887 1 SM6B_RAT
45 43 53.1 994 1 CLC1_MOUSE

ALIGNMENTS

RESULT 1
C11P_HUMAN
ID C11P_HUMAN STANDARD; PRT: 199 AA.
AC O9NS71.
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Call protein.
DE Call protein.
GN CALL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RX MEDLINE=20296773; PubMed=10835488;
RA Yoshikawa Y., Mukai H., Hino F., Asada K., Kato I.;
RT "Isolation of two novel genes, down-regulated in gastric cancer."
RL Jpn. J. Cancer Res. 91:459-463(2000).
CC -I- TISSUE SPECIFICITY: Expressed in stomach. No expression is
CC detected in cancer tissue or gastric cancer cell lines.
CC
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CC
CC EMBL: AB039886; BAA92433.1; -.
DR MTM: 606402; -.
DR SEQUENCE 199 AA; 21999 MW; C099B8B9A1338D7A CRC64;
SO
Query Match 100.0%; Score 81; DB 1; Length 199;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLQKGGPGPPPK 14
Db 118 KKLQKGGPGPPPK 131
RESULT 2
C11P_MOUSE
ID C11P_MOUSE STANDARD; PRT: 184 AA.
AC Q9CR36; Q9D7K7; Q9CFZ5;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Call protein homolog.
GN CALL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Stomach, and Tongue;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyushaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
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 DR EMBL; AK008990; BAB26010.1; -
 DR EMBL; AK008622; BAB25784.1; -
 DR EMBL; AK008641; BAB25801.1; -
 DR EMBL; AK008647; BAB25805.1; -
 DR EMBL; AK008672; BAB25856.1; -
 DR EMBL; AK008745; BAB25872.1; -
 DR EMBL; AK008933; BAB25975.1; -
 DR EMBL; AK008956; BAB25988.1; -
 DR EMBL; AK009145; BAB26103.1; -
 DR EMBL; AK019050; BAB31525.1; -
 FT CONFLICT 113 113 P -> L (IN REF. 1: BAB26103).
 SQ SEQUENCE 184 AA; 20134 MW; 288982F0404FFA8B CRC64;
 Query Match 72.8%; Score 59; DB 1; Length 184;
 Best Local Similarity 71.4%; Pred. No. 0.18;
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KRLOGKGGGPPPK 14
 Db 102 KEQKGGGPPPK 115
 I: :|||||
 RESULT 3
 ID UVRB_ECOLI STANDARD; PRT; 673 AA.
 AC P07025;
 DT 01-APR-1998 (Rel. 07, Created)
 DT 01-APR-1998 (Rel. 07, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Exonuclease ABC subunit B.
 GN UVRB OR B0779 OR Z0998 OR ECS0857.
 OS Escherichia coli, and
 OS Escherichia coli, O157:H7.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia
 OX NCBI_TaxID=562, 83334;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=86176773; PubMed=3008099;
 RA Backendorf C., Spaik H., Barbeiro A.P., van de Putte P.;
 RT "Structure of the uvrB gene of Escherichia coli. Homology with other
 RL DNA repair enzymes and characterization of the uvrB5 mutation.";
 RN Nucleic Acids Res. 14:2877-2890(1986).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86176755; PubMed=3515321;
 RA Arkan E., Kulkarni M.S., Thomas D.C., Sancar A.;
 RT "Sequences of the E. coli uvrB gene and protein.";
 RL Nucleic Acids Res. 14:2637-2650(1986).
 [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=K12 / MG1655;
 MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:12453-1474(1997).
 [4]
 RP SEQUENCE FROM N.A.
 RX STRAIN=O157:H7 / EDL933 / ATCC 700927;
 MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Postell G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamocis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
 RL Nature 409:529-533(2001).
 [5]
 RP SEQUENCE FROM N.A.
 RX STRAIN=O157:H7 / RIMD 0509952;
 MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
 RL O157:H7 and genomic comparison with a laboratory strain K-12.";
 RN DNA Res. 8:11-22(2001).
 [6]
 RP SEQUENCE OF 168-673 FROM N.A.
 RX STRAIN=K12;
 MEDLINE=97061202; PubMed=8905232;
 RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K.,
 RA Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S.,
 RA Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y.,
 RA Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H.,
 RA Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
 RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
 RL corresponding to the 12.7-28.0 min region on the linkage map.";
 RN DNA Res. 3:137-155(1996).
 [7]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 619-673.
 MEDLINE=20123894; PubMed=10631326;
 RA Sohi M., Alexandrovich A., Moolenaar G., Visse R., Goosen N.,
 RA Vernede X., Fontecilla-Camps J.C., Champness J., Sanderson M.R.;
 RT "Crystal structure of Escherichia coli UvrB C-terminal domain, and a
 RL model for UvrB-uvrC interaction.";
 RN FEBS Lett. 465:161-164(2000).
 [8]
 RP STRUCTURE BY NMR OF 619-673
 MEDLINE=99257571; PubMed=10371161;
 RA Alexandrovich A., Sanderson M.R., Moolenaar G.F., Goosen N.,
 RA Lane A.N.;
 RT "NMR assignments and secondary structure of the UvrC binding domain of
 RN UvrB.";

```

[2]
SEQUENCE OF 138-532 FROM N.A.
Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,
Margolin J.F.:
Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
-1- SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).
-1- SIMILARITY: BELONGS TO THE CGT-48 FAMILY OF WD-REPEAT PROTEINS.
-----
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or send an email to license@isb-sib.ch).
-----
EMBL: AF151806; AAD34043.1; -.
EMBL: AY007138; AAG01999.1; ALT_INIT.
InterPro: IPR001680; WD40.
Pfam: PF00400; WD40; 4.
SMART: SM00320; WD40; 3.
PROSITE: PS00678; WD_REPEATS.1; 1.
PROSITE: PS50082; WD_REPEATS.2; 1.
PROSITE: PS50294; WD_REPEATS_REGION; 1.
DR Hypothetical protein; Repeat; WD repeat.
KW REPEAT 225 264 WD 1.
FT REPEAT 269 309 WD 2.
FT REPEAT 315 356 WD 3.
FT REPEAT 357 395 WD 4.
FT REPEAT 397 438 WD 5.
FT REPEAT 447 488 WD 6.
FT REPEAT 519 532 GKALMYRLHHYSDF -> ARP (IN REF. 1).
FT CONFLICT
SEQUENCE 532 AA; 59103 MW; 2DA86FDFASDDF7A1 CRC64;

Query Match 59.3%; Score 48; DB 1; Length 532;
Best Local Similarity 80.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 5 KGKGGGPPPK 14
| | | | | | |
Db 8 GAGKGGPPPK 17

RESULT 5
MYCN SERCA
ID MYCN_SERCA STANDARD; PRT; 427 AA.
AC
P26014;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE N-myc proto-oncogene protein.
GN MYCN.
OS Serinus canaria (Canary).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Fringillidae;
OC Carduelinae; Serinus.
OX NCBI_TaxID=9135;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=91141534; PubMed=1996121;
RA Collum R.G., Clayton D.F., Alt F.W.;
RT "Structure and expression of canary myc family genes.";
RL Mol. Cell. Biol. 11:1770-1776(1991).
CC -1- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
CC BHLH PROTEIN. BINDS DNA AS AN HETERODIMER WITH MAX.
CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.
-----
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 CC or send an email to license@isb-sib.ch)
 CC -----

CC EMBL; M64598; AAA49540.1; -
 CC EMBL; M64251; AAA49540.1; JOINED.
 CC PIR; A39695; A39695.
 CC HSSP; P25912; 1HLO.
 CC TRANSFAC; T02381; -
 CC InterPro; IPR003015; HLH_Myc.
 CC InterPro; IPR001092; HLH_dlm.
 CC Pfam; PF00010; HLH; 1.
 CC Pfam; PF01056; Myc_N_term; 1.
 CC PRINTS; PR00044; LEUZIPRMYC.
 CC SMART; SM00353; HLH; 1.
 CC PROSITE; PS00038; HELIX_LOOP_HELIX; 1.
 CC Nuclear protein; DNA-binding; Proto-oncogene; Phosphorylation.
 CC DOMAIN 212 219 POLY-SER.
 CC FT DOMAIN 220 242 ASP/GLU-RICH (ACIDIC).
 CC FT DNA_BIND 343 356 BASIC DOMAIN.
 CC FT DOMAIN 357 397 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
 CC FT DOMAIN 396 417 LEUCINE-ZIPPER (POTENTIAL).
 CC FT MOD_RES 224 224 PHOSPHORYLATION (BY CK2)
 CC FT MOD_RES 226 226 (BY SIMILARITY).
 CC FT PHOSPHORYLATION (BY CK2)
 CC FT (BY SIMILARITY).
 CC SEQUENCE 427 AA; 47140 MW; 5631PFER615AE54B CRC64;

Query Match 56.8%; Score 46; DB 1; Length 427;
 Best Local Similarity 61.5%; Pred. No. 23;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 KKLQKGGGPPPP 13
 Db 144 EKLQKTPAAPPP 156
 :||| | | | |

RESULT 6
 ID DYNL_CAEEL STANDARD; PRT; 830 AA.
 AC P39055;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE DYNamin (EC 3.6.1.50).
 GN DYN-1
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=97439883; PubMed=9294229;
 RA Clark S.G., Shurland D.L., Meyerowitz E.M., Bargmann C.I.,
 RA van der Bliek A.M.;
 RT "A dynamin GTPase mutation causes a rapid and reversible temperature-
 RT inducible locomotion defect in *C. elegans*";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:10438-10443(1997).
 RN [2]
 RP REVISIONS TO C-TERMINUS.
 RC STRAIN=BRISTOL N2;
 RA van der Bliek A.M.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: MICROTUBULE-ASSOCIATED FORCE-PRODUCING PROTEIN INVOLVED
 CC IN PRODUCING MICROTUBULE BUNDLES AND ABLE TO BIND AND HYDROLYZE
 CC GTP. MOST PROBABLY INVOLVED IN VESICULAR TRAFFICKING PROCESSES, IN
 CC PARTICULAR ENDOCYTOSIS.
 CC -!- CATALYTIC ACTIVITY: GTP + H(2)O = GDP + phosphate.
 CC -!- SUBCELLULAR LOCATION: MICROTUBULE-ASSOCIATED.
 CC -!- SIMILARITY: BELONGS TO THE DYNAMIN FAMILY.

CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch)
 CC -----

CC EMBL; L29031; AAB72228.2; -
 CC HSSP; Q05193; 2DYN.
 CC InterPro; IPR001401; Dynamain.
 CC InterPro; IPR000375; Dynamain_central.
 CC InterPro; IPR003130; GED.
 CC InterPro; IPR001849; PH.
 CC Pfam; PF00350; dynamain; 1.
 CC Pfam; PF01031; dynamain_2; 1.
 CC Pfam; PF02212; GED; 1.
 CC Pfam; PF00169; PH; 1.
 CC PRINTS; PR00195; DYNAMIN.
 CC SMART; SM00053; DYNC; 1.
 CC SMART; SM00302; GED; 1.
 CC SMART; SM00233; PH; 1.
 CC PROSITE; PS00410; DYNAMIN; 1.
 CC PROSITE; PS00003; PH_DOMAIN; 1.
 CC Hydrolase; Motor protein; GTP-binding; Microtubules; Multigene family;
 KW Endocytosis.
 FT NP_BIND 40 47 GTP (BY SIMILARITY).
 FT NP_BIND 138 142 GTP (BY SIMILARITY).
 FT NP_BIND 207 210 GTP (BY SIMILARITY).
 FT DOMAIN 519 624 PH.
 FT SEQUENCE 830 AA; 93348 MW; FC3D7106D079EDC5 CRC64;

Query Match 56.8%; Score 46; DB 1; Length 830;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 GPGGPPPP 13
 Db 818 GPGGPPPP 824
 :||| | | | |

RESULT 7
 ID DPOD_MESAU STANDARD; PRT; 1103 AA.
 AC P97283; P97284;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE DNA polymerase delta catalytic subunit (EC 2.7.7.7).
 GN POLD1.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liu Z., Mishra N.C.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: POSSESSES TWO ENZYMATIC ACTIVITIES: DNA SYNTHESIS
 CC (POLYMERASE) AND AN EXONUCLEOTIC ACTIVITY THAT DEGRADES SINGLE
 CC STRANDED DNA IN THE 3' TO 5' DIRECTION. REQUIRED WITH ITS
 CC ACCESSORY PROTEINS (PROLIFERATING CELL NUCLEAR ANTIGEN (PCNA) AND
 CC REPLICATION FACTOR C (RFC) OR ACTIVATOR 1) FOR LEADING STRAND
 CC SYNTHESIS. ALSO INVOLVED IN COMPLETING OKAZAKI FRAGMENTS INITIATED
 CC BY THE DNA POLYMERASE ALPHA/PRIMASE COMPLEX (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
 CC + {DNA}(N).
 CC -!- SUBUNIT: HETEROTETRAMER COMPOSED OF SUBUNITS OF 125 kDa, 50 kDa,
 CC 66 kDa and 12 kDa. The 125 kDa SUBUNIT CONTAINS THE POLYMERASE

RT of potential sugar-binding subsites.";

RL J. Biotechnol. 57:91-100(1997).

RN [2]

RX X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND MUTAGENESIS.

RA MacKenzie L.F., Sulzenbacher G., Divine C., Jones T.A., Woeldike H.F.,

RA Schuelin M., Withers S.G., Davies G.J.;

RT "Crystal structure of the family 7 endoglucanase I (Cel7B) from

RT Humicola insolens at 2.2 Å resolution and identification of the

RT catalytic nucleophile by trapping of the covalent glycosyl-enzyme

RT intermediate.";

RL Biochem. J. 335:409-416(1998).

CC -1- FUNCTION: THE BIOLOGICAL CONVERSION OF CELLULOSE TO GLUCOSE

CC GENERALLY REQUIRES THREE TYPES OF HYDROLYTIC ENZYMES:

CC (1) ENDOGLUCANASES WHICH CUT INTERNAL BETA-1,4-GLUCOSIDIC BONDS;

CC (2) EXOCELLULOBIODERIVATIVES THAT CUT THE DISSACCHARIDE CELLOBIOSE

CC FROM THE NONREDUCING END OF THE CELLULOSE POLYMER CHAIN;

CC (3) BETA-1,4-GLUCOSIDASES WHICH HYDROLYZE THE CELLOBIOSE AND OTHER

CC SHORT CELLO-OLIGOSACCHARIDES TO GLUCOSE.

CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic

CC linkages in cellulose.

CC -1- SUBUNIT: MONOMER.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY C (FAMILY 7 OF GLYCOSYL

CC HYDROLASES).

DR PDB; 1A39; 02-MAR-99.

DR PDB; 2A39; 16-FEB-99.

DR InterPro: IPR001722; Glyco_hydro_7.

DR Pfam; PF00840; Glyco_hydro_7; 1.

DR PRINTS; PR00734; GLHYDRIASE7.

DR ProDom; PD186135; Glyco_hydro_7; 1.

KW Cellulose degradation; Hydrolase; Glycosidase; Glycoprotein;

KW 3D-structure.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT ACT_SITE 197 197 NUCLEOPHILE.

FT ACT_SITE 202 202 PROTON DONOR.

FT DISULFID 18 24

FT DISULFID 51 73

FT DISULFID 63 69

FT DISULFID 140 365

FT DISULFID 172 195

FT DISULFID 176 194

FT DISULFID 215 234

FT DISULFID 223 228

FT DISULFID 239 315

FT CARBOHYD 89 89 N-LINKED (GLCNAC: . . .).

FT CARBOHYD 247 247 N-LINKED (GLCNAC: . . .).

SQ SEQUENCE 402 AA; 44577 MW; E0C6D31375D1635F CRC64;

Query Match 55.6%; Score 45; DB 1; Length 402;

Best Local Similarity 47.4%; Pred. No. 29;

Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 KLGKGGG-----PPPK 14

Db : : | | | | |

42 RAELGGGCGDGNPPPK 60

RESULT 10

FES_FSVST STANDARD; PRT; 477 AA.

AC P00543;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Tyrosine-protein kinase transforming protein FES (EC 2.7.1.112).

GN V-FES.

OS Feline sarcoma virus (strain Snyder-Theilen).

OC Viruses; Retroviral viruses; Retroviridae; Mammalian type C retroviruses.

OX NCBI_TaxID=11780;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83050963; PubMed=6183005;

RX MEDLINE=83050963; PubMed=6183005;

RA Hampe A., Laprevotte I., Galibert F., Fedele L.A., Sherr C.J.;

RT "Nucleotide sequences of feline retroviral oncogenes (v-fes) provide

RT evidence for a family of tyrosine-specific protein kinase genes.";

RL Cell 30:775-785(1982).

CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

CC tyrosine phosphate.

CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-FES

CC POLYPEPTIDE.

CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC

CC DOMAIN. BELONGS TO THE FES/FPS SUBFAMILY.

CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.

CC -----

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CC -----

DR EMBL; J02088; AAA3046.2; .

DR PIR; A00652; TMVGS.

DR HSP; P11362; IFGK.

DR InterPro: IPR000719; Euk_pkinase.

DR InterPro: IPR000980; SH2.

DR InterPro: IPR001245; Tyr_pkinase.

DR Pfam; PF00069; pkinase; 1.

DR Pfam; PF00017; SH2; 1.

DR PRINTS; PR00401; SH2DOMAIN.

DR PRINTS; PR00109; TYRKINASE.

DR SMART; SM00252; SH2; 1.

DR SMART; SM00219; TyrKc; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS50001; SH2; 1.

KW Polyprotein; Tyrosine-protein kinase; Oncogene; Transferase;

KW ATP-binding; phosphorylation; SH2 domain.

FT DOMAIN 115 204 SH2.

FT NP_BIND 216 477 PROTEIN KINASE.

FT BINDING 222 230 ATP (BY SIMILARITY).

FT ACT_SITE 245 245 ATP (BY SIMILARITY).

FT MOD_RES 338 338 BY SIMILARITY.

FT MOD_RES 368 368 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

SQ SEQUENCE 477 AA; 53756 MW; BB87EDB4E7A3BEB5 CRC64;

Query Match 55.6%; Score 45; DB 1; Length 477;

Best Local Similarity 66.7%; Pred. No. 35;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KLGKGGGPPPP 13

Db : : | | | | |

42 KLEQLGPGGPPPP 53

RESULT 11

FES_FSVGA STANDARD; PRT; 609 AA.

AC P00542;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Tyrosine-protein kinase transforming protein FES (EC 2.7.1.112).

GN V-FES.

OS Feline sarcoma virus (strain Gardner-Arnstein) (Ga-FesV) (Gardner-

OS Arnstein feline leukemia oncovirus B).

OC Viruses; Retroviral viruses; Retroviridae; Gammaretrovirus.

OX NCBI_TaxID=11774;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83050963; PubMed=6183005;

Thú Sep 5 11:23:38 2002

Hampe A., Laprevotte I., Galibert F., Fedele L.A., Sherr C.J.;
"Nucleotide sequences of feline retroviral oncogenes (v-fes) provide
evidence for a family of tyrosine-specific protein kinase genes.";
Cell 30:775-785(1982).
-1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
tyrosine phosphate.
-1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-FES
POLYPEPTIDE.
-1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
DOMAIN. BELONGS TO THE FES/FPS SUBFAMILY.
-1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.

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EMBL; J02087; AAA43041.1; --
PIR; A00651; TVMVGC.
HSP; P11362; IFGK.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001060; FCH.
InterPro; IPR000980; SH2.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00611; FCH; 1.
Pfam; PF00069; pkinase; 1.
Pfam; PF00017; SH2; 1.
PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00109; TYRKINASE.
SMART; SM00055; FCH; 1.
SMART; SM00252; SH2; 1.
SMART; SM00219; TyKc; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50001; SH2; 1.
Protein; Tyrosine-protein kinase; Oncogene; Transferase;
ATP-binding; Phosphorylation; SH2 domain.
DOMAIN 247 336 SH2
DOMAIN 348 609 PROTEIN KINASE
NP_BIND 354 362 ATP (BY SIMILARITY).
BINDING 377 377 ATP (BY SIMILARITY).
ACT_SITE 470 470 ATP (BY SIMILARITY).
MOD_RES 500 500 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SEQUENCE 609 AA; 68769 MW; 53D4919757CF3A3 CRC64;

Query Match 55.68; Score 45; DB 1; Length 609;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KLOGKGPGGPPP 13
||: ||| |||
Db 174 KLEQLGPGGPPP 185

RESULT 12
FES_FELCA
ID FES_FELCA STANDARD; PRT; 820 AA.
AC P14238;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE proto-oncogene tyrosine-protein kinase FES/FPS (EC 2.7.1.112) (C-FES).
GN FES OR FPS.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
NCBI_Taxid=9685;
RN [1]

SEQUENCE FROM N.A.
MEDLINE=87198954; PubMed=3553615;
Roelbroek A.J.M., Schalcken J.A., Onnekink C., Bloemers H.P.J.,
van de Ven W.J.M.;
"Structure of the feline c-fes/fps proto-oncogene: genesis of a
retroviral oncogene";
J. Virol. 61:2009-2016(1987).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
tyrosine phosphate.
-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
DOMAIN. BELONGS TO THE FES/FPS SUBFAMILY.
-!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.

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EMBL; M16705; AAA30808.1; JOINED.
EMBL; M16686; AAA30808.1; JOINED.
EMBL; M16667; AAA30808.1; JOINED.
EMBL; M16668; AAA30808.1; JOINED.
EMBL; M16669; AAA30808.1; JOINED.
EMBL; M16670; AAA30808.1; JOINED.
EMBL; M16671; AAA30808.1; JOINED.
EMBL; M16706; AAA30808.1; JOINED.
EMBL; M16672; AAA30808.1; JOINED.
EMBL; M16673; AAA30808.1; JOINED.
EMBL; M16674; AAA30808.1; JOINED.
EMBL; M16698; AAA30808.1; JOINED.
EMBL; M16700; AAA30808.1; JOINED.
EMBL; M16701; AAA30808.1; JOINED.
EMBL; M16702; AAA30808.1; JOINED.
EMBL; M16704; AAA30808.1; JOINED.
PIR; A27824; TVCTFF.
HSP; P11362; 1FGK.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001060; FCH.
InterPro; IPR000980; SH2.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00611; FCH; 1.
Pfam; PF00069; pkinase; 1.
Pfam; PF00017; SH2; 1.
PRINTS; PR00109; TYRKINASE.
SMART; SM00055; FCH; 1.
SMART; SM00252; SH2; 1.
SMART; SM00219; TyrKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50001; SH2; 1.
KW transferase; Tyrosine-protein kinase; Proto-oncogene; ATP-binding;
Phosphorylation; SH2 domain.
FT DOMAIN 458 547 SH2.
FT DOMAIN 559 820 PROTEIN KINASE.
FT NP_BIND 565 573 ATP (BY SIMILARITY).
FT BINDING 588 588 ATP (BY SIMILARITY).
FT ACT_SITE 681 681 BY SIMILARITY.
FT MOD_RES 711 711 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SOURCE F3A52B750236834E CRC64;

```

Query Match      55.6%; Score 45; DB 1; Length 820;
Best Local Similarity 66.7%; Pred. No. 58;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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DT 01-FEB-1996 (Rel. 33; Last sequence update)
 DT 01-FEB-1996 (Rel. 33; Last annotation update)
 DE proto-oncogene tyrosine-protein kinase FES/FPS (EC 2.7.1.112) (C-FES).
 FE FES OR FPS.
 OS *Felis silvestris catus* (Cat).
 GN Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]

```

RESULT 13
FES_HUMAN
ID FES_HUMAN STANDARD; PRT; 822 AA.
AC P07332;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Proto-oncogene tyrosine-protein kinase FES/FPS (EC 2.7.1.112) (C-FES).
GN FES OR FPS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90191711; PubMed=2179816;
RA Alcalay M., Antolini F., van de Ven W.J., Lanfranccone L.,
RA Grignani F., Pelicci P.G.;
RT "Characterization of human and mouse c-fes cDNA clones and
RT identification of the 5' end of the gene.";
RL Oncogene 5:267-275(1990).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86055727; PubMed=4065096;
RA Roebroek A.J.M., Schalken J.A., Verbeek J.S., van den Ouweland A.M.W.,
RA Onnekink C., Bloemers H.P.J., van de Ven W.J.M.;
RT "The structure of the human c-fes/fps proto-oncogene.";
RL EMBO J. 4:2897-2903(1985).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN. BELONGS TO THE FES/FPS SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X52192; CAA36438.1; -
CC EMBL; X06292; CAA29619.1; -
CC PIR; A24673; TVHUFF.
CC PIR; A60188; A60188.
CC HSSP; P11362; 1FGK.
CC MIM; 190030;
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR001060; FCH.
CC InterPro; IPR000980; SH2.
CC InterPro; IPR001245; Tyr_pkinase.
CC Pfam; PF00611; FCH; 1.
CC Pfam; PF00069; pkinase; 1.
CC Pfam; PF00017; SH2; 1.
CC PRINTS; PR00401; SH2DOMAIN.
CC PRINTS; PR00109; TYRKINASE.
CC SMART; SM00055; FCH; 1.
CC SMART; SM00252; SH2; 1.
CC SMART; SM00219; TyrKc; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
CC PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS50001; SH2; 1.
CC Transferrase; Tyrosine-protein kinase; Proto-oncogene; ATP-binding;
KW Phosphorylation; SH2 domain.
FT DOMAIN 460 549
FT DOMAIN 561 822
FT NP_BIND 567 575
FT BINDING 590 590
FT ACT_SITE 683 683
FT MOD_RES 713 713
FT
FT (BY SIMILARITY).

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FT CONFLICT 719 719 S -> L (IN REF. 2).
SQ SEQUENCE 822 AA; 93470 MW; ADA0B8F7D2666356 CRC64;

Query Match
Best Local Similarity 55.6%; Score 45; DB 1; Length 822;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KLGKPGGGPPP 13
Db 387 KLEHLGPGGPPP 398
||: ||| |||
||: ||| |||

RESULT 14
YPUB_KLEPN STANDARD; PRT; 142 AA.
ID YPUB_KLEPN STANDARD; PRT; 142 AA.
AC P20775;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in PULS 3'-region (Fragment).
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89291709; PubMed=2661532;
RA D'Enfert C., Pugsley A.P.;
RT "Klebsiella pneumoniae puls gene encodes an outer membrane
RT lipoprotein required for pullulanase secretion.";
RL J. Bacteriol. 171:3673-3679(1989).
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M29097; AAA61979.1; -
CC PIR; D32880; D32880.
CC KW Hypothetical protein.
CC FT NON_TER 142 142
CC SQ SEQUENCE 142 AA; 16447 MW; 03ED03BFB63242D0 CRC64;

Query Match
Best Local Similarity 54.3%; Score 44; DB 1; Length 142;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 QGKPGGGPPP 14
Db 50 KGKGGKGGKPPR 60
||| ||| |||
||| ||| |||

RESULT 15
RRAS_HUMAN STANDARD; PRT; 218 AA.
ID RRAS_HUMAN STANDARD; PRT; 218 AA.
AC P10301;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Ras-related protein R-Ras (P23).
OS RRAS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87078390; PubMed=3098437;

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Thu Sep 5 11:23:38 2002

RA Lowe D.G., Capon D.J., Delwart E., Sakaguchi A.Y., Naylor S.L.,
 RA Goeddel D.V.;
 RT "Structure of the human and murine R-ras genes, novel genes closely
 RL related to ras proto-oncogenes.";
 RL Cell 48:137-146(1987).
 CC -!- SUBCELLULAR LOCATION: INNER SURFACE OF PLASMA MEMBRANE POSSIBLY
 CC WITH ATTACHMENT REQUIRING ACYLATION OF THE C-TERMINAL CYSTEINE
 CC (BY SIMILARITY WITH RAS).
 CC -!- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE R-RAS SUB-FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M14949; AAA60256.1; -.
 CC EMBL; M14948; AAA60256.1; JOINED.
 CC PIR; A26159; TVHURR.
 CC HSPP; P01112; 1PLL.
 CC SWISS-2DPAGE; P10301; HUMAN.
 CC MIM; 165090; -.
 CC InterPro; IPR003577; Ras.
 CC InterPro; IPR001806; Ras_trnsfrmng.
 CC Pfam; PF00071; ras; 1.
 CC PRINTS; PR00449; RASTRNSFRMNG.
 CC SMART; SM00173; RAS; 1.
 KW GTP-binding; Prenylation; Lipoprotein.
 FT NP_BIND 36 43 GTP (BY SIMILARITY).
 FT NP_BIND 83 87 GTP (BY SIMILARITY).
 FT NP_BIND 142 145 GTP (BY SIMILARITY).
 FT DOMAIN 58 66 EFFECTOR REGION (BY SIMILARITY).
 FT LIPID 215 215 GERANYL-GERANYL (BY SIMILARITY).
 SQ SEQUENCE 218 AA; 23480 MW; 437F73170670EB28 CRC64;

Query Match 54.3%; Score 44; DB 1; Length 218;
 Best Local Similarity 77.8%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 KGKGGGPPP 13
 DB 18 GPGGDDPPP 26

Search completed: September 4, 2002, 17:05:05
 Job time: 1131 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 17:01:33 ; Search time 124.34 seconds
(without alignments)
19.478 Million cell updates/sec

Title: US-09-821-726-3
Perfect score: 81
Sequence: 1 KKLQKGGGPPPK 14

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL19.*

- 1: sp.archaea.*
- 2: sp.bacteria.*
- 3: sp.fungi.*
- 4: sp.human.*
- 5: sp.invertebrate.*
- 6: sp.mammal.*
- 7: sp.mhc.*
- 8: sp.organelle.*
- 9: sp.phage.*
- 10: sp.plant.*
- 11: sp.rodent.*
- 12: sp.virus.*
- 13: sp.vertibrate.*
- 14: sp.unclassified.*
- 15: sp.virus.*
- 16: sp.bacteriap.*
- 17: sp.archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	60	74.1	1677	11 070373	070373 mus musculus
2	52	64.2	467	4 Q9H9F1	Q9H9F1 homo sapien
3	50	61.7	333	2 Q9APQ3	Q9APQ3 uncultured
4	49	60.5	212	2 Q9APJ1	Q9APJ1 methylobact
5	48	59.3	547	11 P97472	P97472 mus musculus
6	48	59.3	547	11 Q91XC0	Q91XC0 mus musculus
7	48	59.3	774	5 Q9V620	Q9V620 drosophila
8	48	59.3	813	5 Q95TY2	Q95TY2 drosophila
9	48	59.3	1289	10 Q9FLQ7	Q9FLQ7 arabidopsis
10	48	59.3	1292	3 Q96WLO	Q96WLO ustilago ma
11	48	59.3	2061	5 Q9VUH9	Q9VUH9 drosophila
12	47	58.0	262	12 Q9DWB2	Q9DWB2 rat cytomeg
13	47	58.0	669	16 Q9PER1	Q9PER1 xylella fas
14	47	58.0	673	2 Q9RBK2	Q9RBK2 xanthomonas
15	47	58.0	1963	5 Q9VSK5	Q9VSK5 drosophila
16	47	58.0	1966	5 Q9NHX6	Q9NHX6 drosophila

17	46	56.8	241	4 095542	095542 homo sapien
18	46	56.8	250	4 075894	075894 homo sapien
19	46	56.8	281	5 095QJ0	095QJ0 caenorhabdi
20	46	56.8	322	13 Q9PTB4	Q9PTB4 brachydanio
21	46	56.8	377	16 069559	069559 mycobacteri
22	46	56.8	495	5 095YB0	095YB0 caenorhabdi
23	46	56.8	549	5 098IB7	098IB7 caenorhabdi
24	46	56.8	551	4 016630	016630 homo sapien
25	46	56.8	561	5 009542	009542 caenorhabdi
26	46	56.8	588	4 098W18	098W18 homo sapien
27	46	56.8	830	5 093176	093176 caenorhabdi
28	46	56.8	1105	11 091V70	091V70 mus musculu
29	46	56.8	1194	5 09W485	09W485 drosophila
30	46	56.8	1215	5 077202	077202 acanthamoeb
31	46	56.8	1256	5 095YA9	095YA9 caenorhabdi
32	46	56.8	1284	5 0960F1	0960F1 drosophila
33	46	56.8	1761	5 P91019	P91019 caenorhabdi
34	45.5	56.2	579	16 Q9Z8K7	Q9Z8K7 chlamydia p
35	45	55.6	153	11 Q9CTM4	Q9CTM4 mus musculu
36	45	55.6	171	10 Q9SSB8	Q9SSB8 arabidopsis
37	45	55.6	316	15 0998S7	0998S7 chimpanzee
38	45	55.6	976	6 Q9MZT1	Q9MZT1 canis fami
39	45	55.6	2703	5 Q9VEG7	Q9VEG7 drosophila
40	45	55.6	2715	5 061603	061603 drosophila
41	44.5	54.9	439	4 Q9H874	Q9H874 homo sapien
42	44.5	54.9	459	4 Q96BH1	Q96BH1 homo sapien
43	44	54.3	149	2 Q9ZGG1	Q9ZGG1 heliobacill
44	44	54.3	172	11 Q9CU12	Q9CU12 mus musculu
45	44	54.3	182	10 Q9C8U3	Q9C8U3 arabidopsis

ALIGNMENTS

RESULT 1

ID 070373 PRELIMINARY: PRT; 1677 AA.
AC 070373:
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE XIN.
GN XIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART MUSCLE;
RX PubMed=9159189;
RA Wang D.-Z., Hu X., Lin J.L.-C., Kitten G.T., Solursh M., Lin J.J.-C.;
RT "Differential display of mRNAs from the atrioventricular region of
developing chicken hearts at stages 15 and 21.";
RL Front. Biosci. 1:al-a15(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART MUSCLE;
RX MEDLINE=99146891; PubMed=10021346;
RA Wang D.-Z., Reiter R.S., Lin J.L.-C., Wang Q., Williams H.S.,
Krob S.L., Schultzeiss T.M., Evans S., Lin J.J.-C.;
RT "Requirement of a novel gene, Xin, in cardiac morphogenesis.";
RL Development 126:1281-1294(1999).
DR EMBL: AF051945; AAC06023.1; -;
DR MGD: MGI:1333878; Xin;
SO SEQUENCE 1677 AA; 182085 MW; A201CFC9A710C7FF CRC64;

Query Match 74.1%; Score 60; DB 11; Length 1677;
Best Local Similarity 81.8%; Pred. No. 1.3;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 4 QGKGGGPPPK 14

Db 574 EGKGGGPPPE 584
:|||||

RESULT 2
Q9H9F1 ID Q9H9F1 PRELIMINARY; PRT; 467 AA.
AC Q9H9F1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CDNA FLJ12800 FIS, CLONE NT2P2002079, WEAKLY SIMILAR TO HISTONE H1,
DE GONADAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.,
RT "NEDO human cDNA sequencing project."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK02862; BAB14278.1; -.
DR InterPro; IPR000637; AT_hook.
DR SMART; SM00384; AT_hook; 1.
SQ SEQUENCE 467 AA; 49648 MW; 287B1BF4CF30B1A1 CRC64;

Query Match 64.2%; Score 52; DB 4; Length 467;
Best Local Similarity 64.3%; Pred. No. 5.8;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 KKLQGGGPPPK 14
:|||||

RESULT 3
Q9APQ3 ID Q9APQ3 PRELIMINARY; PRT; 333 AA.
AC Q9APQ3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE EXCISION NUCLEASE SUBUNIT B (FRAGMENT).
GN UVRB.
OS uncultured bacterium pCosHEL.
OC Bacteria; environmental samples.
OX NCBI_TaxID=143796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20575196; PubMed=11133432;
RA Entcheva P., Liebl W., Johann A., Hartsch T., Streit W.R.;
RT "Direct cloning from enrichment cultures, a reliable strategy for
RT isolation of complete operons and genes from microbial consortia."
RL Appl. Environ. Microbiol. 67:89-99(2001).
DR EMBL; AF250772; AAG60567.1; -.
DR HSSP; P56981; 1D9X.
DR InterPro; IPR001410; DEAD.
FT NON_TER 333
FT NON_TER 333
SQ SEQUENCE 333 AA; 38152 MW; E6401C01A8A46DEF CRC64;

Query Match 61.7%; Score 50; DB 2; Length 333;
Best Local Similarity 72.7%; Pred. No. 8.3;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 LOGKGGGPPPK 13
*

Db 135 LSGRGGPPPP 145
:|||||

RESULT 4
Q9APJ1 ID Q9APJ1 PRELIMINARY; PRT; 212 AA.
AC Q9APJ1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PUTATIVE REGULATOR FOR GRANULA-ASSOCIATED PROTEIN.
DE METHYLOBACTERIUM EXTORTUENS.
OS Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Methylobacterium group; Methylobacterium.
OX NCBI_TaxID=408;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AM1;
RX MEDLINE=21142531; PubMed=11208803;
RA Korotkova N., Lidstrom M.E.;
RT "Connection between Poly-beta-Hydroxybutyrate Biosynthesis and Growth
RT on C1 and C2 Compounds in the Methylophilic Methylobacterium extortuens
RT AM1."
RL J. Bacteriol. 183:1038-1046(2001).
DR EMBL; AF287907; AAK11535.1; -.
SQ SEQUENCE 212 AA; 23141 MW; 4121BD0E8A3FBAC3 CRC64;

Query Match 60.5%; Score 49; DB 2; Length 212;
Best Local Similarity 88.9%; Pred. No. 7.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 GKGGGPPPP 13
:|||||

RESULT 5
P97472 ID P97472 PRELIMINARY; PRT; 547 AA.
AC P97472;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE AJUBA.
GN JUB OR AJUBA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99263009; PubMed=10330178;
RA Goyal R.K., Lin P., Kanungo J., Payne A.S., Muslin A.J.,
RA Longmore G.D.;
RT "Ajuba, a novel LIM protein, interacts with Grb2, augments mitogen-
RT activated protein kinase activity in fibroblasts, and promotes meiotic
RT maturation of Xenopus oocytes in a Grb2- and Ras-dependent manner."
RL Mol. Cell. Biol. 19:4379-4389(1999).
CC -1- SIMILARITY: CONTAINS 3 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
CC TONS.
DR EMBL; U79776; AAB38287.1; -.
DR HSSP; Q05158; 1QLI.
DR MGD; MGI:1341886; Jub.
DR InterPro; IPR001781; LIM.
DR Pfam; PF00412; LIM; 3.
DR ProDom; PD000094; LIM; 3.
DR SMART; SM00132; LIM; 3.
DR PROSITE; PS00478; LIM_DOMAIN_1; 2.
DR PROSITE; PS00023; LIM_DOMAIN_2; 3.
KW LIM domain; Metal-binding; Zinc.
SQ SEQUENCE 547 AA; 57901 MW; C326772AC1C441B2 CRC64;

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merklov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Smith H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J., Yao Q.A.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhao Q., Zheng L.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195 (2000).
 DR EMBL; AE003824; AAF58619.1; -;
 DR FlyBase; FBgn0033654; PRich_extensn.
 DR InterPro; IPR002965; PRich_extensn.
 DR PRINTS; PR01217; PRICHEXTENS.
 SQ SEQUENCE 774 AA; 83718 MW; 04A64D97952CF90D CRC64;

Query Match 59.3%; Score 48; DB 5; Length 774;
 Best Local Similarity 61.5%; Pred. No. 38;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 KKLOGKPGGPPPP 13
 : : | | | | |
 Db 366 QKSPGPGGAPPP 378

RESULT 8
 Q95TY2 PRELIMINARY; PRT; 813 AA.
 AC Q95TY2;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE GH22790P.
 GN CG8991.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Y, CN BW SP;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Stampanoni M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY058444; AAL13673.1; -;
 SQ SEQUENCE 813 AA; 88199 MW; 9B9F9571EA08308C CRC64;

Query Match 59.3%; Score 48; DB 5; Length 813;
 Best Local Similarity 61.5%; Pred. No. 40;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 KKLOGKPGGPPPP 13
 : : | | | | |

Query Match 59.3%; Score 48; DB 11; Length 547;
 Best Local Similarity 53.8%; Pred. No. 27;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 KKLOGKPGGPPPP 13
 : : | | | | |
 Db 93 QRFEGSPGGPPPP 105

RESULT 6
 Q91XC0 PRELIMINARY; PRT; 547 AA.
 AC Q91XC0;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE SIMILAR TO AJUBA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SALIVARY GLAND;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC011035; AAH11035.1; -;
 SQ SEQUENCE 547 AA; 57919 MW; C326772AC1C155B2 CRC64;

Query Match 59.3%; Score 48; DB 11; Length 547;
 Best Local Similarity 53.8%; Pred. No. 27;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 KKLOGKPGGPPPP 13
 : : | | | | |
 Db 93 QRFEGSPGGPPPP 105

RESULT 7
 Q9V620 PRELIMINARY; PRT; 774 AA.
 AC Q9V620;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE CG8991 PROTEIN.
 GN CG8991.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=107311132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blazer V.G., Champs M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Db 405 QKSPGPGCAPPP 417

RESULT 9

Q9FLQ7 ID Q9FLQ7 PRELIMINARY; PRT; 1289 AA.
 AC Q9FLQ7
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE GB|AAD23008.1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=98290546; PubMed=9628582;
 RA Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. IV.
 RT Sequence features of the regions of 1,456,315 bp covered by nineteen
 RT physically assigned pl and TAC clones.";
 RL DNA Res. 5:41-54(1998).
 DR EMBL: AB010070; BAB11454.1; -;
 DR InterPro: IPR002965; P_rich_extensn.
 DR PRINTS: PR01217; PRICEXTENS.
 SO SEQUENCE 1289 AA; 137558 MW; 898E55A2A618F5E0 CRC64;

Query Match

Best Local Similarity 59.3%; Score 48; DB 10; Length 1289;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 GKPGGPP 13

|:|:|:|:|

Db 1142 GRGPGAPP 1150

RESULT 10

Q96WLO ID Q96WLO PRELIMINARY; PRT; 1292 AA.
 AC Q96WLO
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE TPR-CONTAINING PROTEIN MQL1.
 GN MQL1.
 OS Ustilago maydis (Smut fungus).
 OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
 OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
 OX NCBI_TaxID=5270;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Loubradou G., Kalmann R.;
 RT "Involvement of the TPR containing protein Mql1 in filamentous growth
 RT of Ustilago maydis.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF268097; AAK58576.1; -;
 SO SEQUENCE 1292 AA; 135886 MW; 543A2702C4E0D610 CRC64;

Query Match

Best Local Similarity 59.3%; Score 48; DB 3; Length 1292;

Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 LQKPGGPP 13

|:|:|:|:|

Db 716 LAAAGPGPP 726

RESULT 11

Q9VUH9 ID Q9VUH9 PRELIMINARY; PRT; 2061 AA.
 AC Q9VUH9
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE CG9425 PROTEIN.
 GN CG9425.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephyroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Gelniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abriel J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Balles R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fodor C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Iacono M., Ibegwan C.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003533; AAF49702.1; -;
 DR FlyBase: FBgn0036451; CG9425.
 DR InterPro: IPR002965; P_rich_extensn.
 DR InterPro: IPR001412; tRNA-synt_1.
 DR InterPro: IPR000571; zf-CCCH.
 DR InterPro: IPR000822; Znf-C2H2.
 DR Pfam: PF00642; zf-CCCH; 1.
 DR PRINTS: PR01217; PRICEXTENS.
 DR SMART: SM00355; Znf.C2H2; 1.
 DR PROSITE: PS00178; AA-TRNA-LIGASE I; UNKNOWN_1.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
 SO SEQUENCE 2061 AA; 225386 MW; B6A15539B5B5CC0E CRC64;

Query Match

Best Local Similarity 59.3%; Score 48; DB 5; Length 2061;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
 RA Marques M.V., Martins E.A.L., Miyaki C.Y., Monteiro-Vitorello C.B.,
 RA Menck C.F.M., Miracca E.C., Nogueira A.L.T.O., Netto L.E.S.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 RA Nhani A., Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A., Jr., Pesquero J.B.,
 RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 RA de Rosa V.E., Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A., Jr.,
 RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
 RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshako M.H.,
 RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
 RA "The genome sequence of the plant pathogen Xylella fastidiosa";
 RL Nature 406:151-159(2000).
 CC -1- SIMILARITY: TO HELICASE C-TERMINAL DOMAIN.
 DR EMBL; AF003935; AAF83777.1; -.
 DR HSSP; P56981; 1D9X.
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR001650; Helicase_C.
 DR InterPro; IPR001943; UVR.
 DR Pfam; PF00271; helicase_C; 1.
 DR Pfam; PF02151; UVR; 1.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELICC; 1.
 DR ATP-binding; Complete proteome; Helicase.
 KW ATP-binding; Complete proteome; Helicase.
 SQ SEQUENCE 669 AA; 75557 MW; 268460383A7125E CRC64;

Query Match 58.0%; Score 47; DB 16; Length 669;
 Best Local Similarity 61.5%; Pred. No. 46;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KKLQKGGGPPPP 13
 Db 311 RHLTGKAPGPPPP 323

RESULT 14
 Q9RBK2 ID Q9RBK2 PRELIMINARY; PRT; 673 AA.
 AC Q9RBK2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE EXCINUCLEASE ABC SUBUNIT B.
 GN UVRB.
 OS Xanthomonas campestris (pv. campestris).
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OC Xanthomonas.
 OX NCBI_TaxID=340;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-XC17;
 RT Tseng Y.H.;
 RT "Cloning and characterization of the uvrB of Xanthomonas campestris
 RT pv. campestris";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF102847; AAD46146.2; -.
 DR HSSP; P56981; 1D9X.
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR001650; Helicase_C.
 DR InterPro; IPR001943; UVR.
 DR Pfam; PF00271; helicase_C; 1.
 DR Pfam; PF02151; UVR; 1.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELICC; 1.
 KW ATP-binding; Helicase.
 SQ SEQUENCE 673 AA; 75855 MW; 976441B101DE3897 CRC64;

RA 3 LOCKGGGPPPP 13
 Db 1361 LRCMPPGPPPP 1371

RESULT 12
 Q9DWB2 ID Q9DWB2 PRELIMINARY; PRT; 262 AA.
 AC Q9DWB2;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE P90.
 GN R90.
 OS Rat cytomegalovirus (strain Maastricht).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Muromegalovirus.
 OX NCBI_TaxID=79700;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAASTRICHT;
 RC MEDLINE=20366325; PubMed=10906222;
 RA Vink C., Beuken E., Bruggeman C.A.;
 RT "Complete DNA sequence of the rat cytomegalovirus genome";
 RL J. Virol. 74:7656-7665(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAASTRICHT;
 RC MEDLINE=20473137; PubMed=11018281;
 RA Gruijthuisen Y.K., Beuken E., Bruggeman C.A., Vink C.;
 RT "Rat cytomegalovirus R89 is a highly conserved gene which expresses a
 RT spliced transcript";
 RL Virology Res. 69:119-130(2000).
 DR EMBL; AF232689; AAF99178.1; -.
 SQ SEQUENCE 262 AA; 27742 MW; 7C8063857113D7B7 CRC64;

Query Match 58.0%; Score 47; DB 12; Length 262;
 Best Local Similarity 70.0%; Pred. No. 18;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QCKGGGPPPP 13
 Db 18 RGRGGGPPSP 27

RESULT 13
 Q9PER1 ID Q9PER1 PRELIMINARY; PRT; 669 AA.
 AC Q9PER1;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE EXCINUCLEASE ABC SUBUNIT B.
 GN XF0967.
 OS Xylella fastidiosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OC Xylella.
 OX NCBI_TaxID=2371;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=9AC5;
 RX MEDLINE=20365717; PubMed=10910347;
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
 RA Alvarenga R., Alves L.M.C., Araya J.E., Bata G.S., Baptista C.S.,
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.N.S.,
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrier H.,
 RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
 RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
 RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,

Query Match 58.0%; Score 47; DB 2; Length 673;
 Best Local Similarity 61.5%; Pred. No. 46;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 KKLGKGGGGPP 13
 : | | | | | | | |
 Db 311 RHLTGKAGGPP 323

RESULT 15

Q9VSK5 PRELIMINARY; PRT; 1963 AA.
 AC Q9VSK5;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE CG6964 PROTEIN.
 GN GUG OR CG6964.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Fandel M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 BA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacieb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003555; AA50413.1;
 DR FlyBase; FBgn0020427; GUG.
 DR InterPro; IPR000949; ELM2.
 DR InterPro; IPR001005; Myb_DNA_bind.
 DR Pfam; PF01448; ELM2; 1.
 DR Pfam; PF00249; myb_DNA-binding; 1.

DR SMART; SM00395; SANT; 1.
 SQ SEQUENCE 1963 AA; 207927 MW; 8F386DE56E66CB68 CRC64;

Query Match 58.0%; Score 47; DB 5; Length 1963;
 Best Local Similarity 87.5%; Pred. No. 1.3e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 GPGGPPPK 14
 : | | | | | | | |
 Db 1156 GPGGPPPK 1163

Search completed: September 4, 2002, 17:01:35
 Job time: 1156 sec

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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:45:01 : Search time 158.52 Seconds
(without alignments)
16.116 Million cell updates/sec

Title: US-09-821-726-2
Perfect score: 125
Sequence: 1 LDTWVKQKQKGGPGAPPKDIMY 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802.*
1: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	72.0	185	20 AAW99667	Human secreted pro
2	90	72.0	185	21 AAB24067	Human PRO1005 prot
3	90	72.0	185	21 AAY87272	Human signal pepti
4	90	72.0	185	21 AAY66686	Membrane-bound pro
5	90	72.0	185	22 AAB65209	Human PRO1005 (UNQ
6	90	72.0	185	22 AAB50957	Human PRO1005 prot
7	90	72.0	186	21 AAB38329	Human secreted pro
8	90	72.0	194	19 AAW69974	Cancer associated
9	90	72.0	194	20 AAY76591	Human ovarian tumo
10	54	43.2	194	22 ABB59646	Drosophila melanog
11	51	40.8	298	16 AAB79655	Human UBC/CDC34 pr

12	51	40.8	298	20 AAY39971	Human UBC/CDC34 p
13	51	40.8	298	21 AAB03179	Human UBC/CDC34 .
14	51	40.8	307	22 ABO07765	Novel human diagno
15	51	40.8	307	22 ABO08168	Novel human diagno
16	51	40.8	378	22 ABB72035	Drosophila melanog
17	51	40.8	465	22 AAG67296	Amino acid sequenc
18	50.5	40.4	127	22 AAO07630	Human polypeptide
19	49	39.2	109	22 AAO05707	Human polypeptide
20	49	39.2	170	11 AAR04129	Stem cell leukaemi
21	49	39.2	206	11 AAR04127	Stem cell leukaemi
22	49	39.2	214	11 AAR05857	Stem cell leukaemi
23	49	39.2	418	22 ABO03314	Novel human diagno
24	49	39.2	1518	22 ABB64829	Drosophila melanog
25	48.5	38.8	415	16 AAW01500	50 kD endoglucanas
26	48.5	38.8	435	12 AAR15240	Humicola insolens
27	48.5	38.8	3080	22 ABB64877	Drosophila melanog
28	48	38.4	140	22 AAO08289	Human polypeptide
29	48	38.4	145	22 ABB71381	Drosophila melanog
30	48	38.4	147	22 AAO06887	Human polypeptide
31	48	38.4	163	22 AAO01151	Human polypeptide
32	48	38.4	367	22 AAM78403	Human protein seq
33	48	38.4	417	21 AAB25777	Human secreted pro
34	48	38.4	417	22 AAB75363	Human transmembran
35	48	38.4	540	21 AAY57930	Arabidopsis thalia
36	48	38.4	1024	21 AAG42350	Arabidopsis thalia
37	48	38.4	1105	21 AAG42349	Arabidopsis thalia
38	48	38.4	1189	21 AAG42348	Arabidopsis thalia
39	47	37.6	52	21 AAB59108	Breast and ovarian
40	47	37.6	85	22 AAU47437	Propionibacterium
41	47	37.6	132	22 AAO05991	Human polypeptide
42	47	37.6	136	22 AAM96230	Human reproductive
43	47	37.6	136	22 AAU18917	Novel prostate gla
44	46.5	37.2	921	22 ABB68780	Drosophila melanog
45	46	36.8	97	21 AAB56449	Arabidopsis thalia

ALIGNMENTS

RESULT 1
AAW99667
ID AAW99667 standard; Protein; 185 AA.
XX
AC AAW99667;
XX
DT 07-JUN-1999 (first entry)
XX
DE Human secreted protein clone ej90_5 protein.

XX
KW Human; secreted protein; nutritional; cytokine; cell proliferation;
KW differentiation; immune stimulating; vaccine; haematopoiesis regulation;
KW tissue growth; chemotactic; chemokinetic; haemostatic; thrombolytic;
KW anti-inflammatory; cadherin; tumour invasion suppressor;
tumour inhibition; gene therapy.

XX Homo sapiens.
XX WO9907840-A1.
XX
XX 18-FEB-1999.
XX
XX 06-AUG-1998; 98WO-US16318.
XX
XX 04-AUG-1998; 98US-0130189.
XX 06-AUG-1997; 97US-0906708.
XX
XX (GEM) GENETICS INST INC.
XX
XX Agostino MJ, Evans C, Jacobs K, Lavallie ER, McCoy JM;
XX Merberg D, Racie LA, Steininger RJ, Treacy M;
XX WPI; 1999-167419/14.
XX
XX N-PSDB; AAX19493.

XX New polynucleotides encoding secreted human proteins - derived from
PT fetal kidney, adult testes, adult brain, adult heart, adult placenta
PT or adult retina cDNA libraries
XX
PS Claim 34; Page 98-99; 107pp; English.
XX
CC The present sequence represents a human secreted protein. The secreted
CC protein can have activities such as: nutritional activity, cytokine and
CC cell proliferation/differentiation activity, immune stimulating (e.g. as
CC vaccines) or suppressing activity, haematopoiesis regulating activity,
CC tissue growth activity, activin/inhibin activity, chemotactic/
CC chemokinetic activity, haemostatic and thrombolytic activity, receptor/
CC ligand activity, anti-inflammatory activity, cadherin/tumour invasion
CC suppressor activity, and tumour inhibition activity. The secreted
CC protein polynucleotides and proteins are predicted to have biological
CC activities which would make them suitable for treating, preventing or
CC ameliorating medical conditions in humans and animals. The
CC polynucleotides are also stated to be useful for gene therapy.
XX
SQ Sequence 185 AA;

Query Match 72.0%; Score 90; DB 20; Length 185;
Best Local Similarity 72.0%; Pred. No. 1.7e-05;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
QY 1 LDTMWKEQK--GKGPGGAPPKDLMY 23
|| :|||:| ||||| ||| |||
Db 97 ldlavkekklgkgpggppkglmly 121

RESULT 2
AAB24067
ID AAB24067 standard; Protein; 185 AA.
XX
AC AAB24067;
XX
XX 29-JAN-2001 (first entry)
XX
DE Human PRO1005 protein sequence SEQ ID NO:34.
XX
KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
KW proliferation; tumorigenesis; identification; cancer; cytostatic;
KW neutrophic; neuroprotective; antiinflammatory; immunosuppressive;
KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
KW neuronal disorder; gliad disorder; astrocytal disorder; angiogenic;
KW hypothalamic disorder; glandular disorder; macrophagal disorder;
KW epithelial disorder; stromal disorder; blastocoeleic disorder;
KW inflammatory disorder; immunologic disorder.
XX
OS Homo sapiens.
XX
XX WO200053755-A2.
XX
XX 14-SEP-2000.
XX
XX 06-JAN-2000; 2000WO-US00376.
XX
XX 08-MAR-1999; 99WO-US05028.
XX 02-JUN-1999; 99WO-US12252.
XX 23-JUN-1999; 99US-0141037.
XX 07-JUL-1999; 99US-0143048.
XX 26-JUL-1999; 99US-0145698.
XX 30-NOV-1999; 99WO-US28313.
XX 20-DEC-1999; 99WO-US30911.
XX 05-JAN-2000; 2000WO-US00219.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
XX Watanabe CK, Wood WI;

DR WPI; 2000-572270/53.
DR N-PSDB; AAC58377.
XX
PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
PT treatment, diagnosis and prevention of cancer .
XX
XX Claim 61; Fig 22; 286pp; English.
XX
CC The present invention describes an isolated antibody that binds to
CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,
CC PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,
CC PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,
CC PRO1187, PRO1281, PRO233, PRO39, PRO834, PRO1317, PRO1710, PRO2094,
CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell
CC growth. The PRO polypeptides and nucleotides are useful in the
CC treatment, diagnosis and prevention of cancer. The antibodies and other
CC anti-tumour compounds maybe used to treat various conditions, including
CC those characterised by overexpression and/or activation of the amplified
CC PRO genes. Exemplary conditions or disorders to be treated with such
CC antibodies and other compounds include benign or malignant tumours
CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,
CC colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic,
CC carcinomas, sarcomas, glioblastomas, and various head and neck tumours),
CC leukaemias and lymphoid malignancies, other disorders such as neuronal,
CC glial, astrocytal, hypothalamic and other glandular, macrophagal,
CC epithelial, stromal and blastocoeleic disorders, and inflammatory,
CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR
CC primers and hybridisation probes used in the isolation of the human PRO
CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human
CC PRO polynucleotide and protein sequences given in the exemplification of
CC the present invention.
XX
SQ Sequence 185 AA;

Query Match 72.0%; Score 90; DB 21; Length 185;
Best Local Similarity 72.0%; Pred. No. 1.7e-05;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
QY 1 LDTMWKEQK--GKGPGGAPPKDLMY 23
|| :|||:| ||||| ||| |||
Db 97 ldlavkekklgkgpggppkglmly 121

RESULT 3
AAY87272
ID AAY87272 standard; Protein; 185 AA.
XX
XX AAY87272;
XX
XX 11-MAY-2000 (first entry)
XX
XX Human signal peptide containing protein HSPP-49 SEQ ID NO:49.
XX
XX Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
XX inflammation; cardiovascular disease; anticancer; anti-inflammatory;
XX antimicrobial; neutrophic; neuroprotective; cardiovascular; hepatotropic;
XX antiasthmatic; gene therapy; cell proliferation; neurological disorder;
XX reproductive disorder; developmental disorder; arteriosclerosis;
XX cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
XX asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
XX Parkinson's disease; Huntington's diseases; ovulatory defect;
XX muscular dystrophy.
XX
XX Homo sapiens.
XX
XX WO200000610-A2.
XX
XX 06-JAN-2000.
XX
XX 25-JUN-1999; 99WO-US14484.
XX
XX 26-JUN-1998; 98US-0090762.

Thu Sep 5 11:23:34 2002

us-09-821-726-2.rag

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PR 31-JUL-1998; 98US-0094983.
PR 01-OCT-1998; 98US-0102686.
PR 11-DEC-1998; 98US-0112129.
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
XX Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
XX Bandman O;
XX
XX WPI; 2000-160673/14.
XX N-PSDB; AAZ98157.
XX
XX New human signal peptide-containing proteins useful in treatment,
XX prevention and diagnosis of e.g. cancer, inflammation and
XX cardiovascular disease
XX
XX Claim 1: Page 193-194; 327pp; English.
XX
XX AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
XX human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have
XX anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,
XX neuroprotective, cardiovascular and antitachycardic activities, and can
XX be used in gene therapy. HSPs can be used to treat or prevent disorders
XX associated with decreased activity or function of HSP. Antagonists of
XX HSP are used to treat or prevent disorders associated with increased
XX activity or function of HSP. Such diseases include cell proliferation
XX (including cancer), inflammation, cardiovascular, neurological,
XX reproductive or developmental disorders, (e.g. arteriosclerosis,
XX cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
XX asthma, Crohn's disease, microbial or other infections, congestive or
XX ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
XX diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP
XX nucleic acids can be used for the recombinant production of HSP, for
XX detecting HSP in standard hybridisation and amplification assays (for
XX diagnosis and monitoring), in gene therapy, as antisense,
XX triplex-forming or ribozyme therapeutics, for detecting related sequences
XX or genetic variations, and for chromosomal mapping. HSP are also used to
XX raise specific antibodies (Ab) and to screen for agonists and
XX antagonists (potential therapeutic agents). Ab are used to diagnose, or
XX monitor, HSP-related diseases (in usual immunoassays), as therapeutic
XX antagonists, in competitive drug screens, and for purification of HSP
XX from natural sources.
XX
XX SQ Sequence 185 AA;

Query Match 72.0%; Score 90; DB 21; Length 185;
Best Local Similarity 72.0%; Pred. No. 1.7e-05;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

Qy 1 LDTWVKQK-GKGGGAPKDLMY 23
Db 97 ldaivkekkigkgpggppkglm 121

RESULT 4
AAY66686
ID AAY66686 standard; protein; 185 AA.
XX
XX AC AAY66686;
XX
XX DT 05-APR-2000 (first entry)
XX
XX DE Membrane-bound protein PRO1005.
XX
XX KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
XX pharmaceutical; receptor immunoadhesin; gene mapping.
XX
XX OS Homo sapiens.
XX
XX PN WO963088-A2.
XX

```

PD 09-DEC-1999.
XX
PF 02-JUN-1999;
XX 99WO-US12252.
PR 02-JUN-1998;
PR 98US-0087607.
PR 02-JUN-1998;
PR 98US-0087609.
PR 02-JUN-1998;
PR 98US-0087759.
PR 03-JUN-1998;
PR 98US-0087827.
PR 04-JUN-1998;
PR 98US-0088021.
PR 04-JUN-1998;
PR 98US-0088025.
PR 04-JUN-1998;
PR 98US-0088028.
PR 04-JUN-1998;
PR 98US-0088029.
PR 04-JUN-1998;
PR 98US-0088030.
PR 04-JUN-1998;
PR 98US-0088033.
PR 04-JUN-1998;
PR 98US-0088326.
PR 05-JUN-1998;
PR 98US-0088167.
PR 05-JUN-1998;
PR 98US-0088202.
PR 05-JUN-1998;
PR 98US-0088212.
PR 05-JUN-1998;
PR 98US-0088217.
PR 09-JUN-1998;
PR 98US-0088655.
PR 10-JUN-1998;
PR 98US-0088722.
PR 10-JUN-1998;
PR 98US-0088730.
PR 10-JUN-1998;
PR 98US-0088734.
PR 10-JUN-1998;
PR 98US-0088738.
PR 10-JUN-1998;
PR 98US-0088740.
PR 10-JUN-1998;
PR 98US-0088741.
PR 10-JUN-1998;
PR 98US-0088742.
PR 10-JUN-1998;
PR 98US-0088810.
PR 10-JUN-1998;
PR 98US-0088811.
PR 10-JUN-1998;
PR 98US-0088824.
PR 10-JUN-1998;
PR 98US-0088825.
PR 10-JUN-1998;
PR 98US-0088826.
PR 11-JUN-1998;
PR 98US-0088858.
PR 11-JUN-1998;
PR 98US-0088861.
PR 11-JUN-1998;
PR 98US-0088863.
PR 11-JUN-1998;
PR 98US-0088876.
PR 12-JUN-1998;
PR 98US-0089090.
PR 12-JUN-1998;
PR 98US-0089105.
PR 16-JUN-1998;
PR 98US-0089440.
PR 16-JUN-1998;
PR 98US-0089512.
PR 16-JUN-1998;
PR 98US-0089514.
PR 17-JUN-1998;
PR 98US-0089532.
PR 17-JUN-1998;
PR 98US-0089538.
PR 17-JUN-1998;
PR 98US-0089598.
PR 17-JUN-1998;
PR 98US-0089599.
PR 17-JUN-1998;
PR 98US-0089600.
PR 17-JUN-1998;
PR 98US-0089653.
PR 18-JUN-1998;
PR 98US-0089801.
PR 18-JUN-1998;
PR 98US-0089907.
PR 18-JUN-1998;
PR 98US-0089908.
PR 19-JUN-1998;
PR 98US-0089947.
PR 19-JUN-1998;
PR 98US-0089948.
PR 19-JUN-1998;
PR 98US-0089952.
PR 22-JUN-1998;
PR 98US-0090246.
PR 22-JUN-1998;
PR 98US-0090252.
PR 22-JUN-1998;
PR 98US-0090254.
PR 23-JUN-1998;
PR 98US-0090349.
PR 23-JUN-1998;
PR 98US-0090355.
PR 24-JUN-1998;
PR 98US-0090429.
PR 24-JUN-1998;
PR 98US-0090431.
PR 24-JUN-1998;
PR 98US-0090435.
PR 24-JUN-1998;
PR 98US-0090444.
PR 24-JUN-1998;
PR 98US-0090445.
PR 24-JUN-1998;
PR 98US-0090461.
PR 24-JUN-1998;
PR 98US-0090472.
PR 24-JUN-1998;
PR 98US-0090535.
PR 24-JUN-1998;
PR 98US-0090538.
PR 24-JUN-1998;
PR 98US-0090540.
PR 24-JUN-1998;
PR 98US-0090557.
PR 25-JUN-1998;
PR 98US-0090676.
PR 25-JUN-1998;
PR 98US-0090678.
PR 25-JUN-1998;
PR 98US-0090688.
PR 25-JUN-1998;
PR 98US-0090690.

18-FEB-2000; 2000WO-US04341.
 22-FEB-2000; 2000WO-US04414.
 24-FEB-2000; 2000WO-US04914.
 24-FEB-2000; 2000WO-US05004.
 02-MAR-2000; 2000WO-US05841.
 15-MAR-2000; 2000WO-US06884.
 20-MAR-2000; 2000WO-US07377.
 (GETH) GENENTECH INC.
 Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 Ferrera N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
 Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 Zhang Z;
 WPI: 2001-032160/04.
 N-PSDB; AAF44169.
 PRO polynucleotides used to produce polypeptides used to target
 bioactive molecules such as toxins, radiolabels or antibodies, to
 specific cells, to cause targeted cell death -
 Claim 12; Fig 139; 935pp; English.
 The present invention describes human secreted and transmembrane PRO
 proteins. The PRO proteins have cytostatic activity. The PRO proteins
 can be used for targeted delivery of bioactive molecules, such as
 toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
 sequences, and their fragments, can be used as hybridisation probes, in
 chromosomal and gene mapping, and in the generation of anti-sense RNA
 and DNA. They may also be used to produce transgenic animals which are
 used to develop and screen therapeutically useful reagents. The PRO
 nucleotide and protein sequence can be used for tissue typing and in
 treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
 AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
 in the isolation of human PRO sequences. AAF44087 to AAF44269 and
 AAF65154 to AAF65300 represent human PRO polynucleotide and protein
 sequences given in the exemplification of the present invention.
 Sequence 185 AA;
 Query Match 72.0%; Score 90; DB 22; Length 185;
 Best Local Similarity 72.0%; Pred. No. 1.7e-05;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
 QY 1 LDTWVKEQK--GKGPGGAPPKDLMY 23
 Db 97 Idalvkekklgkgpgpppgkglmy 121
 RESULT 6
 ID AAB50957 standard; Protein; 185 AA.
 XX AAB50957;
 AC AAB50957;
 XX 21-MAR-2001 (first entry)
 XX Human PRO1005 protein.
 DE Human; PRO; cytostatic; neurotropic; neuroprotective; respiratory general;
 KW antinflammatory; angiogenic; immunosuppressive; immunostimulant;
 KW PRO agonist; cancer; inflammatory disorder; immunological disorder.
 XX Homo sapiens.
 XX WO200073348-A2.
 XX 07-DEC-2000.
 XX 30-MAY-2000; 2000WO-US14941.
 02-JUN-1999; 99WO-US12252.
 22-JUN-1999; 99US-0140650.
 23-JUN-1999; 99US-0141037.
 23-JUN-1999; 99US-0144758.
 01-SEP-1999; 99WO-US20111.
 08-SEP-1999; 99WO-US20594.
 29-OCT-1999; 99US-0162506.
 30-NOV-1999; 99WO-US28313.
 01-DEC-1999; 99WO-US28634.
 02-DEC-1999; 99WO-US28551.
 16-DEC-1999; 99WO-US30095.
 20-DEC-1999; 99WO-US30989.
 06-JAN-2000; 2000WO-US00376.
 11-FEB-2000; 2000WO-US03565.
 18-FEB-2000; 2000WO-US04341.
 18-FEB-2000; 2000WO-US04342.
 02-MAR-2000; 2000WO-US05841.
 03-MAR-2000; 2000US-0187202.
 10-MAR-2000; 2000WO-US06319.
 15-MAR-2000; 2000WO-US06884.
 30-MAR-2000; 2000WO-US08439.
 17-MAY-2000; 2000WO-US13705.
 (GETH) GENENTECH INC.
 Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
 Shelton DL, Smith V, Watanabe CK, Wood WI;
 WPI: 2001-016509/02.
 N-PSDB; AAC91559.
 Twenty eight nucleic acids encoding PRO polypeptides which are useful
 for treating various tumors, e.g. breast cancer, and other
 inflammatory, angiogenic and immunological disorders -
 Claim 31; Fig 14; 188pp; English.
 The present sequence is one of twenty eight novel PRO polypeptides. The
 PRO polypeptides and their agonists, including antibodies, peptides, and
 small molecule agonists, may be used to treat various tumors, e.g.,
 cancers such as breast cancer, ovarian cancer, renal cancer, colorectal
 cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,
 central nervous system cancer, melanoma or leukaemia. They are also
 useful for treating other disorders such as neuronal, glial, astrocytal,
 hypothalamic and other glandular, macrophagal, epithelial, stromal and
 blastocoeleic disorders, and inflammatory, angiogenic and immunological
 disorders.
 Sequence 185 AA;
 Query Match 72.0%; Score 90; DB 22; Length 185;
 Best Local Similarity 72.0%; Pred. No. 1.7e-05;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
 QY 1 LDTWVKEQK--GKGPGGAPPKDLMY 23
 Db 97 Idalvkekklgkgpgpppgkglmy 121
 RESULT 7
 ID AAB38329 standard; Protein; 186 AA.
 XX AAB38329;
 AC AAB38329;
 XX 31-JAN-2001 (first entry)
 XX Human secreted protein encoded by gene 9 clone HNSA53.
 DE Immunosuppressive; antiarthritic; antirheumatic; antiproliferative;
 KW cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective;

KW nootropic; antibacterial; virucide; fungicide; opthalmological; human;
 KW vulnerary; gene therapy; infection; secreted protein.
 XX Homo sapiens.
 XX WO200061623-A1.
 XX 19-OCT-2000.
 XX 06-APR-2000; 2000WO-US08979.
 XX 09-APR-1999; 99US-0128693.
 XX 26-APR-1999; 99US-0130991.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Ruben SM, Ni J, Komatsoulis GA, Rosen CA, Soppet DR, Shi Y;
 PI Lafleur DW, Olsen HS, Ebner R, Florence KA, Moore PA, Birse CE;
 PI Young PE;
 XX WPI; 2000-647418/62.
 XX New nucleic acid molecules encoding 62 human secreted proteins for
 PT diagnosing, preventing, treating or ameliorating medical conditions and
 PT used as food additives or preservatives -
 XX Claim 11; Page 598; 716pp; English.
 XX Sequences AAB38321-B38396 represent the amino acid sequences of 62
 CC human secreted proteins encoded by the genes AAC69512-C69587. The genes
 CC and proteins are useful for preventing, ameliorating or treating medical
 CC conditions, e.g. by protein or gene therapy. The genes are isolated from
 CC a range of human tissues disclosed in the specification. The nucleic
 CC acids, proteins, antibodies and (ant)agonists are useful in the
 CC diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.
 CC rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms
 CC of the breast or liver; (c) cardiovascular disorders e.g. cardiac
 CC arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e)
 CC angiogenesis; (f) nervous system disorders e.g. Alzheimer's disease; (g)
 CC infections caused by bacteria, viruses and fungi; and (h) ocular
 CC disorders e.g. corneal infection. The polypeptides can also be used to
 CC aid wound healing and epithelial cell proliferation, to prevent skin
 CC aging due to sunburn, to maintain organs before transplantation, for
 CC supporting cell culture of primary tissues, to regenerate tissues and in
 CC chemotaxis.
 XX SQ Sequence 186 AA;

Query Match 72.0%; Score 90; DB 21; Length 186;
 Best Local Similarity 72.0%; Pred. No. 1.7e-05;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
 QY 1 LDTMWKEQK--GKGPGGAPPKDLMY 23
 || :|||: ||||| ||| |||
 Db 97 ldlvkekklqgpgpgppkglmly 121

RESULT 8
 ID AAW69974
 XX AAW69974 standard; Protein; 194 AA.
 AC AAW69974;
 XX 16-NOV-1998 (first entry)
 XX Cancer associated protein.
 DE Cancer; PCR; Northern blotting; ribonuclease protection assay;
 KW diagnosis; metastatic cancer.
 XX Synthetic.
 OS Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
 XX

PN WO9837187-A1.
 XX 27-AUG-1998.
 XX 18-FEB-1998; 98WO-JP00667.
 XX 21-FEB-1997; 97JP-0052508.
 XX (TAKI) TAKARA SHUZO CO LTD.
 XX Asada K, Hino F, Kato I, Mukai H, Yoshikawa Y;
 XX WPI; 1998-467552/40.
 XX Detection of cancer cells in tissue samples - by changes in mRNA
 PT expression compared to normal tissue of specific cancer-associated
 PT gene sequences
 XX Claim 14; Page 64-65; 92pp; Japanese.
 XX The cancer associated proteins AAW69974-W69976 where used in the method
 CC of the invention to detect cancer cells in tissue samples or biological
 CC fluids. They are detected by monitoring the change in mRNA expression
 CC as compared to normal tissue of one or more cancer-associated genes
 CC whose cDNA stringently hybridises to cancer associated gene nucleic acid
 CC fragments. The change in expression may be an increase or a decrease
 CC compared to normal tissue. The mRNA expression may be determined by
 CC PCR, Northern blotting or ribonuclease protection assay, or by
 CC determining the change in the amount of protein encoded by the gene(s) as
 CC compared to normal tissue, for example by using a labelled antibody
 CC recognising the protein. Detection of cancer cells for cancer diagnosis,
 CC including detection of metastatic cancer cells in tissues other than the
 CC primary tumour site.
 XX SQ Sequence 194 AA;
 Query Match 72.0%; Score 90; DB 19; Length 194;
 Best Local Similarity 72.0%; Pred. No. 1.8e-05;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
 QY 1 LDTMWKEQK--GKGPGGAPPKDLMY 23
 || :|||: ||||| ||| |||
 Db 106 ldlvkekklqgpgpgppkglmly 130

RESULT 9
 AAY76591
 ID AAY76591 standard; Protein; 194 AA.
 XX AAY76591;
 AC AAY76591;
 XX 10-APR-2000 (first entry)
 XX Human ovarian tumor EST fragment encoded protein 87.
 DE Expressed sequence tag; EST; human; ovarian tumor; anticancer;
 KW gene therapy; treatment.
 XX Homo sapiens.
 OS DE19817557-A1.
 XX 21-OCT-1999.
 XX 09-APR-1998; 98DE-1017557.
 XX 09-APR-1998; 98DE-1017557.
 XX (META-) METAGEN GES GENOMFORSCHUNG MBH.
 XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
 XX

DR WPI: 1999-591920/51.
 DR N-PSDB; AAZ77487.
 XX
 PT New nucleic acid sequences expressed in ovarian, and some other, cancer
 PT tissues, and derived polypeptides, for treatment of ovarian cancer and
 PT identification of therapeutic agents.
 XX
 PS Claim 25; Page 279; 310pp; German.
 XX
 CC This invention describes novel nucleic acid (cDNA) sequences (A) which
 CC have anticancer activity and are highly expressed in ovarian tumor
 CC tissue (and some also in testis and breast cancer tissue). The products
 CC of the invention can be used for gene therapy. (A) are used (i) for
 CC recombinant expression of polypeptides (B) and (ii) to isolate complete
 CC genes. (B) are used (i) to identify agents suitable for treatment of
 CC ovarian cancer; (ii) directly for treating this form of cancer
 CC (including expression from gene therapy vectors) and (iii) for generation
 CC of specific antibodies. (A) are identified by assembling ESTs (expressed
 CC sequence tags) from a particular tissue type before comparison of
 CC expression patterns. This allows a significantly longer fragment of the
 CC gene to be revealed, so should reduce the number of failures associated
 CC with the fact that ESTs from different libraries may represent different
 CC parts of the same unknown gene, distorting the estimated frequency of
 CC occurrence in a particular tissue. AAY76505-Y76638 represent protein
 CC fragments encoded by the human ovarian tumor cDNA library derived EST
 CC fragments represented in AAZ77450-Z77572.
 XX
 SQ Sequence 194 AA;
 Query Match 72.0%; Score 90; DB 20; Length 194;
 Best Local Similarity 72.0%; Pred. No. 1.8e-05;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
 QY 1 LDTMVKEQK--GKGPGGAPKDLMY 23
 Db 106 ldlvkekklqgkgpggppkglmly 130
 ||:||||:||||| |||||
 RESULT 10
 ABB59646
 ID ABB59646 standard; Protein: 1194 AA.
 XX
 AC ABB59646;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 5730.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 XX (PEKE) PE CORP NY.
 PA
 XX Venter JC, Adams M, Li PWD, Myers EW;
 PI
 XX WPI: 2001-656860/75.
 DR
 DR N-PSDB; ABL03749.
 XX
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -

XX Disclosure; SEQ ID NO 5730; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 1194 AA;
 Query Match 43.2%; Score 54; DB 22; Length 1194;
 Best Local Similarity 64.3%; Pred. No. 24;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 5 VKEQKKGKGGGAPP 18
 Db 613 mkspngngpggapp 626
 :| | | | | | | |
 RESULT 11
 AAR79655
 ID AAR79655 standard; Protein: 298 AA.
 XX
 AC AAR79655;
 XX
 DT 06-DEC-1995 (first entry)
 XX
 DE Human UBC/CDC34 protein.
 XX
 KW Ubiquitin-conjugating enzyme; UBC/CDC34; cell cycle;
 KW cell proliferation; cancer; psoriasis; fibrosis.
 XX
 OS Homo sapiens.
 XX
 PN WO9518974-A.
 XX
 PD 13-JUL-1995.
 XX
 PF 04-JAN-1995; 95WO-US00164.
 XX
 PR 13-SEP-1994; 94US-0305520.
 PR 04-JAN-1994; 94US-0176937.
 PR 23-MAY-1994; 94US-0247904.
 PR 27-MAY-1994; 94US-0250795.
 XX
 XX (MITO-) MITOTIX INC.
 PA
 XX Cottarel G, Draetta G, Eckstein JW, Gyuris J, Rolfe M;
 XX WPI: 1995-255137/33.
 DR
 DR N-PSDB; AAO97845.
 XX
 XX Identifying inhibitors of ubiquitin mediated proteolysis of cell cycle
 PT regulatory proteins - also new ubiquitin conjugating enzymes, their
 PT related nucleic acid, vectors, antibodies etc., useful for regulating
 PT e.g. cell proliferation
 XX
 XX Disclosure; Page 107-108; 157pp; English.
 PS
 XX Human UBC3/CDC34 cDNA (given in AAO97845) was amplified from a HeLa
 CC cell cDNA library. The gene was subcloned into a baculovirus or
 CC PGEX vector for expression of recombinant UBC/CDC34 in Sf9 insect
 CC or E. coli cells for use as a component of an in vitro ubiquitin
 CC conjugating system.
 XX

SQ Sequence 298 AA;

Query Match 40.8%; Score 51; DB 16; Length 298;
 Best Local Similarity 61.5%; Pred. No. 16;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 KEQKGKGGGAPP 18
 : : | : : : : :
 Db 21 eeeagggpggssp 33

RESULT 12

AA39971
 ID AAY39971 standard; Protein; 298 AA.

XX AC AAY39971;

XX DT 15-DEC-1999 (first entry)

XX DE Human UBC3/CDC34 protein sequence.

XX KW Ubiquitin conjugating enzyme; UbCE; ubiquitin-mediated proteolysis;
 cell-cycle regulatory protein; ubiquitination inhibitor; atherosclerosis;
 KW proliferative disorder; cancer; restenosis; tissue connective disorder;
 KW wound healing; fibrosis disorder; rheumatoid arthritis; scleroderma;
 KW insulin dependent diabetes mellitus; glomerulonephritis; cirrhosis;
 KW diagnosis; therapy; UBC3/CDC34.

XX OS Homo sapiens.

XX PN US5968761-A.

XX PD 19-OCT-1999.

XX PF 07-JUN-1995; 95US-0486663.

XX PR 04-JAN-1994; 94US-0176937.

XX PR 23-MAY-1994; 94US-0247904.

XX PR 13-SEP-1994; 94US-0250795.

XX PA (MITO-) MITOTIX INC.

XX PI Chiu MI, Cottarel G, Berlin V, Damagnez V, Draetta G, Rolfe M;

XX DR WPI; 1999-590402/50.

XX DR N-PSDB; AAZ27573.

XX PT Identifying ubiquitination inhibitors using novel ubiquitin conjugating

XX PT enzymes -

XX PS Example 2; Column 99-102; 61pp; English.

XX CC This sequence is the human UBC3/CDC34 protein. The invention relates
 to assays for identifying an inhibitor of ubiquitin-mediated proteolysis
 of a cell-cycle regulatory protein comprising contacting a candidate
 agent with an ubiquitin-conjugating system and measuring the level of
 ubiquitination. The ubiquitin-conjugating system comprises:
 (a) a reconstituted protein mixture including a ubiquitin conjugating
 enzyme (UbCE) produced by the expression of a nucleic acid which
 hybridizes under high stringency conditions to human UbCE, *Candida*
 albicans UbCE, or *Schizosaccharomyces pombe* UbCE coding sequences;
 (b) a regulatory protein; and (c) ubiquitin. The polynucleotides are
 useful for identifying ubiquitination inhibitors. The polynucleotides are
 polypeptides, antisense compounds and antibodies against them may also be
 useful for the treatment and/or diagnosis of proliferative disorders
 (e.g. cancer, atherosclerosis, or restenosis), tissue connective
 disorders, controlling wound healing, and disorders characterized by
 fibrosis (e.g. rheumatoid arthritis, insulin dependent diabetes mellitus,
 glomerulonephritis, cirrhosis, and scleroderma).

XX SQ Sequence 298 AA;

Query Match 40.8%; Score 51; DB 20; Length 298;
 Best Local Similarity 61.5%; Pred. No. 16;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 KEQKGKGGGAPP 18
 : : | : : : : :
 Db 21 eeeagggpggssp 33

RESULT 13

AA3179
 ID AAB03179 standard; Protein; 298 AA.

XX AC AAB03179;

XX DT 23-OCT-2000 (first entry)

XX DE Human UBC/CDC34.

XX KW UBC/CDC34; ubiquitin conjugating enzyme; ubiquitin mediated proteolysis;
 human; cellular protein half life; ubiquitination inhibitor; p53;
 KW cyclin; cell cycle regulator; myc deregulation; human papillomavirus;
 KW HPV-18 E6 protein; cervical cancer; skin cancer; epidermal hyperplasia;
 KW epidermal neoplasia; psoriasis; connective tissue disorder;
 KW wound healing; cytostatic; antiproliferative; anticancer; antipsoriatic.

XX OS Homo sapiens.

XX PN US6068982-A.

XX PD 30-MAY-2000.

XX PF 17-DEC-1996; 96US-0767942.

XX PR 07-JUN-1995; 95US-0486663.

XX PR 04-JAN-1994; 94US-0176937.

XX PR 23-MAY-1994; 94US-0247904.

XX PR 27-MAY-1994; 94US-0250795.

XX PR 13-SEP-1994; 94US-0305520.

XX PA (MITO-) MITOTIX INC.

XX PI Chiu MI, Cottarel G, Berlin V, Draetta G, Damagnez V, Rolfe M;

XX DR WPI; 2000-410854/35.

XX DR N-PSDB; AAA61626.

XX PT Identifying an inhibitor of ubiquitin mediated proteolysis of

XX PT regulatory protein for treating cancers involves measuring

XX PT ubiquitination levels of the protein in the presence of candidate agent

XX PT in an eukaryotic cell -

XX PS Example 2; Column 117-118; 73pp; English.

XX CC The invention relates to a method of identifying an inhibitor of
 ubiquitin-mediated proteolysis of a cell cycle regulatory protein
 comprising contacting an engineered eukaryotic cell with a candidate
 agent. The eukaryotic cells is engineered to express a recombinant
 human, *Candida albicans* or *Schizosaccharomyces pombe* ubiquitin-
 conjugating enzyme (AAB03169-H03171), a cell cycle regulatory protein
 (such as p53) and ubiquitin. The specification also discloses novel
Candida albicans and *Schizosaccharomyces pombe* ubiquitin-conjugating
 enzymes, caubCE and spubCE (AAB03170, AAB03171), and two novel human
 ubiquitin-conjugating enzymes, hUbCE and rapUBC (AAB03169, AAB03173).
 The ubiquitin-mediated proteolysis system is the major pathway for the
 selective, controlled degradation of intracellular proteins in
 eukaryotic cells. In particular, this system controls the half-lives of
 cellular proteins, and is important in controlling the levels of proteins
 involved in cell cycle progression. Alterations in the ubiquitination of
 these proteins may therefore play a role in the development of cancers.
 For example, human papillomaviruses such as HPV-18 encode a transforming

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protein, E6 (AAB03176), which combines with a cellular E6-associated protein (E6-AP; AAB03177) to stimulate the ubiquitination of p53, thus targeting it for degradation. The ubiquitination inhibitors identified according to the method of the invention are useful for treatment of cervical cancers and connective tissue disorders and for controlling the wound healing process. They are also useful in treatment of hyperplastic epidermal conditions such as psoriasis, neoplastic epidermal conditions, skin cancers e.g., basal cell carcinomas, squamous cell carcinomas. The inhibitors are useful for deregulating myc expression and rendering the cells sensitive to chemotherapeutic treatment or to upset the balance of transformed cells and cause apoptosis to occur. Inhibitors of ubiquitin-mediated degradation of cyclins are useful as antiproliferative agents. The present sequence represents human UBC/CDC34.

XX Sequence 298 AA;

Query Match 40.8%; Score 51; DB 21; Length 298;
Best Local Similarity 61.5%; Pred. No. 16;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 KEQKKGKGGGAPP 18
:|: | |||||
Db 21 eeeagggpgspp 33

RESULT 14
ABG07765
ID ABG07765 standard; Protein: 307 AA.

XX AC ABG07765;
XX DT 13-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #7756.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX WPI: 2001-639362/73.

XX DR N-PSDB; AAS71952.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity

XX Claim 20; SEQ ID NO 38124; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as

CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 307 AA;

Query Match 40.8%; Score 51; DB 22; Length 307;
Best Local Similarity 61.5%; Pred. No. 16;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 KEQKKGKGGGAPP 18
:|: | |||||
Db 21 eeeagggpgspp 33

RESULT 15
ABG08168
ID ABG08168 standard; Protein: 307 AA.

XX AC ABG08168;

XX DT 13-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #8159.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX WPI: 2001-639362/73.

XX DR N-PSDB; AAS72355.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity

XX Claim 20; SEQ ID NO 38527; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical

CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations in
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX

SQ Sequence 307 AA;

Query Match 40.8%; Score 51; DB 22; Length 307;
 Best Local Similarity 61.5%; Pred. No. 16;

Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 KEQKGGGGGAPP 18

Db 21 eeeagggggspp 33
 :|: | |||:|

Search completed: September 4, 2002, 16:45:02
 Job time: 378 sec

Thu Sep 5 11:23:34 2002

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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:46:05 ; Search time 57.74 Seconds
(without alignments)
9.730 Million cell updates/sec

Title: US-09-821-726-2
Perfect score: 125
Sequence: 1 LDMVKEQKGGPGGAPKDLMY 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	40.8	298	3	US-08-767-942A-25
2	46	36.8	467	4	US-09-002-361-3
3	46	36.8	496	4	US-09-002-361-2
4	45.5	36.4	402	3	US-08-709-974A-1
5	45.5	36.4	402	3	US-08-709-974A-5
6	45.5	36.4	415	2	US-08-833-642A-5
7	45.5	36.4	415	3	US-08-709-974A-4
8	45.5	36.4	415	4	US-09-069-632-1
9	45.5	36.4	435	1	US-08-361-920-27
10	45.5	36.4	435	1	US-08-479-939-27
11	45.5	36.4	435	1	US-08-483-432-27
12	45.5	36.4	435	1	US-09-069-632-3
13	45	36.0	265	2	US-08-484-905-119
14	45	36.0	265	3	US-08-481-985B-119
15	45	36.0	265	4	US-08-370-476-119
16	45	36.0	298	5	PCT-US95-02689-41
17	45	36.0	298	5	US-08-207-481-39
18	45	36.0	992	4	US-08-890-865A-1
19	44	35.2	402	2	US-08-709-979A-3
20	43	34.4	9	2	US-08-460-890A-57
21	43	34.4	9	3	US-08-167-641C-57
22	43	34.4	9	4	US-08-460-971A-57
23	43	34.4	9	4	US-08-462-040-57
24	43	34.4	321	1	US-08-362-670B-26
25	43	34.4	321	3	US-08-333-576C-26
26	43	34.4	321	4	US-08-808-324-26
27	43	34.4	321	5	PCT-US94-14030A-26

28	43	34.4	456	2	US-08-709-979A-1	Sequence 1, Appli
29	43	34.4	456	3	US-08-709-974A-11	Sequence 11, Appl
30	43	34.4	880	4	US-09-378-255-6	Sequence 6, Appli
31	43	34.4	880	4	US-09-141-212-2	Sequence 2, Appli
32	43	34.4	880	4	US-09-141-212-4	Sequence 4, Appli
33	43	34.4	880	4	US-09-552-351-4	Sequence 4, Appli
34	43	34.4	880	4	US-09-251-372-6	Sequence 6, Appli
35	43	34.4	880	4	US-09-561-138-2	Sequence 2, Appli
36	43	34.4	880	4	US-09-561-138-4	Sequence 4, Appli
37	43	34.4	880	4	US-09-715-336-6	Sequence 6, Appli
38	43	34.4	880	4	US-09-811-241-6	Sequence 2, Appli
39	43	34.4	880	4	US-09-802-839-4	Sequence 4, Appli
40	42	33.6	246	3	US-08-675-885-2	Sequence 2, Appli
41	42	33.6	296	2	US-08-700-637-4	Sequence 4, Appli
42	42	33.6	307	1	US-07-982-112-2	Sequence 2, Appli
43	42	33.6	378	4	US-09-500-569-10	Sequence 10, Appli
44	42	33.6	819	4	US-09-651-856-15	Sequence 15, Appli
45	42	33.6	1060	3	US-08-931-820-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-767-942A-25
; Sequence 25, Application US/08767942A
; Patent No. 6068982
; GENERAL INFORMATION:
; APPLICANT: Rolfe, Mark
; APPLICANT: Chiu, M. Isabel
; APPLICANT: Berlin, Vivian
; APPLICANT: Damagnez, Veronique
; APPLICANT: Draetta, Giulio
; APPLICANT: Guillaume, Cottarel
; TITLE OF INVENTION: UBIQUITIN CONJUGATING ENZYMES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,942A
; FILING DATE: 17-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-029.04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 298 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-767-942A-25

Query Match 40.8%; Score 51; DB 3; Length 298;
Best Local Similarity 61.5%; Pred. No. 4.9;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 KEQKGGPGGAPP 18
: : : | | | | |

Db 21 EEEAGGGGSGPP 33

RESULT 2
US-09-002-361-3
; Sequence 3, Application US/09002361
; Patent No. 6329516
; GENERAL INFORMATION:
; APPLICANT: Halling, Blaik
; TITLE OF INVENTION: Lepidopteran GABA-Gated Chloride
; TITLE OF INVENTION: Channels
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/002,361
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-09-002-361-3

Query Match 36.8%; Score 46; DB 4; Length 467;
Best Local Similarity 40.0%; Pred. No. 41;
Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 LDTMVKEQKGKGGGAPPKD 20
I: : : || || || ||
Db 380 LENTINGARGPAGPAPPAD 399

RESULT 3
US-09-002-361-2
; Sequence 2, Application US/09002361
; Patent No. 6329516
; GENERAL INFORMATION:
; APPLICANT: Halling, Blaik
; TITLE OF INVENTION: Lepidopteran GABA-Gated Chloride
; TITLE OF INVENTION: Channels
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543

Query Match 36.8%; Score 46; DB 4; Length 467;
Best Local Similarity 40.0%; Pred. No. 41;
Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 LDTMVKEQKGKGGGAPPKD 20
I: : : || || || ||
Db 380 LENTINGARGPAGPAPPAD 399

RESULT 4
US-08-709-974A-1
; Sequence 1, Application US/08709974A
; Patent No. 6117664
; GENERAL INFORMATION:
; APPLICANT: Sch lein, Martin
; APPLICANT: Rosholm, Peter
; APPLICANT: Nielsen, Jack Bech
; APPLICANT: Hansen, Svend Aage
; APPLICANT: von der Osten, Claus
; TITLE OF INVENTION: No. 6117664el Alkaline Cellulases
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6117664o No. 6117664disk of No. 6117664th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,974A
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta
; REGISTRATION NUMBER: 35,127y
; REFERENCE/DOCKET NUMBER: 4160.414-US
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-709-974A-1

Query Match 36.4%; Score 45.5; DB 3; Length 402;
Best Local Similarity 36.7%; Pred. No. 42;
Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;

QY 1 LDTM---VKEQKKGPGGA-----PPKDL 21
DB 33 LDSLSHPHRAEGLGPGCGDGNPPPKDV 62

RESULT 5
US-08-709-974A-5
Sequence 5, Application US/08709974A
Patent No. 6117664
GENERAL INFORMATION:
APPLICANT: Sch lein, Martin
APPLICANT: Rosholm, Peter
APPLICANT: Nielsen, Jack Bech
APPLICANT: Hansen, Svend Aage
APPLICANT: von der Osten,Claus
TITLE OF INVENTION: No. 6117664el Alkaline Cellulases
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6117664o No. 6117664disk of No. 6117664th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,974A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta
REGISTRATION NUMBER: 35,127Y
REFERENCE/DOCKET NUMBER: 4160.414-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-709-974A-5

Query Match 36.4%; Score 45.5; DB 3; Length 402;
Best Local Similarity 36.7%; Pred. No. 42;
Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;

QY 1 LDTM---VKEQKKGPGGA-----PPKDL 21
DB 33 LDSLSHPHRAEGLGPGCGDGNPPPKDV 62

RESULT 6
US-08-833-642A-5
Sequence 5, Application US/08833642A
Patent No. 5883066
GENERAL INFORMATION:
APPLICANT: Ivan M. A. J. Herbots et al.
TITLE OF INVENTION: Liquid Detergent Compositions
Containing Cellulase and Amine
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jackie Ann Zurcher
ADDRESSEE: Dinsmore & Shohl LLP
STREET: 255 E. Fifth Street
STREET: 1900 Chemed Center
CITY: Cincinnati
STATE: Ohio
COUNTRY: USA
ZIP: 45202
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,642A
FILING DATE: April 8, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Zurcher, J. A. P42,251
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: CM551C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (513) 977-8377
TELEFAX: (513) 977-8141
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-642A-5

Query Match 36.4%; Score 45.5; DB 2; Length 415;
Best Local Similarity 36.7%; Pred. No. 43;
Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;

QY 1 LDTM---VKEQKKGPGGA-----PPKDL 21
DB 33 LDSLSHPHRAEGLGPGCGDGNPPPKDV 62

RESULT 7
US-08-709-974A-4
Sequence 4, Application US/08709974A
Patent No. 6117664
GENERAL INFORMATION:
APPLICANT: Sch lein, Martin
APPLICANT: Rosholm, Peter
APPLICANT: Nielsen, Jack Bech
APPLICANT: Hansen, Svend Aage
APPLICANT: von der Osten,Claus
TITLE OF INVENTION: No. 6117664el Alkaline Cellulases
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6117664o No. 6117664disk of No. 6117664th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,974A
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta
; REGISTRATION NUMBER: 35,127Y
; REFERENCE/DOCKET NUMBER: 4160.414-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-709-974A-4

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Query Match          36.4%; Score 45.5; DB 3; Length 415;
Best Local Similarity 36.7%; Pred. No. 43;
Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;

QY 1 LDTM---VKEQKKGPGGA-----PPKDL 21
   |||: : |||||
Db 33 LDSLHPHRAEGLPGCGDGNPPPKDV 62

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RESULT 8

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US-09-069-632-1
; Sequence 1, Application US/09069632
; Patent No. 6261828
; GENERAL INFORMATION:
; APPLICANT: Lund, Henrik
; TITLE OF INVENTION: A Process For Combined Desizing
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6261828o No. 6261828disk of No. 6261828th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,632
; FILING DATE: 29-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK96/00469
; FILING DATE: 15-NOV-1996
; APPLICATION NUMBER: 1278/95
; FILING DATE: 15-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta
; REGISTRATION NUMBER: 35,127
; REFERENCE/DOCKET NUMBER: 4588.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 415 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-069-632-1

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Query Match          36.4%; Score 45.5; DB 4; Length 415;
Best Local Similarity 36.7%; Pred. No. 43;
Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;

QY 1 LDTM---VKEQKKGPGGA-----PPKDL 21
   |||: : |||||
Db 33 LDSLHPHRAEGLPGCGDGNPPPKDV 62

```

RESULT 9

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US-08-361-920-27
; Sequence 27, Application US/08361920
; Patent No. 5457046
; GENERAL INFORMATION:
; APPLICANT: Woeldike, Helle F.
; APPLICANT: Hagen, Frederick
; APPLICANT: Hjort, Carsten M.
; APPLICANT: Sven, Hastrup
; TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5457046o No. 5457046disk of No. 5457046th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,920
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/940,860
; FILING DATE: 28-OCT-1992
; APPLICATION NUMBER: DK 1158/90
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK91/00124
; FILING DATE: 08-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3435.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-867-0298
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-361-920-27

```

```

Query Match          36.4%; Score 45.5; DB 1; Length 435;
Best Local Similarity 36.7%; Pred. No. 46;
Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;

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Thu Sep 5 11:23:34 2002

```
QY 1 LDTM---VKEQKGGGGA-----PPKDL 21
    ||::: : : |||||
Db 53 LDSLSHPHRAEGLGPGCGDGNPPPKDV 82

RESULT 10
US-08-479-939-27
; Sequence 27, Application US/08479939
; Patent No. 5686593
; GENERAL INFORMATION:
; APPLICANT: Woeldike, Helle F.
; APPLICANT: Hagen, Frederick
; APPLICANT: Hjort, Carsten M.
; APPLICANT: Sven, Hastrup
; TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5763254o No. 5763254disk of No. 5763254th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,432
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,920
; FILING DATE:
; APPLICATION NUMBER: US 07/940,860
; FILING DATE: 28-OCT-1992
; APPLICATION NUMBER: DK 1158/90
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK91/00124
; FILING DATE: 08-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3435.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-867-0298
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-432-27

Query Match 36.4%; Score 45.5; DB 1; Length 435;
Best Local Similarity 36.7%; Pred. No. 46;
Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;

QY 1 LDTM---VKEQKGGGGA-----PPKDL 21
    ||::: : : |||||
Db 53 LDSLSHPHRAEGLGPGCGDGNPPPKDV 82

RESULT 12
US-09-069-632-3
; Sequence 3, Application US/09069632
; Patent No. 6261828
; GENERAL INFORMATION:
; APPLICANT: Lund, Henrik
; TITLE OF INVENTION: A Process For Combined Desizing
; TITLE OF INVENTION: And Stone-Washing of Dyed Denim
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6261828o No. 6261828disk of No. 6261828th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
```

ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,632
FILING DATE: 29-APR-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK96/00469
FILING DATE: 15-NOV-1996
APPLICATION NUMBER: 1278/95
FILING DATE: 15-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 4588.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-069-632-3

Query Match 36.4%; Score 45.5; DB 4; Length 435;
Best Local Similarity 36.7%; Pred. No. 46;
Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;
QY 1 LDTW---VKEQKGGKGGGA-----PPKDL 21
|||: : : ||||| |||||
Db 53 LDSLSHPHRAEGLGPGGCDGWNPPPKDV 82

RESULT 13
US-08-484-905-119
Sequence 119, Application US/08484905
Patent No. 5976551
GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: An Altered Major Histocompatibility
TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
TITLE OF INVENTION: Determinant
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,905
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 03495.0106-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 119:
SEQUENCE CHARACTERISTICS:
LENGTH: 265 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-905-119

Query Match 36.0%; Score 45; DB 2; Length 265;
Best Local Similarity 36.4%; Pred. No. 32;
Matches 8; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
QY 1 LDTWVKEQKGGKGGAPPKDL 22
|||: : : ||||| |||||
Db 243 LGLFIRHSQKGRGPPAGLL 264

RESULT 14
US-08-481-985B-119
Sequence 119, Application US/08481985B
Patent No. 6011146
GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,985B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0106-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 119:
SEQUENCE CHARACTERISTICS:

Query Match 36.0%; Score 45; DB 4; Length 265;
 Best Local Similarity 36.4%; Pred. No. 32;
 Matches 8; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 LDTMVKEQKGGGAPPKDL 22
 DB 243 LGLFIRHRQKGGPPAGLL 264

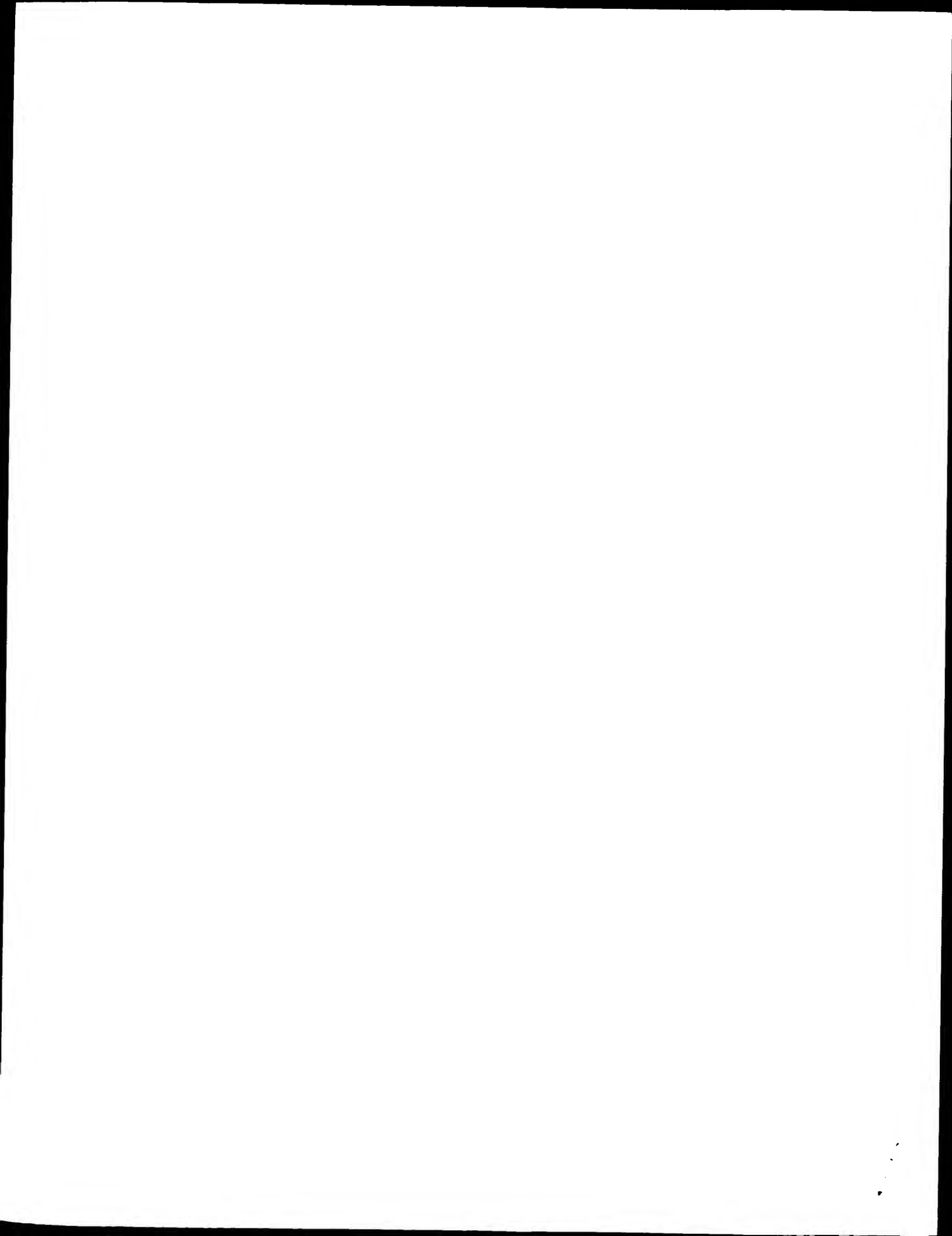
Search completed: September 4, 2002, 16:46:06
 Job time: 327 sec

LENGTH: 265 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-481-985B-119

Query Match 36.0%; Score 45; DB 3; Length 265;
 Best Local Similarity 36.4%; Pred. No. 32;
 Matches 8; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 LDTMVKEQKGGGAPPKDL 22
 DB 243 LGLFIRHRQKGGPPAGLL 264

RESULT 15
 US-08-370-476-119
 ; Sequence 119, Application US/08370476
 ; Patent No. 6153408
 ; GENERAL INFORMATION:
 ; APPLICANT: Mottez, Estelle
 ; APPLICANT: Abastado, Jean-Pierre
 ; APPLICANT: Kourilsky, Philippe
 ; APPLICANT: Lone, Yu-Chun
 ; APPLICANT: Ojcius, David
 ; APPLICANT: Casrouge, Armanda
 ; TITLE OF INVENTION: Altered Major Histocompatibility Complex
 ; TITLE OF INVENTION:
 ; NUMBER OF SEQUENCES: 127
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ; ADDRESS: Dunner
 ; STREET: 1300 I Street, N.W., Suite 700
 ; CITY: Washington
 ; STATE: D.C.
 ; ZIP: 20005-3315
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/370,476
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/117,575
 ; FILING DATE: 07-SEP-1993
 ; APPLICATION NUMBER: US 08/072,787
 ; FILING DATE: 06-JUN-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/801,818
 ; FILING DATE: 05-DEC-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/792,473
 ; FILING DATE: 15-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Meyers, Kenneth J.
 ; REGISTRATION NUMBER: 25,146
 ; REFERENCE/DOCKET NUMBER: 05243.0001-01000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-408-4000
 ; TELEFAX: 202-408-4400
 ; INFORMATION FOR SEQ ID NO: 119:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 265 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-370-476-119



Thu Sep 5 11:23:34 2002

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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:59:19 : Search time 704.77 seconds
(without alignments)
11.487 Million cell updates/sec

Title: US-09-821-726-2

Perfect score: 125

Sequence: 1 LDTMWKEQKGKGGAPKPDLMY 23

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_Main.*

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- 4: /cgn2_6/ptodata/2/paa/US080_COMB.pep.*
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- 8: /cgn2_6/ptodata/2/paa/US084_COMB.pep.*
- 9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
- 10: /cgn2_6/ptodata/2/paa/US086_COMB.pep.*
- 11: /cgn2_6/ptodata/2/paa/US087_COMB.pep.*
- 12: /cgn2_6/ptodata/2/paa/US088_COMB.pep.*
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- 26: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	125	100.0	23	22	US-09-821-726-2
2	125	100.0	184	22	US-09-821-726-16
3	90	72.0	25	22	US-09-821-726-10
4	90	72.0	150	13	US-08-906-708-24
5	90	72.0	182	20	US-09-684-524-212
6	90	72.0	182	24	US-10-050-704-212
7	90	72.0	185	1	PCT-US98-16318-18
					Sequence 2, Appli
					Sequence 16, Appl
					Sequence 10, Appl
					Sequence 24, Appl
					Sequence 212, App
					Sequence 18, Appl

8	90	72.0	185	15	US-09-130-189-18	Sequence 18, Appl
9	90	72.0	185	20	US-09-684-524-105	Sequence 105, App
10	90	72.0	185	21	US-09-709-238-211	Sequence 211, App
11	90	72.0	185	21	US-09-746-783-146	Sequence 146, App
12	90	72.0	185	22	US-09-821-726-13	Sequence 13, Appl
13	90	72.0	185	23	US-09-941-992-211	Sequence 211, App
14	90	72.0	185	23	US-09-989-279-211	Sequence 211, App
15	90	72.0	185	23	US-09-989-293A-211	Sequence 211, App
16	90	72.0	185	23	US-09-989-721-211	Sequence 211, App
17	90	72.0	185	23	US-09-989-722-211	Sequence 211, App
18	90	72.0	185	23	US-09-989-723-211	Sequence 211, App
19	90	72.0	185	23	US-09-989-724-211	Sequence 211, App
20	90	72.0	185	23	US-09-989-725-211	Sequence 211, App
21	90	72.0	185	23	US-09-989-726-211	Sequence 211, App
22	90	72.0	185	23	US-09-989-727-211	Sequence 211, App
23	90	72.0	185	23	US-09-989-728-211	Sequence 211, App
24	90	72.0	185	23	US-09-989-729A-211	Sequence 211, App
25	90	72.0	185	23	US-09-989-730-211	Sequence 211, App
26	90	72.0	185	23	US-09-989-731-211	Sequence 211, App
27	90	72.0	185	23	US-09-989-732-211	Sequence 211, App
28	90	72.0	185	23	US-09-989-734-211	Sequence 211, App
29	90	72.0	185	23	US-09-989-735-211	Sequence 211, App
30	90	72.0	185	23	US-09-989-862-211	Sequence 211, App
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32	90	72.0	185	23	US-09-990-436-211	Sequence 211, App
33	90	72.0	185	23	US-09-990-437-211	Sequence 211, App
34	90	72.0	185	23	US-09-990-438-211	Sequence 211, App
35	90	72.0	185	23	US-09-990-439-211	Sequence 211, App
36	90	72.0	185	23	US-09-990-440-211	Sequence 211, App
37	90	72.0	185	23	US-09-990-441-211	Sequence 211, App
38	90	72.0	185	23	US-09-990-442-211	Sequence 211, App
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40	90	72.0	185	23	US-09-990-444-211	Sequence 211, App
41	90	72.0	185	23	US-09-990-456-211	Sequence 211, App
42	90	72.0	185	23	US-09-990-562-211	Sequence 211, App
43	90	72.0	185	23	US-09-990-711-211	Sequence 211, App
44	90	72.0	185	23	US-09-990-726-211	Sequence 211, App
45	90	72.0	185	23	US-09-991-073-211	Sequence 211, App

ALIGNMENTS

RESULT 1
US-09-821-726-2
; Sequence 2, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: CASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-821-726-2

Query Match 100.0%; Score 125; DB 22; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.4e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDTMWKEQKGKGGAPKPDLMY 23
|||||
Db 1 LDTMWKEQKGKGGAPKPDLMY 23

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RESULT 2
US-09-821-726-16
; Sequence 16, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-821-726-16

Query Match
Best Local Similarity 100.0%; Score 125; DB 22; Length 184;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDTWVKEQKGKGGAPPKDLMY 23
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Db 97 LDTWVKEQKGKGGAPPKDLMY 119

RESULT 3
US-09-821-726-10
; Sequence 10, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-821-726-10

Query Match
Best Local Similarity 72.0%; Score 90; DB 22; Length 25;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTWVKEQK--GKGGAPPKDLMY 23
| | : | | | | | | | | | | | | | | |
Db 1 LDALVKEKKLOGKGGPPPKGLMY 25

RESULT 4
US-08-906-708-24
; Sequence 24, Application US/08906708
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; APPLICANT: Agostino, Michael J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING THEM
```

```
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,708
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: P-41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-906-708-24

Query Match
Best Local Similarity 72.0%; Score 90; DB 13; Length 150;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTWVKEQK--GKGGAPPKDLMY 23
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Db 97 LDALVKEKKLOGKGGPPPKGLMY 121

RESULT 5
US-09-684-524-212
; Sequence 212, Application US/09684524
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039p1
; CURRENT APPLICATION NUMBER: US/09/684,524
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 212
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-684-524-212

Query Match
Best Local Similarity 72.0%; Score 90; DB 20; Length 182;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTWVKEQK--GKGGAPPKDLMY 23
| | : | | | | | | | | | | | | | | |
Db 97 LDALVKEKKLOGKGGPPPKGLMY 121
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us-09-821-726-2.rapm

Thu Sep 5 11:23:34 2002

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RESULT 8
US-09-130-189-18
; Sequence 18, Application US/09130189
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI6051A
; CURRENT APPLICATION NUMBER: US/09/130,189
; CURRENT FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-130-189-18

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Query Match 72.0%; Score 90; DB 15; Length 185;
Best Local Similarity 72.0%; Pred. No. 0.00048;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

Qy 1 LDTMWKEQK--GKGPGGAPPKDLMY 23
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Db 97 LDALVKEKKLOGKGGPPPKGLMY 121

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RESULT 9
US-09-684-524-105
; Sequence 105, Application US/09684524
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/09/684,524
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-684-524-105

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Query Match 72.0%; Score 90; DB 20; Length 185;
Best Local Similarity 72.0%; Pred. No. 0.00048;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

Qy 1 LDTMWKEQK--GKGPGGAPPKDLMY 23
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Db 97 LDALVKEKKLOGKGGPPPKGLMY 121

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RESULT 10
US-09-709-238-211
; Sequence 211, Application US/09709238
; GENERAL INFORMATION:

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RESULT 6
US-10-050-704-212
; Sequence 212, Application US/10050704
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/10/050,704
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 09/684,524
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 212
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-704-212

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Query Match 72.0%; Score 90; DB 24; Length 182;
Best Local Similarity 72.0%; Pred. No. 0.00047;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

Qy 1 LDTMWKEQK--GKGPGGAPPKDLMY 23
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Db 97 LDALVKEKKLOGKGGPPPKGLMY 121

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RESULT 7
PCT-US98-16318-18
; Sequence 18, Application PC/TUS9816318
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI6051A
; CURRENT APPLICATION NUMBER: PCT/US98/16318
; CURRENT FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US98-16318-18

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Query Match 72.0%; Score 90; DB 1; Length 185;
Best Local Similarity 72.0%; Pred. No. 0.00048;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

Qy 1 LDTMWKEQK--GKGPGGAPPKDLMY 23
   |||:|:~| ||||| ||| |||
Db 97 LDALVKEKKLOGKGGPPPKGLMY 121

```

APPLICANT: Baker, Kevin
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Yuan, Jean
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding the Same
FILE REFERENCE: P2730R1C1
CURRENT APPLICATION NUMBER: US 09/709,238
CURRENT FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: US 60/087,607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: US 60/087,609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: US 60/087,759
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: US 60/087,827
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,326
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: US 60/088,167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: US 60/088,202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: US 60/088,212
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PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: US 60/088,655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: US 60/088,722
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: US 60/088,730
PRIOR FILING DATE: 1998-06-10
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PRIOR APPLICATION NUMBER: US 60/088,738
PRIOR FILING DATE: 1998-06-10
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PRIOR APPLICATION NUMBER: US 60/088,741
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PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: US 60/088,810
PRIOR FILING DATE: 1998-06-10
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PRIOR APPLICATION NUMBER: US 60/089,090
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PRIOR FILING DATE: 1998-06-12
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,676
PRIOR FILING DATE: 1998-06-25

Howes, Steven H.
Fechtel, Kim
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
ENCODING THEM
NUMBER OF SEQUENCES: 231
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/746,783
FILING DATE: 21-Dec-2000
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Milasincic, Debra J.
REGISTRATION NUMBER: 46,931
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 146:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
STRANDEDNESS: <unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 146:
PS-09-746-783-146

Query Match	72.0%;	Score 90;	DB 21;	Length 185;
Best Local Similarity	72.0%;	Pred. No. 0.00048;		
Matches	18. Conservative	2; Mismatches	3; Indels	2; Gaps

QY 1 LDTMVKEQK--GKGPGGAPPKDLMY 23
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97 IDAIVKEKKLOGKGGPPPKGLMY 121

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RESULT 12
US-09-821-726-13
; Sequence 13, Application US/09821726
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; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND
; FILE REFERENCE: 21459/20913
; CURRENT APPLICATION NUMBER: US/09/821-726-13
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-821-726-13

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Query Match          72.0%; Score 90; DB 22; Length 185;
Best Local Similarity 72.0%; Pred. No. 0.00048;
Matches 18; Conservative 2; Mismatches 3; Indels

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3	PRIOR APPLICATION NUMBER:	US 60/090,688
4	PRIOR FILING DATE:	1998-06-25
5	PRIOR APPLICATION NUMBER:	US 60/090,690
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7	PRIOR APPLICATION NUMBER:	US 60/090,691
8	PRIOR FILING DATE:	1998-06-25
9	PRIOR APPLICATION NUMBER:	US 60/090,694
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16	PRIOR FILING DATE:	1998-06-25
17	PRIOR APPLICATION NUMBER:	US 60/090,863
18	PRIOR FILING DATE:	1998-06-25
19	PRIOR APPLICATION NUMBER:	US 60/091,358
20	PRIOR FILING DATE:	1998-07-01
21	PRIOR APPLICATION NUMBER:	US 60/091,360
22	PRIOR FILING DATE:	1998-07-01
23	PRIOR APPLICATION NUMBER:	US 60/091,478
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26	PRIOR FILING DATE:	1998-07-02
27	PRIOR APPLICATION NUMBER:	US 60/091,519
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29	PRIOR APPLICATION NUMBER:	US 60/091,544
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33	PRIOR APPLICATION NUMBER:	US 60/091,628
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40	PRIOR FILING DATE:	1998-07-02
41	PRIOR APPLICATION NUMBER:	US 60/091,978
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43	PRIOR APPLICATION NUMBER:	US 60/091,982
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45	PRIOR APPLICATION NUMBER:	US 60/092,182
46	PRIOR FILING DATE:	1998-07-09
47	PRIOR APPLICATION NUMBER:	US 60/092,472
48	PRIOR FILING DATE:	1998-07-10
49	PRIOR APPLICATION NUMBER:	US 60/093,339
50	PRIOR FILING DATE:	1998-07-20
51	PRIOR APPLICATION NUMBER:	US 60/094,651
52	PRIOR FILING DATE:	1998-07-30

Query Match	72.0%;	Score 90;	DB 21;	Length 185;
Best Local Similarity	72.0%;	Pred. No. 0.00048;		
Matches 18: Conservative	2;	Mismatches 3;	Indels	

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07 TDAIVKEFKIACKGPGGGPPPKGLMY 121

RESULT 11
US-09-746-783-146
Sequence 146, Application US/09746783
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
McCoy, John M.
LaVallee, Edward R.
Racie, Lisa A.
Treacy, Maurice
Spaulding, Vikki
Agostino, Michael

Db 97 LDALVKKKLOGKGGPPKGLMY 121
RESULT 13
US-09-941-992-211
; Sequence 211, Application US/09941992
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C1
; CURRENT APPLICATION NUMBER: US/09/941,992
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR APPLICATION NUMBER: 60/090254

us-09-821-726-2.rapm

Thu Sep 5 11:23:34 2002

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301C56
; CURRENT APPLICATION NUMBER: US/09/989,279
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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; Query Match 72.0%; Score 90; DB 23; Length 185;
; Best Local Similarity 72.0%; Pred. No. 0.00048;
; Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
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; RESULT 14
; US-09-989-279-211
; Sequence 211, Application US/09989279

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; PRIOR APPLICATION NUMBER: 60/090431
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; PRIOR APPLICATION NUMBER: 60/092472

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Query Match 72.0%; Score 90; DB 23; Length 185;
 Best Local Similarity 72.0%; Pred. No. 0.00048;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

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QY 1 LDTMVKDQK--GKPGGAPPKDLMY 23
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Db 97 LDALVKEKLGKGGPGPPKGLMY 121

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RESULT 15
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 ; Sequence 211, Application US/09989293A
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone

us-09-821-726-2.rapm

Thu Sep 5 11:23:34 2002

APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavini, Ivar J.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2730PLC66
 CURRENT APPLICATION NUMBER: US/09/989,293A
 CURRENT FILING DATE: 2001-11-20
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 PRIOR FILING DATE: 1997-06-16
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 PRIOR APPLICATION NUMBER: 60/065186
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 PRIOR APPLICATION NUMBER: 60/088655
 PRIOR FILING DATE: 1998-06-09
 PRIOR APPLICATION NUMBER: 60/088734
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088738
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088742
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088810
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088824
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088826
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088858
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088861
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088876
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/089105
 PRIOR FILING DATE: 1998-06-12
 PRIOR APPLICATION NUMBER: 60/089440
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089512
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089514
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089532
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089538
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089598
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089599
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089600
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089653
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089801
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089907
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089908
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089947
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/089948
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/089952
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/090246
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090252
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090254
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090349
 PRIOR FILING DATE: 1998-06-23
 PRIOR APPLICATION NUMBER: 60/090355
 PRIOR FILING DATE: 1998-06-23
 PRIOR APPLICATION NUMBER: 60/090429
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090431
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090435
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090444
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090445
 PRIOR FILING DATE: 1998-06-24

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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472
```

```
Query Match 72.0%; Score 90; DB 23; Length 185;
Best Local Similarity 72.0%; Pred. NO. 0.00048;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
```

```
QY 1 LDTWKEQK--GKGPGGAPPKDLMY 23
Db 97 LDALVKEKKLOGKPGGPPKGLMY 121
||:||||| ||||| |||||
```

Search completed: September 4, 2002, 16:59:19
Job time: 1040 sec


```

RESULT 2
US-09-720-533-49
; Sequence 49, Application US/09720533
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: LAL, Preeti
; APPLICANT: TANG, Y. Tom
; APPLICANT: GORGONE, Gina A.
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AKERBLOM, Ingrid E.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: YUE, Henry
; APPLICANT: PATTERSON, Chandra
; APPLICANT: REDDY, Roopa
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: BANDMAN, Olga
; TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
; FILE REFERENCE: PF-0541 PCT
; CURRENT APPLICATION NUMBER: US/09720, 533
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/090,762; 60/094,983; 60/102,686; 60/112,129
; PRIOR FILING DATE: 1998-06-26; 1998-07-31; 1998-10-01; 1998-12-11
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PERL Program
; SEQ ID NO 49
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte Clone No: 2593853
US-09-720-533-49

```

```

Query Match 72.0%; Score 90; DB 5; Length 185;
Best Local Similarity 72.0%; Pred. No. 0.00012;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMVKEQK--GKGPGGAPPKDLMY 23
   ||:||||| ||||| |||||
Db 97 LDALVKEKKLQKGPGGPPKGLMY 121

```

```

RESULT 3
US-10-119-480-148
; Sequence 148, Application US/10119480
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C1
; CURRENT APPLICATION NUMBER: US/10/119,480
; CURRENT FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 246
; Remaining Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-119-480-148

```

```

Query Match 72.0%; Score 90; DB 6; Length 185;
Best Local Similarity 72.0%; Pred. No. 0.00012;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMVKEQK--GKGPGGAPPKDLMY 23
   ||:||||| ||||| |||||
Db 97 LDALVKEKKLQKGPGGPPKGLMY 121

```

```

RESULT 4
US-10-216-159A-148
; Sequence 148, Application US/10216159A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C6
; CURRENT APPLICATION NUMBER: US/10/216,159A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-159A-148

```

```

Query Match 72.0%; Score 90; DB 6; Length 185;
Best Local Similarity 72.0%; Pred. No. 0.00012;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMVKEQK--GKGPGGAPPKDLMY 23
   ||:||||| ||||| |||||
Db 97 LDALVKEKKLQKGPGGPPKGLMY 121

```

```

RESULT 5
US-10-216-162-148
; Sequence 148, Application US/10216162
; GENERAL INFORMATION:

```


us-09-821-726-2.rpn

Thu 'Sep 5 11:23:35 2002

```

; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC2
; CURRENT APPLICATION NUMBER: US/10/216,162
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 1997-10-28
; PRIOR FILING DATE: 1997-10-31
; PRIOR FILING DATE: 1997-12-17
; PRIOR FILING DATE: 1998-03-20
; PRIOR FILING DATE: 1998-03-25
; PRIOR FILING DATE: 1998-03-26
; PRIOR FILING DATE: 1998-03-27
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-163-148

Query Match 72.0%; Score 90; DB 6; Length 185;
Best Local Similarity 72.0%; Pred. No. 0.00012;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

Qy 1 LDTWVKEOK--GKPGGAPPKDLMY 23
   ||:||||:| ||||| ||| |||
Db 97 LDALVKEKKLOGKGGPPKGLMY 121

RESULT 7
US-10-216-164-148
; Sequence 148, Application US/10216164
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC5
; CURRENT APPLICATION NUMBER: US/10/216,164
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 1997-10-31
; PRIOR FILING DATE: 1997-12-17
; PRIOR FILING DATE: 1998-03-20
; PRIOR FILING DATE: 1998-03-25
; PRIOR FILING DATE: 1998-03-26
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-162-148

```

```

; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC2
; CURRENT APPLICATION NUMBER: US/10/216,162
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 1997-10-31
; PRIOR FILING DATE: 1997-12-17
; PRIOR FILING DATE: 1998-03-20
; PRIOR FILING DATE: 1998-03-25
; PRIOR FILING DATE: 1998-03-26
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-162-148

Query Match 72.0%; Score 90; DB 6; Length 185;
Best Local Similarity 72.0%; Pred. No. 0.00012;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

Qy 1 LDTWVKEOK--GKPGGAPPKDLMY 23
   ||:||||:| ||||| ||| |||
Db 97 LDALVKEKKLOGKGGPPKGLMY 121

RESULT 6
US-10-216-163-148
; Sequence 148, Application US/10216163
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC3
; CURRENT APPLICATION NUMBER: US/10/216,163

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; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-164-148

Query Match
Best Local Similarity 72.0%; Score 90; DB 6; Length 185;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMVKEQK--GKPGGAPPKDLMY 23
   ||:||||| ||||| |||||
Db 97 LDALVKEKKLOGKGGPPPKGLMY 121

```

```

RESULT 8
US-10-216-165-148
; Sequence 148, Application US/10216165
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC7
; CURRENT APPLICATION NUMBER: US/10/216,165
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-165-148

```

```

Query Match
Best Local Similarity 72.0%; Score 90; DB 6; Length 185;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMVKEQK--GKPGGAPPKDLMY 23
   ||:||||| ||||| |||||
Db 97 LDALVKEKKLOGKGGPPPKGLMY 121

```

```

RESULT 9
US-10-216-166-148
; Sequence 148, Application US/10216166
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC9
; CURRENT APPLICATION NUMBER: US/10/216,166
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-166-148

```

```

Query Match
Best Local Similarity 72.0%; Score 90; DB 6; Length 185;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMVKEQK--GKPGGAPPKDLMY 23
   ||:||||| ||||| |||||
Db 97 LDALVKEKKLOGKGGPPPKGLMY 121

RESULT 10
US-10-216-167-148
; Sequence 148, Application US/10216167
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc

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Thu Sep 5 11:23:35 2002

```

; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC4
; CURRENT APPLICATION NUMBER: US/10/216,167
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-167-148

Query Match 72.0%; Score 90; DB 6; Length 185;
Best Local Similarity 72.0%; Pred. No. 0.00012;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMVKEQK--GKGPGGAPPKDLMY 23
   ||:||||:| ||||| ||| |||
Db 97 LDALVKEKKLQGGPGGPPKGLMY 121

RESULT 11
US-10-216-168-148
; Sequence 148, Application US/10216168
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC8
; CURRENT APPLICATION NUMBER: US/10/216,168
; CURRENT FILING DATE: 2002-08-09
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-167-148

Query Match 72.0%; Score 90; DB 6; Length 185;
Best Local Similarity 72.0%; Pred. No. 0.00012;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMVKEQK--GKGPGGAPPKDLMY 23
   ||:||||:| ||||| ||| |||
Db 97 LDALVKEKKLQGGPGGPPKGLMY 121

RESULT 11
US-10-216-168-148
; Sequence 148, Application US/10216168
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC10
; CURRENT APPLICATION NUMBER: US/10/216,168
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-167-148

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; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-168-148

Query Match 72.0%; Score 90; DB 6; Length 185;
Best Local Similarity 72.0%; Pred. No. 0.00012;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMVKEQK--GKGPGGAPPKDLMY 23
   ||:||||:| ||||| ||| |||
Db 97 LDALVKEKKLQGGPGGPPKGLMY 121

RESULT 12
US-10-216-160-148
; Sequence 148, Application US/10216160
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC8
; CURRENT APPLICATION NUMBER: US/10/216,160
; CURRENT FILING DATE: 2002-08-09
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-160-148

Query Match 72.0%; Score 90; DB 6; Length 185;
Best Local Similarity 72.0%; Pred. No. 0.00012;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMVKEQK--GKGPGGAPPKDLMY 23
   ||:||||:| ||||| ||| |||
Db 97 LDALVKEKKLQGGPGGPPKGLMY 121

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RESULT 13
 US-10-218-849-148
 ; Sequence 148, Application US/10218849
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530P1C11
 ; CURRENT APPLICATION NUMBER: US/10/218,849
 ; CURRENT FILING DATE: 2002-08-12
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 148
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-218-849-148

Query Match 72.0%; Score 90; DB 6; Length 185;
 Best Local Similarity 72.0%; Pred. No. 0.00012;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

Qy 1 LDTMYKEQK--GKPGGAPPKDLMY 23
 || :|||:| ||||| ||| |||
 Db 97 LDALVKEKKLQKGGPPPKGLMY 121

RESULT 14
 US-10-218-930-148
 ; Sequence 148, Application US/10218930
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530P1C13
 ; CURRENT APPLICATION NUMBER: US/10/218,930
 ; CURRENT FILING DATE: 2002-08-12
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 148
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-218-930-148

Query Match 72.0%; Score 90; DB 6; Length 185;
 Best Local Similarity 72.0%; Pred. No. 0.00012;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

Qy 1 LDTMYKEQK--GKPGGAPPKDLMY 23
 || :|||:| ||||| ||| |||
 Db 97 LDALVKEKKLQKGGPPPKGLMY 121
 RESULT 15
 US-10-219-003-148
 ; Sequence 148, Application US/10219003
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530P1C12
 ; CURRENT APPLICATION NUMBER: US/10/219,003
 ; CURRENT FILING DATE: 2002-08-12
 ; Prior Application Number: 10/119,480
 ; Prior Filing Date: 2002-04-09
 ; Prior Application Number: 60/059113
 ; Prior Filing Date: 1997-09-17
 ; Prior Application Number: 60/062287
 ; Prior Filing Date: 1997-10-17
 ; Prior Application Number: 60/063549
 ; Prior Filing Date: 1997-10-28
 ; Prior Application Number: 60/064103
 ; Prior Filing Date: 1997-10-31
 ; Prior Application Number: 60/069873
 ; Prior Filing Date: 1997-12-17
 ; Prior Application Number: 60/078910
 ; Prior Filing Date: 1998-03-20
 ; Prior Application Number: 60/079294
 ; Prior Filing Date: 1998-03-25
 ; Prior Application Number: 60/079656
 ; Prior Filing Date: 1998-03-26
 ; Prior Application Number: 60/079728
 ; Prior Filing Date: 1998-03-27
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 ; Prior Filing Date: 1998-04-15
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 ; Prior Filing Date: 1998-06-17
 ; Prior Application Number: 60/089538
 ; Prior Filing Date: 1998-06-17
 ; Prior Application Number: 60/089905
 ; Prior Filing Date: 1998-06-18
 ; Prior Application Number: 60/090472
 ; Prior Filing Date: 1998-06-24
 ; Prior Application Number: 60/090557
 ; Prior Filing Date: 1998-06-24
 ; Prior Application Number: 60/090691
 ; Prior Filing Date: 1998-06-25
 ; Prior Application Number: 60/090695
 ; Prior Filing Date: 1998-06-25

us-09-821-726-2.rapn

Thu 'Sep 5 11:23:35 2002

; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/095302
 ; PRIOR FILING DATE: 1998-08-04
 ; PRIOR APPLICATION NUMBER: 60/095318
 ; PRIOR FILING DATE: 1998-08-04
 ; PRIOR APPLICATION NUMBER: 60/095916
 ; PRIOR FILING DATE: 1998-08-10
 ; PRIOR APPLICATION NUMBER: 60/096146
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 ; PRIOR APPLICATION NUMBER: 60/097986
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 ; PRIOR FILING DATE: 1999-11-16
 ; PRIOR APPLICATION NUMBER: 60/169445
 ; PRIOR FILING DATE: 1999-12-07
 ; PRIOR APPLICATION NUMBER: 60/169495
 ; PRIOR FILING DATE: 1999-12-07
 ; PRIOR APPLICATION NUMBER: 60/169835
 ; PRIOR FILING DATE: 1999-12-07

Query Match 72.08; Score 90; DB 6; Length 185;

Best Local Similarity 72.08; Pred. No. 0.00012;

Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMVKQK--GKPGGAPPKDLMY 23

|| :|||: ||||| ||| |||

Db 97 LDALVKKLQKGGPPPKGLMY 121

Search completed: September 4, 2002, 17:04:23

Thu Sep 5 11:23:35 2002

us-09-821-726-2.rapn

Page 8

Job time: 1154 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 17:05:03 ; Search time 34.18 Seconds
(without alignments)
26.055 Million cell updates/sec

Title: US-09-821-726-2
Perfect score: 125
Sequence: 1 LDTMWKEQKGKPGCGAPPKDLMY 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	125	100.0	184	1	C11P_MOUSE
2	90	72.0	199	1	C11P_HUMAN
3	51	40.8	378	1	HMAN_DROME
4	49	39.2	331	1	YPUB_KLEPN
5	49	39.2	331	1	TAL_HUMAN
6	47	37.6	233	1	HB2A_RAT
7	47	37.6	263	1	HB2B_RAT
8	46	36.8	267	1	TRUA_CHLMU
9	46	36.8	267	1	CHLTR
10	46	36.8	268	1	HB2X_HUMAN
11	46	36.8	398	1	ACOC_BACSU
12	46	36.8	423	1	VIAR_MOUSE
13	45.5	36.4	402	1	GUNT_HUMIN
14	45	36.0	137	1	LSM4_MOUSE
15	45	36.0	139	1	LSM4_HUMAN
16	45	36.0	160	1	PETD_SCOB
17	45	36.0	263	1	HB2K_MOUSE
18	45	36.0	263	1	HB2S_MOUSE
19	45	36.0	263	1	HB2U_MOUSE
20	45	36.0	265	1	HB2A_MOUSE
21	45	36.0	265	1	HB2D_MOUSE
22	45	36.0	265	1	HB2Q_MOUSE
23	45	36.0	302	1	CCDC_CAFEL
24	45	36.0	992	1	AXN1_MOUSE
25	45	36.0	3414	1	POLG_TBEVH
26	45	36.0	3414	1	POLG_TBEVW
27	44.5	35.6	264	1	COLI_MAGNE
28	44.5	35.6	267	1	COLI_HUMAN
29	44.5	35.6	267	1	COLI_PIG
30	44	35.2	172	1	CH18_DROME
31	44	35.2	211	1	CAB4_HUMAN
32	44	35.2	375	1	SOX3_MOUSE
33	44	35.2	471	1	S61A_YARLI

RESULT 1

ID	CLIP_MOUSE	STANDARD	PRT	184 AA
AC	Q9CR36; Q9D7K7; Q9CTZ5;			
DT	01-MAR-2002 (Rel. 41, Created)			
DT	01-MAR-2002 (Rel. 41, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	CALL protein homolog.			
GN	CALL			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Stomach, and Tongue;			
RX	MEDLINE=21085660; PubMed=11217851;			
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Aizawa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,			
RA	Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,			
RA	Saito K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,			
RA	Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,			
RA	Schrml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,			
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,			
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,			
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,			
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,			
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,			
RA	Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,			
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,			
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,			
RA	Hayashizaki Y.;			
RT	"Functional annotation of a full-length mouse cDNA collection.";			
RL	Nature 409:685-690(2001).			
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DR	EMBL; AK008990; BAB26010.1;			
DR	EMBL; AK008632; BAB25784.1;			
DR	EMBL; AK008641; BAB25801.1;			
DR	EMBL; AK008647; BAB25805.1;			
DR	EMBL; AK008722; BAB25856.1;			
DR	EMBL; AK008745; BAB25872.1;			
DR	EMBL; AK008933; BAB25975.1;			
DR	EMBL; AK008956; BAB25988.1;			
DR	EMBL; AK009145; BAB26103.1;			
DR	EMBL; AK019050; BAB31525.1;			

RP SEQUENCE FROM N.A.
RA Schneuwly S., Kuroiwa A., Baumgartner P., Gehring W.J.;
RT "Structural organization and sequence of the homeotic gene
RT Antennapedia of *Drosophila melanogaster*.";
RL EMBO J. 5:733-739(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87089828; PubMed=2879222;
RA Stroehrer V.L., Jorgensen E.M., Garber R.L.;
RT "Multiple transcripts from the Antennapedia gene of *Drosophila*
RT melanogaster".;
RL Mol. Cell. Biol. 6:4667-4675(1986).
RN [3]
RP SEQUENCE FROM N.A.
RA Celniker S.E., Pfeiffer B., Knafels J., Martin C.H., Mayeda C.A.,
RA Palazzolo M.J.;
RT "Complete sequence of the Antennapedia complex of *Drosophila*.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadien E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Evangelista C.C., Ferraz C., Ferrier S., Finkbeiner S.,
RA Fodor C.A., Godfrey A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glisler A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J.D., Puri V., Reese M.C.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtkars R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissensbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-f., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.-H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [5]
RP SEQUENCE OF 296-378 FROM N.A.
RX MEDLINE=84205674; PubMed=6327065;
RA McGinnis W., Garber R.L., Wirz J., Kuroiwa A., Gehring W.J.;
RT "A homologous protein-coding sequence in *Drosophila* homeotic genes
RT and its conservation in other metazoans.";
RL Cell 37:403-408(1984).
RN [6]
RP SEQUENCE OF 296-364 FROM N.A.
RX MEDLINE=84248068; PubMed=6330741;
RA Scott M.P., Weiner A.J.;
RT "Structural relationships among genes that control development:
RT sequence homology between the Antennapedia, Ultrabithorax, and fushi
RT tarazu loci of *Drosophila*.";


```

RL  Proc. Natl. Acad. Sci. U.S.A. 81:4115-4119(1984).
RN  [7]
RP  SEQUENCE OF 297-357 FROM N.A.
RX  MEDLINE=86079516; PubMed=2416463;
RA  Reguluski M., Harding K., Kostriken R., Karch F., Levine M.,
RA  McGinnis W.;
RT  "Homeo box genes of the Antennapedia and bithorax complexes of
RT  Drosophila.";
RL  Cell 43:71-80(1985).
RN  [8]
RP  STRUCTURE BY NMR OF HOMEBOX.
RX  MEDLINE=90317820; PubMed=2164583;
RA  Billeter M., Qian Y.-Q., Otting G., Mueller M., Gehring W.J.,
RA  Wuethrich K.;
RT  "Determination of the three-dimensional structure of the Antennapedia
RT  homeodomain from Drosophila in solution by 1H nuclear magnetic
RT  resonance spectroscopy.";
RL  J. Mol. Biol. 214:183-197(1990).
RN  [9]
RP  STRUCTURE BY NMR OF HOMEBOX.
RX  MEDLINE=94087721; PubMed=7903397;
RA  Qian Y.-Q., Otting G., Billeter M., Mueller M., Gehring W.J.,
RA  Wuethrich K.;
RT  "Nuclear magnetic resonance spectroscopy of a DNA complex with the
RT  uniformly 13C-labeled Antennapedia homeodomain and structure
RT  determination of the DNA-bound homeodomain.";
RL  J. Mol. Biol. 234:1070-1083(1993).
RN  [10]
RP  STRUCTURE BY NMR OF HOMEBOX.
RX  MEDLINE=94087722; PubMed=7903398;
RA  Billeter M., Qian Y.-Q., Otting G., Mueller M., Gehring W.J.,
RA  Wuethrich K.;
RT  "Determination of the nuclear magnetic resonance solution structure
RT  of an Antennapedia homeodomain-DNA complex.";
RL  J. Mol. Biol. 234:1084-1097(1993).
RN  [11]
RP  STRUCTURE BY NMR OF 279-363.
RX  MEDLINE=93066318; PubMed=1359544;
RA  Qian Y.-Q., Otting G., Furukubo-Tokinaga K., Affolter M.,
RA  Gehring W.J., Wuethrich K.;
RT  "NMR structure determination reveals that the homeodomain is
RT  connected through a flexible linker to the main body in the
RT  Drosophila Antennapedia protein.";
RL  Proc. Natl. Acad. Sci. U.S.A. 89:10738-10742(1992).
RN  [12]
RP  X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 297-356.
RX  MEDLINE=98363212; PubMed=9699632;
RA  Fraenkel E., Pabo C.O.;
RT  "Comparison of X-ray and NMR structures for the Antennapedia
RT  homeodomain-DNA complex.";
RL  Nat. Struct. Biol. 5:692-697(1998).
CC  -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC  A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC  SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC  -!- FUNCTION: THIS HOMEOBOX PROTEIN CONTROLS DEVELOPMENT OF THE CELLS
CC  IN THE MESOTHORAX SEGMENTS.
CC  -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC  -!- SIMILARITY: BELONGS TO THE ANT P FAMILY OF HOMEBOX PROTEINS.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; X03790; CAA27417.1;
DR  EMBL; X03791; CAA27417.1; JOINED.
DR  EMBL; K01948; AAZ28373.1; ALT_SEQ.
DR  EMBL; AE001572; AAD19793.1;
DR  EMBL; AE003673; AAG22205.1;
DR  EMBL; M14496; AAA28376.1;

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DR  EMBL; M20704; AAA70214.1;
DR  EMBL; M20705; AAA70216.1;
DR  EMBL; M12009; AAA79241.1;
DR  PIR; A03318; A03318.
DR  PIR; A23450; A23450.
DR  PIR; A23450; A23450.
DR  PIR; C24780; C24780.
DR  PIR; A25400; A25400.
DR  PDB; 1HOM; 31-OCT-93.
DR  PDB; 2HOA; 31-OCT-93.
DR  PDB; 1AHD; 31-OCT-93.
DR  PDB; 1SAN; 30-APR-94.
DR  PDB; 9ANT; 18-NOV-98.
DR  TRANSFAC; T00026;
DR  FlyBase; FBgn0000095; Antp.
DR  InterPro; IPR001827; Antennapedia.
DR  InterPro; IPR001356; Homeobox.
DR  Pfam; PF00046; homeobox; 1.
DR  PRINTS; PR00025; ANTENNAPEDIA.
DR  PRINTS; PR00024; HOMEBOX.
DR  SMART; SM00389; HOX; 1.
DR  PROSITE; PS00027; HOMEBOX_1; 1.
DR  PROSITE; PS00032; ANTENNAPEDIA; 1.
DR  PROSITE; PS00711; HOMEBOX_2; 1.
KW  Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW  3D-structure.
FT  DOMAIN 76 81 GLN-RICH (OPA-REPEAT).
FT  DOMAIN 110 155 GLN-RICH (OPA-REPEAT).
FT  DOMAIN 283 288 ANTP-TYPE HEXAPEPTIDE.
FT  DNA_BIND 297 356 HOMEBOX.
FT  CONFLICT 300 300 G -> E (IN REF. 7).
FT  HELIX 306 318
FT  HELIX 324 334
FT  HELIX 335 335
FT  TURN 339 350
FT  HELIX 339 350
FT  TURN 351 355
FT  TURN 358 359
SQ  SEQUENCE 378 AA; 42761 MW; D653232A8622D055 CRC64;

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Query Match 40.8%; Score 51; DB 1; Length 378;

Best Local Similarity 45.0%; Pred. No. 5.2;

Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 4 MVKEQKGGKGGAPPKDLMY 23

DB 230 MYQQSGVPPVPGAPPGGMH 249

RESULT 4

YPUB_KLEPN STANDARD; PRT; 142 AA.

AC P20775;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical protein in PULS 3' region (Fragment).

OS Klebsiella pneumoniae.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Klebsiella.

OX NCBI_TaxID=573;

RN [1]

SEQUENCE FROM N.A.

RP MEDLINE=89291709; PubMed=2661532;

RA D'Enfert C., Pugsley A.P.;

RT "Klebsiella pneumoniae pulS gene encodes an outer membrane

RT lipoprotein required for pullulanase secretion.";

RL J. Bacteriol. 171:3673-3679(1989).

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DR EMBL; M29097; AAA61979.1; -;
 KW PIR: D32880; D32880.
 KW Hypothetical protein.
 FT NON_TER 142
 SQ SEQUENCE 142 AA; 16447 MW; 03ED03FBF63242D0 CRC64;

Query Match 39.2%; Score 49; DB 1; Length 142;
 Best Local Similarity 66.7%; Pred. No. 3.7;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 8 QKKGKGGGAPPK 19
 Db 49 RKKGKGGKPPR 60
 :|||||
 :|||||

RESULT 5
 TAL_HUMAN STANDARD; PRT; 331 AA.
 AC P17542;
 DT 01-AUG-1990 (rel. 15, Created)
 DT 01-NOV-1991 (rel. 20, Last sequence update)
 DT 01-MAR-2002 (rel. 41, Last annotation update)
 DE T-cell acute lymphocytic leukemia-1 protein (TAL-1 protein) (STEM cell
 DE protein) (T-cell leukemia/lymphoma-5 protein).
 OS TAL1 OR SCL OR TCL5.
 GN Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]

RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RX MEDLINE-91061750; PubMed-2247063;
 RA Aplan P.D., Begley C.G., Bertness V., Nussmeier M., Ezquerro A.,
 RA Colligan J., Kirsch I.R.;
 RT "The SCL gene is formed from a transcriptionally complex locus.";
 RL Mol. Cell. Biol. 10:6426-6435(1990).
 RN [2]
 RN SEQUENCE FROM N.A.
 RA Graham D.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE OF 118-331 FROM N.A.
 RC TISSUE=Bone marrow;
 RX MEDLINE-90099309; PubMed-2602361;
 RA Begley C.G., Aplan P.D., Denning S.M., Haynes B.F., Waldmann T.A.,
 RA Kirsch I.R.;

RT "The gene SCL is expressed during early hematopoiesis and encodes a
 RT differentiation-related DNA-binding motif";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:10128-10132(1989).
 RN [4]
 RN SEQUENCE OF 181-331 FROM N.A.
 RX MEDLINE-90151616; PubMed-2303035;
 RA Chen Q., Cheng J.-T., Tsai L.H., Schneider N., Buchanan G.,
 RA Carroll A., Crist W., Ozanne B., Siciliano M.J., Baer R.;
 RT "The tal gene undergoes chromosome translocation in T cell leukemia
 RT and potentially encodes a helix-loop-helix protein.";
 RL EMO J. 9:415-424(1990).
 RN [5]
 RN SEQUENCE OF 106-148 FROM N.A.
 RX MEDLINE-91037802; PubMed-2230650;
 RA Chen Q., Yang C.Y.C., Tsan J.T., Xia Y., Ragab A.H., Peiper S.C.,
 RA Carroll A., Baer R.;

RT "Coding sequences of the tal-1 gene are disrupted by chromosome
 RT translocation in human T cell leukemia.";
 RL J. Exp. Med. 172:1403-1408(1990).
 RN [6]
 RN FUNCTION.
 RP MEDLINE-93011002; PubMed-1396592;

RA

RA Aplan P.D., Nakahara K., Orkin S.H., Kirsch I.R.;
 RT "The SCL gene product: a positive regulator of erythroid
 RT differentiation.";
 RL EMBO J. 11:4073-4081(1992).
 RN [7]
 RN PHOSPHORYLATION.
 RX MEDLINE-93173511; PubMed-8437851;
 RA Cheng J.-T., Hsu H.-L., Hwang L.-Y., Baer R.;
 RT "Products of the TAL1 oncogene: basic helix-loop-helix proteins
 RT phosphorylated at serine residues.";
 RL Oncogene 8:677-683(1993).
 CC -1- FUNCTION: IMPLICATED IN THE GENESIS OF HEMOPOIETIC MALIGNANCIES.
 CC IT MAY PLAY AN IMPORTANT ROLE IN HEMOPOIETIC DIFFERENTIATION.
 CC SERVES AS A POSITIVE REGULATOR OF ERYTHROID DIFFERENTIATION.
 CC TO THE LIM DOMAIN CONTAINING PROTEIN RHOMBOTIN-2.
 CC -1- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
 CC BHLH PROTEIN. FORMS HETERODIMERS WITH EL2 AND E47. BINDS TO DRG1.
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: PP42-TAL1 (SHOWN HERE),
 CC PP39-TAL1 AND PP22-TAL1; ARE PRODUCED BY ALTERNATIVE SPLICING. THE
 CC SPLICING PATTERN IS CELL-LINEAGE DEPENDENT.
 CC -1- TISSUE SPECIFICITY: LEUKEMIC STEM CELL.
 CC -1- DOMAIN: THE HELIX-LOOP-HELIX DOMAIN IS NECESSARY AND SUFFICIENT
 CC FOR THE INTERACTION WITH DRG1.
 CC -1- PTM: PHOSPHORYLATED ON SERINE RESIDUES.
 CC -1- DISEASE: SOME T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) (A FORM
 CC OF STEM-CELL LEUKEMIA) ARE CHARACTERIZED BY A CHROMOSOMAL
 CC TRANSLOCATION T(1;4)(p32;q11) WHICH INVOLVES TAL1 AND T-CELL
 CC RECEPTOR ALPHA CHAIN (TCRA) GENES.
 CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
 CC TRANSCRIPTION FACTORS.

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CC EMBL; M61108; AAA36600.1; -;
 DR EMBL; M61103; -; NOT_ANNOTATED_CDS.
 DR EMBL; M61104; -; NOT_ANNOTATED_CDS.
 DR EMBL; M61105; -; NOT_ANNOTATED_CDS.
 DR EMBL; M63572; -; NOT_ANNOTATED_CDS.
 DR EMBL; AL135960; CAB72103.1; -;
 DR EMBL; M63589; AAA36599.1; -;
 DR EMBL; M63576; AAA36599.1; JOINED.
 DR EMBL; M63584; AAA36599.1; JOINED.
 DR EMBL; M29038; AAA36598.1; -;
 DR EMBL; X51990; CAA36246.1; -;
 DR EMBL; X58621; CAA41476.1; ALT_SEQ.
 DR EMBL; X58622; CAA41477.1; -;
 DR PIR; A34519; A34519.
 DR PIR; A36358; A36358.
 DR HSSP; P10085; IMDY.
 DR TRANSFAC; T00790; -;
 DR MIM; 187040; -;
 DR InterPro; IPR003015; HLH_Myc.
 DR InterPro; IPR001092; HLH_dim.
 DR Pfam; PF00010; HLH; 1.
 DR SMART; SM00353; HLH; 1.
 DR PROSITE; PS00038; HELIX_LOOP_HELIX; 1.
 KW DNA-binding; Transcription regulation; Differentiation;
 KW Proto-oncogene; Chromosomal translocation; Alternative splicing;
 KW Phosphorylation.
 FT DOMAIN 89 132 PRO-RICH
 FT DNA_BIND 187 199 BASIC DOMAIN
 FT DOMAIN 200 240 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
 FT DOMAIN 263 274 POLY-GLY.
 FT VARSELIC 1 25 MISSING (IN ISOFORM PP39-TAL1).
 FT VARSELIC 1 175 MISSING (IN ISOFORM PP22-TAL1).
 SQ SEQUENCE 331 AA; 34270 MW; 33BEE31589DBE7C7 CRC64;

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RESULT# 7
HB2B_RAT
ID HB2B_RAT STANDARD; PRT; 263 AA.
AC P29826;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE RT1 class II histocompatibility antigen, B-1 beta chain precursor
DE (RT1.B-beta(1)).
DE
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=101116;
RX [1]
SEQUENCE FROM N.A.
RC STRAIN=LEWIS; TISSUE=Bone marrow;
EX MEDLINE=91316148; PubMed=1859846;
RA Syta-Jedelhauser J., Wendling U., Reske K.;
RT *Complete coding nucleotide sequence of cDNA for the class II RT1.B
RL beta 1 chain of the Lewis rat.;
RL Biochim. Biophys. Acta 1089:414-416(1991).
CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -----
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CC -----
CC EMBL; X56596; CAA39934.1; -
CC PIR; S16999; HLRTBB.
CC HSSP; P06343; IIAK.
CC InterPro; IPR003006; Iq_MHC.
CC InterPro; IPR003597; Iq_cl.
CC InterPro; IPR000353; MHC_II_beta.
CC Pfam; PF00047; Iq; 1.
CC Pfam; PF00969; MHC_II_beta; 1.
CC ProDom; PD000328; MHC_II_beta; 1.
CC SMART; SM00407; IGel; 1.
CC PROSITE; PS00290; IG_MHC; 1.
CC MHC_II; Transmembrane; Glycoprotein; Signal.
KW SIGNAL
FT 1 27 POTENTIAL
FT CHAIN 28 263 RT1 CLASS II HISTOCOMPATIBILITY ANTIGEN,
FT B-1 BETA CHAIN.
FT 28 120 EXTRACELLULAR BETA-1.
FT 121 214 EXTRACELLULAR BETA-2.
FT 215 224 CONNECTING PEPTIDE.
FT 225 245
FT 246 263 CYTOPLASMIC TAIL.
FT 263 263 BY SIMILARITY.
FT 42 104 BY SIMILARITY.
FT 143 199 BY SIMILARITY.
FT 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD SEQUENCE 263 AA; 29935 MW; 11127ABBE6139204 CRC64;
SQ
Query Match 37.6%; Score 47; DB 1; Length 263;
Best Local Similarity 36.4%; Pred. No. 13;
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

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Db	241	LGLFIRHKRQKGRGPPAGLL	262
RESULT	8		
TRUA_CHLMU			
ID	TRUA_CHLMU	STANDARD:	PRT: 267 AA.
AC	Q9PJT0:		
DT	16-OCT-2001	(Rel. 40. Created)	

DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE tRNA pseudouridine synthase A (EC 4.2.1.70) (Pseudouridylylate synthase
 GN I) (Pseudouridine synthase I) (Uracil hydrolyase).
 DE TRUA OR TC0748.
 OS Chlamydia muridarum.
 CC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=83560;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MOPN / NIGG;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heideberg J.F.,
 RA White O., Hickey E.K., Peterson J., Otterback T., Berry K., Bass S.,
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RA "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
 RT pneumoniae AR39."; 28:1397-1406(2000).
 RL Nucleic Acids Res. 28:1397-1406(2000).
 CC -!- FUNCTION: FORMATION OF PSEUDOURIDINE AT POSITIONS 38, 39 AND 40 IN
 CC THE ANTICODON STEM AND LOOP OF TRANSFER RNAs (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: Uracil + D-ribose 5-phosphate = pseudouridine
 CC 5'-phosphate + H(2)O.
 CC -!- SIMILARITY: BELONGS TO THE TRUA FAMILY OF PSEUDOURIDINE SYNTHASES.
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 CC -----
 DR EMBL; AE002343; AAF39555.1;
 DR TIGR; TC0748;
 DR InterPro; IPR001406; PseudoU_synth_1.
 DR Pfam; PF01416; PseudoU_synth_1;
 KW Lyase; tRNA processing; Complete proteome.
 FT ACT_SITE 52 52 BY SIMILARITY.
 SQ SEQUENCE 267 AA; 30413 MW; CBEDB3B568EDBB7 CRC64;

 Query Match 36.8%; Score 46; DB 1; Length 267;
 Best Local Similarity 42.9%; Pred. No. 19;
 Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

 QY 1 LDTWVKEQKGKGGGAPPKDL 21
 | : | : | | | | |
 DB 221 LEMLEKKDRKGGPPSAPPYGL 241

 RESULT 9
 TRUA_CHLTR
 ID TRUA_CHLTR STANDARD; PRT; 267 AA.
 AC 084469;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE tRNA pseudouridine synthase A (EC 4.2.1.70) (Pseudouridylylate synthase
 GN I) (Pseudouridine synthase I) (Uracil hydrolyase).
 OS Chlamydia trachomatis.
 CC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D/UV-3/CX;
 RX MEDLINE=99000809; PubMed=9784136;
 RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
 RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
 RA Davis R.W.;
 RT "Genome sequence of an obligate intracellular pathogen of humans:

RT Chlamydia trachomatis."; Science 282:754-759(1998).
 RL -!- FUNCTION: FORMATION OF PSEUDOURIDINE AT POSITIONS 38, 39 AND 40 IN
 CC THE ANTICODON STEM AND LOOP OF TRANSFER RNAs (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: Uracil + D-ribose 5-phosphate = pseudouridine
 CC 5'-phosphate + H(2)O.
 CC -!- SIMILARITY: BELONGS TO THE TRUA FAMILY OF PSEUDOURIDINE SYNTHASES.
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 CC -----
 DR EMBL; AE001320; AAC68063.1;
 DR InterPro; IPR001406; PseudoU_synth_1.
 DR Pfam; PF01416; PseudoU_synth_1;
 KW Lyase; tRNA processing; Complete proteome.
 FT ACT_SITE 53 53 BY SIMILARITY.
 SQ SEQUENCE 267 AA; 30427 MW; 917EA49E394B3CB3 CRC64;

 Query Match 36.8%; Score 46; DB 1; Length 267;
 Best Local Similarity 42.9%; Pred. No. 19;
 Matches 9; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

 QY 1 LDTWVKEQKGKGGGAPPKDL 21
 | : | : | | | | |
 DB 221 LDMLATKDRKGGPPSAPPYGL 241

 RESULT 10
 HB2X_HUMAN
 ID HB2X_HUMAN STANDARD; PRT; 268 AA.
 AC P05538;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE HLA class II histocompatibility antigen, DX beta chain precursor.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87250501; PubMed=3036828;
 RA Jonsson A.K., Hyldig-Nielsen J.J., Servenius B., Larhammar D.,
 RA Andersson G., Joergensen F., Peterson P.A., Rask L.;
 RT "Class II genes of the human major histocompatibility complex.
 RT Comparisons of the DQ and DX alpha and beta genes."; J. Biol. Chem. 262:8767-8777(1987).
 RN [2]
 RP SEQUENCE OF 38-125 FROM N.A.
 RX MEDLINE=85216510; PubMed=3858830;
 RA Okada K., Boss J.M., Prentice H., Spies T., Mengler R., Auffray C.,
 RA Lillie J.W., Grossberger D., Strominger J.L.;
 RT "Gene organization of DC and DX subregions of the human major
 RT histocompatibility complex."; Proc. Natl. Acad. Sci. U.S.A. 82:3410-3414(1985).
 CC -----
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 CC -----
 DR EMBL; M29614; -; NOT_ANNOTATED_CDS.
 DR EMBL; M29615; -; NOT_ANNOTATED_CDS.
 DR EMBL; M11136; -; NOT_ANNOTATED_CDS.

DR PIR: D29312; D29312.
 DR HSSP: P13760; 2SEB.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003397; Ig_c1.
 DR InterPro: IPR000353; MHC_II_beta.
 DR Pfam: PF00047; Ig_1.
 DR Pfam: PF00969; MHC_II_beta; 1.
 DR ProDom: PD000328; MHC_II_beta; 1.
 DR SMART: SM00407; Ig_c1; 1.
 DR PROSITE: PS00290; Ig_MHC; 1.
 KW MHC II; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 32
 FT CHAIN 33 268
 FT
 FT DX BETA CHAIN.
 FT DOMAIN 33 126
 FT DOMAIN 127 229
 FT TRANSMEM 230 250
 FT DOMAIN 251 268
 FT DISULFID 47 110
 FT DISULFID 148 204
 FT CARBOHYD 51 51
 SQ SEQUENCE 268 AA; 30386 MW; 2746ED6CC5D44AF2 CRC64;
 Query Match 36.8%; Score 46; DB 1; Length 268;
 Best Local Similarity 34.8%; Pred. No. 19;
 Matches 8; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
 QY 1 LDTWKEOKGKGGPGAPPKDLMY 23
 Db 246 LGLIHRHKGKGGPPGACGLLH 268
 RESULT 11
 ACOC_BACSU STANDARD; PRT; 398 AA.
 ID ACOC_BACSU STANDARD; PRT; 398 AA.
 AC O31550; 2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Dihydrolipoamide acetyltransferase component of acetoin cleaving
 DE system (EC 2.3.1.12) (Acetoin dehydrogenase E2 component).
 GN ACOC
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AC327;
 RX MEDLINE=97124190; PubMed=8969503;
 RA Yamamoto H., Uchiyama S., Sekiguchi J.;
 RT "Cloning and sequencing of a 40.6 Kb segment in the 73 degrees-76
 RT degrees region of the Bacillus subtilis chromosome containing genes
 RT for trehalose metabolism and acetoin utilization.";
 RL Microbiology 142:3057-3065(1996).
 CC
 CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
 CC acetylhydrolipoamide.
 CC -!- COFACTOR: THE E2 COMPONENT CONTAINS ONE COVALENTLY-BOUND LIPOYL
 CC COFACTOR (PROBABLE).
 CC -!- PATHWAY: ACETOIN CATABOLISM.
 CC -!- SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.
 CC -!- SIMILARITY: CONTAINS 1 LIPOYL-BINDING DOMAIN.
 CC
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 CC
 CC EMBL; D49729; BAA08566.1; -;
 CC EMBL; D49730; BAA08567.1; -;
 CC EMBL; AB030013; BAA89050.1; -;
 CC GCRDB; GCR_1611; -;
 DR
 DR EMBL; D78509; BAA24294.1; -;
 DR HSSP: P07016; IEZO.
 DR Subtilist; BG12560; acoc.
 DR InterPro: IPR001078; 2Oxoacid_dh.
 DR InterPro: IPR000089; Biotin_lioyl.
 DR InterPro: IPR003016; Liopyl.
 DR InterPro: IPR004167; e3 binding.
 DR Pfam: PF00198; 2-oxoacid_dh; 1.
 DR Pfam: PF00364; biotin_lioyl; 1.
 DR Pfam: PF02817; e3_binding; 1.
 DR ProDom: PD001115; 2Oxoacid_dh; 1.
 DR PROSITE: PS00189; Liopyl; FALSE_NEG.
 KW Transferase; Acyltransferase; Liopyl; Complete proteome.
 FT DOMAIN 1 76
 FT BINDING 43 43
 FT ACT_SITE 371 371
 FT ACT_SITE 375 375
 SQ SEQUENCE 398 AA; 42885 MW; 559564C27C1C64F6 CRC64;
 Query Match 36.8%; Score 46; DB 1; Length 398;
 Best Local Similarity 56.2%; Pred. No. 28;
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 5 VKEQKGGKGGPGAPPKD 20
 Db 134 LKOLKGTGPGGRIVKD 149
 RESULT 12
 VIAR_MOUSE STANDARD; PRT; 423 AA.
 ID VIAR_MOUSE STANDARD; PRT; 423 AA.
 AC O62463; O62464; O90YH2;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Vasopressin V1a receptor (V1aR) (Vasculer/hepatic-type arginine
 DE vasopressin receptor) (Antidiuretic hormone receptor 1a) (AVPR V1a).
 GN AVPR1A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Onodera Y., Maekawa K., Arai Y.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ;
 RX MEDLINE=20132529; PubMed=10669045;
 RA Kikuchi S., Tanoue A., Goda N., Matsuo N., Tsujimoto G.;
 RT "Structure and sequence of the mouse V1a and V1b vasopressin receptor
 RT genes";
 RL Jpn. J. Pharmacol. 81:388-392(1999).
 CC
 CC -!- FUNCTION: RECEPTOR FOR ARGinine VASOPRESSIN. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE A PHOSPHATIDYL-
 CC INOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC EMBL; D49729; BAA08566.1; -;
 CC EMBL; D49730; BAA08567.1; -;
 CC EMBL; AB030013; BAA89050.1; -;
 CC GCRDB; GCR_1611; -;
 DR

GCRDb; GCR_1612; -
 DR MGD; MGI:1859216; Avpr1a.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHOOPS.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS00262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 52 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 53 76 1 (POTENTIAL).
 FT DOMAIN 77 88 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 89 110 2 (POTENTIAL).
 FT DOMAIN 111 125 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 126 147 3 (POTENTIAL).
 FT DOMAIN 148 168 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 169 190 4 (POTENTIAL).
 FT DOMAIN 191 220 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 221 241 5 (POTENTIAL).
 FT DOMAIN 242 298 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 299 318 6 (POTENTIAL).
 FT DOMAIN 319 335 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 337 356 7 (POTENTIAL).
 FT DOMAIN 357 423 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 27 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 124 205 BY SIMILARITY.
 FT VARIANT 41 42 PP -> RR.
 FT VARIANT 55 55 V -> F.
 SQ SEQUENCE 423 AA; 47181 MW; C75AFFID0A082CC6 CRC64;

 Query Match 36.8%; Score 46; DB 1; Length 423;
 Best Local Similarity 50.0%; Pred. No. 29;
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

 QY 6 KEQKGGKGGGAPPKDL 21
 Db 30 REAAGLEGSGSPGDV 45

 RESULT 13
 ID GUNI_HUMIN STANDARD; PRT; 402 AA.
 AC P56680;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Endoglucanase I (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase).
 GN CEL7B.
 OS Humicola insolens.
 OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
 OX NCBI_TaxID=34413;
 RN [1]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT S37W/P39W.
 RX MEDLINE=97475713; PubMed=9335168;
 RA Davies G.J., Ducros V., Lewis R.J., Borchert T.V., Schulein M.;
 RT "Oligosaccharide specificity of a family 7 endoglucanase: Insertion
 RT of potential sugar-binding subsites.";
 RL J. Biotechnol. 57:91-100(1997).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND MUTAGENESIS.
 RX MEDLINE=98437137; PubMed=9761741;
 RA Mackenzie L.F., Sulzenbacher G., Divne C., Jones T.A., Woeldike H.F.,
 RA Schulein M., Withers S.G., Davies G.J.;
 RT "Crystal structure of the family 7 endoglucanase I (Cel7B) from
 RT Humicola insolens at 2.2 A resolution and identification of the
 RT catalytic nucleophile by trapping of the covalent glycosyl-enzyme
 RT intermediate.";
 RL Biochem. J. 335:409-416(1998).
 CC -!- FUNCTION: THE BIOLOGICAL CONVERSION OF CELLULOSE TO GLUCOSE
 CC GENERALLY REQUIRES THREE TYPES OF HYDROLYTIC ENZYMES:
 CC (1) ENDOGLUCANASES WHICH CUT INTERNAL BETA-1,4-GLUCOSIDIC BONDS;
 CC (2) EXOCELLULOBIODERIVATIVES THAT CUT THE DISSACCHARIDE CELLOBIOSE

FROM THE NONREDUCING END OF THE CELLULOSE POLYMER CHAIN;
 (3) BETA-1,4-GLUCOSIDASES WHICH HYDROLYZE THE CELLOBIOSE AND OTHER
 SHORT CELLO-OLIGOSACCHARIDES TO GLUCOSE.
 -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 linkages in cellulose.
 -!- SUBUNIT: MONOMER.
 -!- SUBCELLULAR LOCATION: Secreted.
 -!- SIMILARITY: BELONGS TO CELLULOSE FAMILY C (FAMILY 7 OF GLYCOSYL
 HYDROLASES).
 PDB; 1A39; 02-MAR-99.
 PDB; 2A39; 16-FEB-99.
 DR InterPro: IPR001722; Glyco_hydro_7.
 DR Pfam: PF00840; Glyco_hydro_7; 1.
 DR PRINTS: PR00734; GLHYDRLASE7.
 DR PRODOM: PD186135; Glyco_hydro_7; 1.
 KW Cellulose degradation; Hydrolase; Glycosidase; Glycoprotein;
 3D-structure.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT ACT_SITE 197 197 NUCLEOPHILE.
 FT ACT_SITE 202 202 PROTON DONOR.
 FT DISULFID 18 24
 FT DISULFID 51 73
 FT DISULFID 63 69
 FT DISULFID 140 365
 FT DISULFID 172 195
 FT DISULFID 176 194
 FT DISULFID 215 234
 FT DISULFID 223 228
 FT DISULFID 239 315
 FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 247 247 N-LINKED (GLCNAC. . .).
 SQ SEQUENCE 402 AA; 44577 MW; E0C6D31375D1635F CRC64;

 Query Match 36.4%; Score 45.5; DB 1; Length 402;
 Best Local Similarity 36.7%; Pred. No. 33;
 Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;

 QY 1 LDTM---VKEQKGGKGGGA-----PPKDL 21
 Db 33 LDSLHPHRAEGLGPGCGDGNPPPKDV 62

 RESULT 14
 ID LSM4_MOUSE STANDARD; PRT; 137 AA.
 AC Q9QX5;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE U6 snRNA-associated Sm-like protein LSM4.
 GN LSM4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hirsch E., Ohashi T., Stamm S., Paessler R.;
 RT "Peri-implantation lethality in mice lacking the Sm motif-containing
 RT protein lsm4.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: BINDS SPECIFICALLY TO THE 3'-TERMINAL U-TRACT OF U6
 CC SNRNA (BY SIMILARITY).
 CC -!- SUBUNIT: LSM SUBUNITS FORM A HETEROMER WITH A DOUGNUT SHAPE.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- SIMILARITY: BELONGS TO THE SNRNP SM PROTEINS FAMILY.
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DR EMBL: AJ249439; CAB65729.1; -.
DR MGD: MGI-1354692; Lsm4.
DR InterPro: IPR001163; snRNP_Sm.
DR Pfam: PF01423; Sm; 1.
KW Nuclear protein; Ribonucleoprotein; mRNA splicing; mRNA processing;
KW RNA-binding.
SQ SEQUENCE 137 AA; 15076 MW; A917E15E61467940 CRC64;

Query Match 36.0%; Score 45; DB 1; Length 137;
Best Local Similarity 72.7%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 KEQKGGPGGA 16
I:|||||
DB 95 KQKGRGMGGA 105

RESULT 15
LSM4 HUMAN
ID LSM4 HUMAN STANDARD; PRT; 139 AA.
AC Q9Y4Z0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE U6 snRNA-associated Sm-like protein LSM4 (Glycine-rich protein) (GRP).
GN LSM4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=99298196; PubMed=10369684;
RA Salgado-Garrido J., Bragado-Nilsson E., Kandel-Lewis S., Seraphin B.;
RT "Sm and Sm-like proteins assemble in two related complexes of deep
RT evolutionary origin.";
RL EMBO J. 18:3451-3462(1999).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=99452783; PubMed=10523320;
RA Achsel T., Brahm H., Kastner B., Bachi A., Wilm M., Luehrmann R.;
RT "A doughnut-shaped heteromer of human Sm-like proteins binds to the
RT 3'-end of U6 snRNA, thereby facilitating U4/U6 duplex formation in
RT vitro.";
RL EMBO J. 18:5789-5802(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Hypothalamus;
RX MEDLINE=20402571; PubMed=10931946;
RA Hu R.-M., Han Z.-G., Song H.-D., Peng Y.-D., Huang Q.-H., Ren S.-X.,
RA Gu Y.-J., Huang C.-H., Li Y.-B., Jiang C.-L., Fu G., Zhang Q.-H.,
RA Gu B.-W., Dai M., Mao Y.-F., Gao G.-F., Rong R., Ye M., Zhou J.,
RA Xu S.-H., Gu J., Shi J.-X., Jin W.-R., Zhang C.-K., Wu T.-M.,
RA Huang G.-Y., Chen Z., Chen M.-D., Chen J.-L.;
RT "Gene expression profiling in the human hypothalamus-pituitary-adrenal
RT axis and full-length cDNA cloning.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:9543-9548(2000).
RN [4]
RP SEQUENCE FROM N.A.
RA Chan E.K.L.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: BINDS SPECIFICALLY TO THE 3'-TERMINAL U-TRACT OF U6
CC SNRNA
CC -!- SUBUNIT: LSM SUBUNITS FORM A HETEROMER WITH A DOUGHNUT SHAPE.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: BELONGS TO THE SNRNP SM PROTEINS FAMILY.
CC -----

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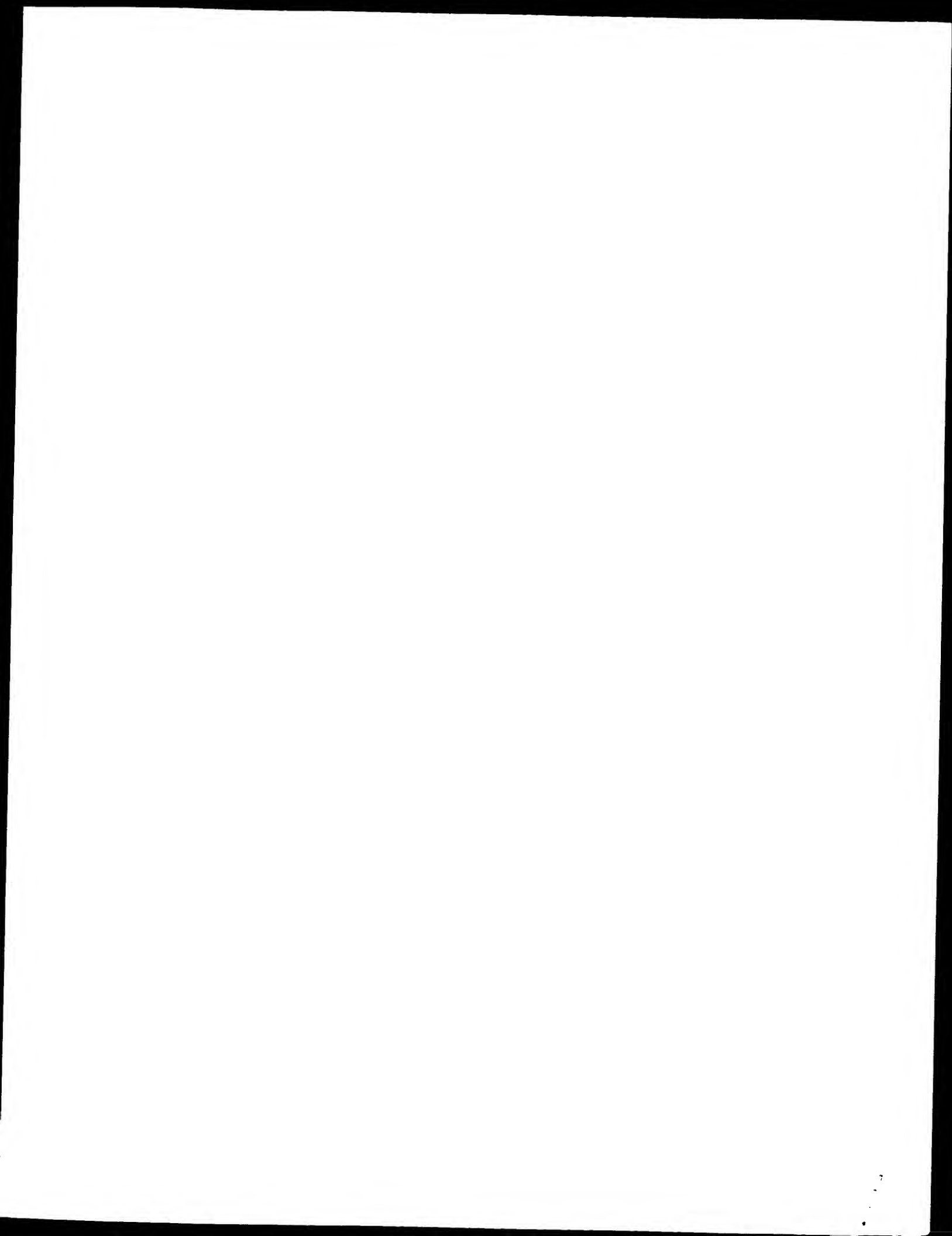
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DR EMBL: AJ238096; CAB45867.1; -.
DR EMBL: AF182290; AAD56228.1; -.
DR EMBL: AF117235; AAF17216.1; -.
DR EMBL: AF251218; AAF90055.1; -.
DR InterPro: IPR001163; snRNP_Sm.
DR Pfam: PF01423; Sm; 1.
KW Nuclear protein; Ribonucleoprotein; mRNA splicing; mRNA processing;
KW RNA-binding.
SQ SEQUENCE 139 AA; 15350 MW; BCEFB20247335A1B CRC64;

Query Match 36.0%; Score 45; DB 1; Length 139;
Best Local Similarity 72.7%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 KEQKGGPGGA 16
I:|||||
DB 97 KQKGRGMGGA 107

Search completed: September 4, 2002, 17:05:04
Job time: 1130 sec



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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:47:29 ; Search time 75.48 Seconds
(without alignments)
29.280 Million cell updates/sec

Title: US-09-821-726-2

Perfect score: 125

Sequence: 1 LDTWKEQKGGPGGAPPKDLMY 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR71.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	59	47.2	1677	T14267	Xin protein, stage
2	51	40.8	153	B71226	hypothetical prote
3	51	40.8	298	A49630	ubiquitin conjugat
4	51	40.8	378	A25399	homeotic protein A
5	50	40.0	269	I54432	MHC class II histo
6	49	39.2	142	D32880	hypothetical prote
7	49	39.2	266	B84351	pseudouridylylate sy
8	49	39.2	331	A36358	T-cell acute lymph
9	48	38.4	263	T50596	probable oxidoredu
10	47	37.6	218	T51887	hypothetical prote
11	47	37.6	233	HURTAB	Rt1 class II histo
12	47	37.6	263	HURTAB	class II histocomp
13	47	37.6	798	T42070	protein serine/thr
14	47	37.6	539	T49456	hypothetical prote
15	47	37.6	4936	AH2515	hypothetical prote
16	46.5	37.2	1240	T30834	nuclear protein SA
17	46	36.8	267	D31669	tRNA pseudouridine
18	46	36.8	267	C71511	probable pseudouri
19	46	36.8	268	D29312	MHC class II histo
20	46	36.8	315	T29525	hypothetical prote
21	46	36.8	398	F69581	acetoin dehydrogen
22	46	36.8	511	S24345	Balbani ring 1 pr
23	46	36.8	709	T34706	fatty acid oxidati
24	46	36.8	886	S07132	hypothetical prote
25	46	36.8	2022	T48818	glucan 1,4-alpha-g
26	46	36.8	4957	T03455	ALR protein - huma
27	46	36.8	5262	T03454	ALR protein - huma
28	45.5	36.4	376	A12339	dihydroorotate oxi
29	45.5	36.4	579	D72092	conserved hypothet

ALIGNMENTS

RESULT 1

T14267

Xin protein, stage early embryo - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T14267

R:Wang, D.Z.; Lin, J.J.C.

submitted to the EMBL Data Library, March 1998

A:Description: Involvement of a novel gene, Xin, in cardiac looping.

A:Reference number: Z17948

A:Accession: T14267

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1677 <W>

A:Cross-references: EMBL:AF051945; NID:g2970645; PID:g2970646; PIDN:RAC06023.1

A:Experimental source: cardiac muscle; stage early embryo

Query Match 47.2%; Score 59; DB 2; Length 1677;
Best Local Similarity 64.3%; Pred. No. 4.9;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 KEQKGGPGGAPPK 19

Db 571 EEEGKGPGGPPE 584

!:::|||||!::

RESULT 2

B71226

hypothetical protein PH0068 - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii

C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000

C:Accession: B71226

R.Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushida, N.; Ogu

DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophil

A:Reference number: A71000; MUID:98344137

A:Accession: B71226

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-153 <W>

A:Cross-references: GB:AF000001; NID:g3236128; PIDN:BAA29137.1; PID:g3256454

A:Experimental source: strain OT3

A>Note: this accession replaces an interim accession for a sequence replaced by GenBa

C:Genetics:

A:Gene: PH0068

C:Superfamily: Pyrococcus horikoshii hypothetical protein PH0068

Query Match 40.8%; Score 51; DB 2; Length 153;
Best Local Similarity 60.0%; Pred. No. 6;

Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LDTMVKEQKGGPGG 15
 |||::|||:: |||
 Db 121 LDTIIEENKGVGG 135

RESULT 3

A:ubiquitin conjugating enzyme - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 05-Nov-1999
 C:Accession: A49630
 R:Pilon, S.E.; Leppig, K.A.; Do, H.N.; Groudine, M.
 Proc. Natl. Acad. Sci. U.S.A. 90, 10484-10488, 1993
 A:Title: Cloning of the human homolog of the CDC34 cell cycle gene by complementation in
 A:Reference number: A49630; MUID:94068425
 A:Accession: A49630
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-298 <RES>
 A:Cross-references: GB:L22005; NID:q388308; PIDN:AAAC37534.1; PID:q388309
 C:Superfamily: human ubiquitin-protein ligase E2

Query Match 40.8%; Score 51; DB 2; Length 298;
 Best Local Similarity 61.5%; Pred. No. 12;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 KEQKGGKGGAPP 18
 :|||::|||:: |||
 Db 21 EEEAGGGGGPPP 33

RESULT 4

A25399
 homeotic protein Antennapedia - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 09-Jun-2000
 C:Accession: A23450; A25400; A25399; A03318; C24780; S02593
 R:Schneuwly, S.; Kuroiwa, A.; Baumgartner, P.; Gehring, W.J.
 EMBO J. 5, 733-739, 1986
 A:Title: Structural organization and sequence of the homeotic gene Antennapedia of Drosophila
 A:Reference number: A23450; MUID:99334708
 A:Accession: A23450
 A:Molecule type: DNA; mRNA
 A:Residues: 1-378 <SCH>
 A:Cross-references: GB:X03790; NID:q7593; PIDN:CAA27417.1; PID:e293776; PID:gl805742
 R:Laughton, A.; Boulet, A.M.; Bermingham Jr., J.R.; Laymon, R.A.; Scott, M.P.
 Mol. Cell. Biol. 6, 4676-4689, 1986
 A:Title: Structure of transcripts from the homeotic antennapedia gene of Drosophila melanogaster
 A:Reference number: A25400; MUID:87089829
 A:Accession: A25400
 A:Molecule type: DNA
 A:Residues: 1-378 <LAU>
 A:Cross-references: GB:M14496; GB:K01950; NID:gl56945; PIDN:AAA28376.1; PID:gl56947
 R:Stroeder, V.L.; Jorgensen, E.M.; Garber, R.L.
 Mol. Cell. Biol. 6, 4667-4675, 1986
 A:Title: Multiple transcripts from the antennapedia gene of Drosophila melanogaster.
 A:Reference number: A25399; MUID:87089828
 A:Accession: A25399
 A:Molecule type: mRNA
 A:Residues: 1-378 <STR>
 A:Cross-references: GB:M20704; GB:M14699; GB:M14701; NID:gl56948; PIDN:AAA70214.1; PID:gl56949
 A:Note: the authors translated the codon TCG for residue 179 as Asp
 R:McGinnis, W.; Garber, R.L.; Wirz, J.; Kuroiwa, A.; Gehring, W.J.
 Cell 37, 403-408, 1984
 A:Title: A homologous protein-coding sequence in Drosophila homeotic genes and its conserved
 A:Reference number: A90847; MUID:84205674
 A:Accession: A03318
 A:Molecule type: DNA
 A:Residues: 1-296-362, 'D' <MCG>
 A:Cross-references: GB:K01948; NID:gl56931; PIDN:AAA28373.1; PID:gl56934

R:Regulski, M.; Harding, K.; Kostriken, R.; Karch, F.; Levine, M.; McGinnis, W.
 Cell 43, 71-80, 1985
 A:Title: Homeo box genes of the Antennapedia and Bithorax complexes of Drosophila.
 A:Reference number: A90874; MUID:86079516
 A:Accession: C24780
 A:Molecule type: DNA
 A:Residues: 297-299, 'E' 301-357 <REG>
 A:Cross-references: GB:M12009; NID:gl56939; PIDN:AAA79241.1; PID:gl56940
 A:Note: the authors translated the codon GAA for residue 300 as Gly and TAC for resid
 R:Bermingham Jr., J.R.; Scott, M.P.
 EMBO J. 7, 3211-3222, 1988
 A:Title: Developmentally regulated alternative splicing of transcripts from the Drosophila
 A:Reference number: S02593; MUID:89030617
 A:Contents: annotation; alternative splicing
 C:Comment: This homeotic protein controls development of cells in the mesothorax segment
 C:Genetics:
 A:Gene: FlyBase:Antp
 A:Cross-references: FlyBase:FBgn00000095
 A:Map position: 3R47.8; 84B1-2
 A:Introns: 207/3; 220/3; 296/1
 C:Superfamily: unassigned homeobox proteins; homeobox homology
 C:Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regul
 F:298-354/Domain: homeobox homology <HOX>

Query Match 40.8%; Score 51; DB 2; Length 378;
 Best Local Similarity 45.0%; Pred. No. 15;
 Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 4 MVKEQKGGKGGAPPKDLMY 23
 :|||::|||:: |||
 Db 230 MYQQSGVPPVPGAPPQGMH 249

RESULT 5

I54432
 MHC class II histocompatibility antigen DQ α -beta chain precursor - human
 N:Alternate names: cell surface glycoprotein DQ α ; HLA-DQB1
 C:Species: Homo sapiens (man)
 C>Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 05-May-2000
 C:Accession: I54432; I67725; I68723; I59623
 R:Takamoto, K.; Yasunami, M.; Kimura, A.; Inoko, H.; Ando, A.; Hirose, T.; Inayama, Y.
 Immunogenetics 25, 343-346, 1987
 A:Title: DQ α beta chain precursor from HLA-DQ α -DQ β consists of six exons and expresses multiple
 A:Reference number: I54432; MUID:87192945
 A:Accession: I54432
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-269 <TSU>
 A:Cross-references: GB:M16276; NID:gl88397; PIDN:AAA59823.1; PID:gl87272
 R:Yasunami, M.
 Fukuoka Igaku Zasshi 79, 153-167, 1988
 A:Title: [Structural analysis of human major histocompatibility complex class II gene
 A:Reference number: I53630; MUID:88226367
 A:Accession: I67725
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 6-269 <PUK>
 A:Cross-references: GB:M57649; NID:gl87852; PIDN:AAA63217.1; PID:gl87853
 R:Lee, B.S.; Bell, J.I.; Rust, N.A.; McDevitt, H.O.
 Immunogenetics 26, 85-91, 1987
 A:Title: Structural and functional variability among DQ beta alleles of DR2 subtypes.
 A:Reference number: I54440; MUID:87278366
 A:Accession: I68723
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 33-83, 'P' 85-122 <LEB>
 A:Cross-references: GB:M17204; NID:gl87906; PIDN:AAA59698.1; PID:gl87907
 R:Singal, D.P.; Oiu, X.; Sood, S.K.
 Tissue Antigens 40, 104-107, 1992
 A:Title: Molecular analysis of novel HLA-DR2.DQ α haplotypes in Asian Indians.
 A:Reference number: I59623; MUID:93031783
 A:Accession: I59623

A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 45-83, P', 85-112 <SIN>
A:Cross-references: GB:M86740; NID:g188221; PIDN:AAA59778.1; PID:g188222
C:Genetics:
A:Gene: GDB:HLA-DQB1; HLA-DW12
A:Cross-references: GDB:120517; OMIM:142857
A:Map position: 6p21.3-6p21.3
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein
F:142-207/Domain: immunoglobulin homology <IMM>

Query Match 40.0%; Score 50; DB 2; Length 269;
Best Local Similarity 34.8%; Pred. No. 14;
Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 LDTMVKEQKGGPGGAPPKDLMY 23
| : : : : | | | | | : : :
Db 247 LGLTIQRSGKGGPGGPPAGLLH 269

RESULT 6
D32880
hypothetical protein (pulB 3' region) - Klebsiella pneumoniae (fragment)
C:Species: Klebsiella pneumoniae
C:Date: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 30-Sep-1993
C:Accession: D32880
R:D'Entert, C.; Pugsley, A.P.
J. Bacteriol. 171, 3673-3679, 1989
A:Title: Klebsiella pneumoniae pulB gene encodes an outer membrane lipoprotein required
A:Reference number: A32880; MUID:89291709
A:Accession: D32880
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-142 <DEN>
A:Cross-references: GB:M29097
C:Superfamily: penicillin-binding protein 1B

Query Match 39.2%; Score 49; DB 2; Length 142;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 QKGGKGGGAPPK 19
| : : : : | | | | : : :
Db 49 RKGGKGGGKPPR 60

RESULT 7
B84351
pseudouridylate synthase I [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 24-May-2001
C:Accession: B84351
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablonski, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: B84160; MUID:20504483
A:Accession: B84351
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-266 <STO>
A:Cross-references: GB:AE004437; NID:g10581435; PIDN:AAG20174.1; GSPDB:GN00138
C:Genetics:
A:Gene: trnA
C:Superfamily: tRNA-pseudouridine synthase I

Query Match 39.2%; Score 49; DB 2; Length 266;
Best Local Similarity 69.2%; Pred. No. 25;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 GKGGGAPPKDLM 22

Best Local Similarity 40.0%; Pred. No. 20;
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 LDTMVKEQKGGPGGAPPKD 20
| : : : : | | | | | : : :
Db 197 IDTVLGDEPVAGPDGVPDAD 216

RESULT 8
A36358
T-cell acute lymphocytic leukemia 1 protein - human
C:Species: Homo sapiens (man)
C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 17-Nov-2000
C:Accession: A36358; A34519; S55280; I38254; S12374
R:Aplan, P.D.; Begley, C.G.; Bertness, V.; Nussmeier, M.; Ezquerro, A.; Colligan, J.; Mol. Cell. Biol. 10, 6426-6435, 1990
A:Title: The SCL gene is formed from a transcriptionally complex locus.
A:Reference number: A36358; MUID:91061750
A:Accession: A36358
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-331 <APL>
A:Cross-references: GB:M61108; NID:g469058; PIDN:AAA36600.1; PID:g337970
R:Begin, C.G.; Aplan, P.D.; Denning, S.M.; Haynes, B.F.; Waldmann, T.A.; Kirsch, I.R. Proc. Natl. Acad. Sci. U.S.A. 86, 10128-10132, 1989
A:Title: The gene SCL is expressed during early hematopoiesis and encodes a different
A:Reference number: A34519; MUID:90099309
A:Accession: A34519
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 118-331 <BEG>
A:Cross-references: GB:M29038; NID:g337958; PIDN:AAA36598.1; PID:g337959
R:Bernard, O.; Lecointe, N.; Jonveaux, P.; Souyri, M.; Mauchauffe, M.; Berger, R.; La Oncogene 6, 1477-1488, 1991
A:Title: Two site-specific deletions and t(1;14) translocation restricted to human T-
A:Reference number: S55280; MUID:91360285
A:Accession: S55280
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-292, 't', 294-331 <BER>
A:Cross-references: EMBL:S53245; NID:g234755; PIDN:AA19683.1; PID:g234756
R:Chen, Q.; Yang, C.Y.; Tsan, J.T.; Xia, Y.; Ragab, A.H.; Peiper, S.C.; Carroll, A.; J. Exp. Med. 172, 1403-1408, 1990
A:Title: Coding sequences of the tal-1 gene are disrupted by chromosome translocation
A:Reference number: I38253; MUID:91037802
A:Accession: I38253
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 106-148 <RES>
A:Cross-references: EMBL:X58622; NID:g36685; PIDN:CAA41477.1; PID:g36686
R:Chen, Q.; Cheng, J.T.; Tsai, L.H.; Schneider, N.; Buchanan, G.; Carroll, A.; Crist, EMO J. 9, 415-424, 1990
A:Title: The tal gene undergoes chromosome translocation in T cell leukemia and poten
A:Reference number: S12374; MUID:90151616
A:Accession: S12374
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 'R', 157-331 <CHE>
A:Cross-references: EMBL:X51990
C:Genetics:
A:Gene: GDB:TAL1; SCL; TCL5
A:Cross-references: GDB:120759; OMIM:187040
A:Map position: lp32-lp32
A:Introns: 180/3
C:Superfamily: lyl-1 protein
C:Keywords: DNA binding; transcription regulation

Query Match 39.2%; Score 49; DB 2; Length 331;
Best Local Similarity 69.2%; Pred. No. 25;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

A:Accession: T42070
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-598 <OGA>
A:Cross-references: EMBL:AB016932; PIDN:BAA32455.1
C:Genetics:
A:Gene: pkad

Query Match 37.6%; Score 47; DB 2; Length 598;
Best Local Similarity 72.7%; Pred. No. 84;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 GKGGGAPPKD 20
| | | | | | | | | |
DB 433 GKGGGGVPAD 443

RESULT 14
T49456
hypothetical protein B14D6.80 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C:Accession: T49456
R:Schulte, U.; Align, V.; Hohelsel, J.; Brandt, P.; Partmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A:Reference number: Z25022
A:Accession: T49456
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-739 <SCH>
A:Cross-references: EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6.80
A:Experimental source: BAC clone B14D6; strain OR74A
C:Genetics:
A:Gene: NCSP:B14D6.80
A:Map position: 6

Query Match 37.6%; Score 47; DB 2; Length 739;
Best Local Similarity 61.5%; Pred. No. 1e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

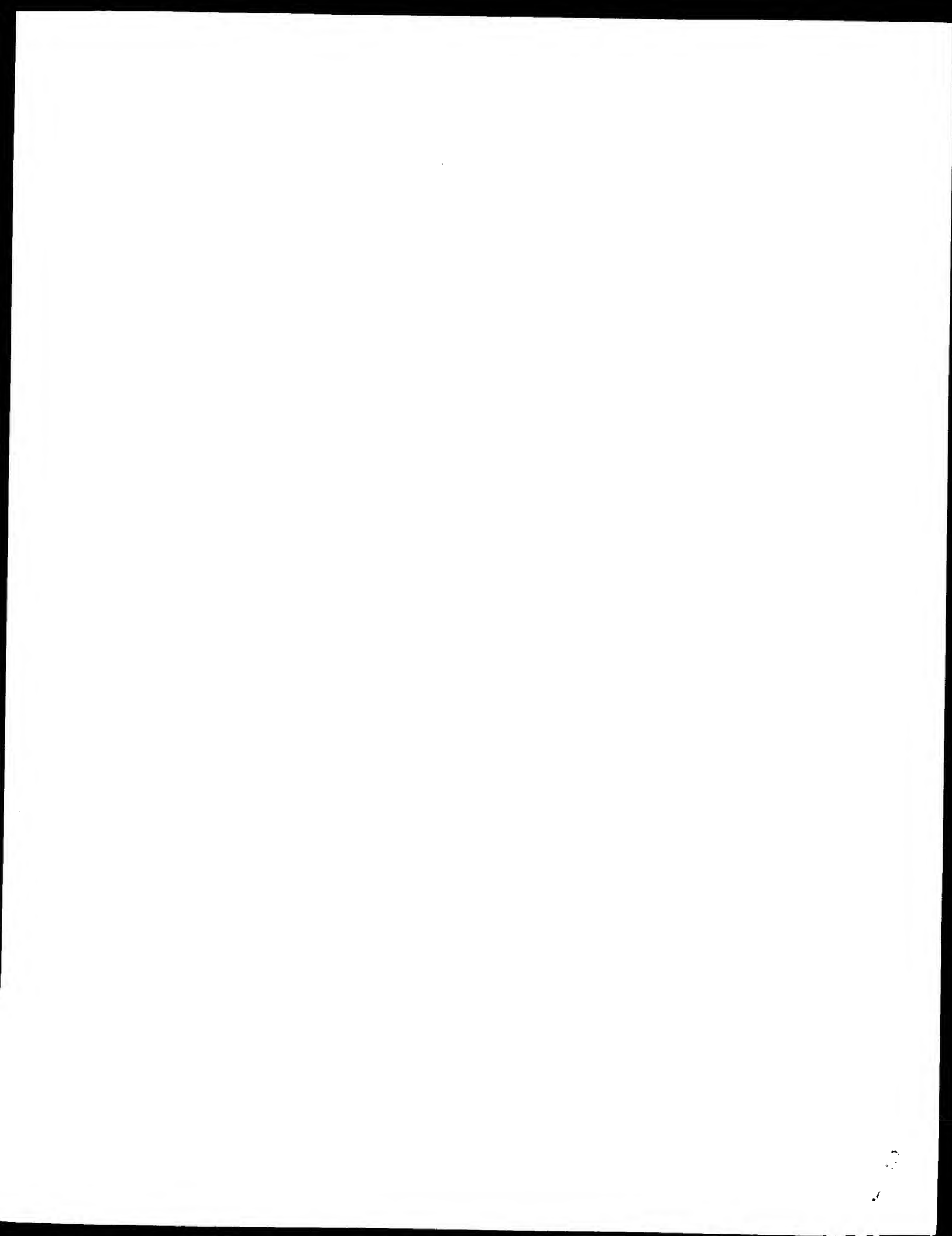
QY 6 KEQKGGGPGAPP 18
: | | | | | | | | | |
DB 217 REQKGGPGASTP 229

RESULT 15
AH2515
hypothetical protein alr7304 [imported] - Anabaena sp. (strain PCC 7120) plasmid pCC7120
C:Species: Anabaena sp.
A:Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C:Accession: AH2515
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AH2515
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-4936 <KUR>
A:Cross-references: GB:BA000020; PIDN:BA878388.1; PID:gl7135842; GSPDB:GN00180
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr7304
A:Genome: plasmid

Query Match 37.6%; Score 47; DB 2; Length 4936;
Best Local Similarity 40.0%; Pred. No. 6.9e+02;
Matches 8; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 LDTMYKEQKGGGAPPKD 20
: | | | | | | | | | |
DB 2312 VDDGIEQNGRDPNNPDPKD 2331

Search completed: September 4, 2002, 16:47:30
Job time: 366 sec



Thu Sep 5 11:23:36 2002

Query Match 41.2%; Score 51.5; DB 4; Length 681;
Best Local Similarity 54.2%; Pred. No. 18;
Matches 13; Conservative 1; Mismatches 5; Indels 5; Gaps 1;

QY 1 LDTMPKFAFSSDEGVGGPGAPK 19
155 LDTMPKFAFSSDEGVGGPGAPK 178

RESULT 5
ID O60307 PRELIMINARY; PRT; 1308 AA.
AC O60307;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DT KIAA0561 PROTEIN (FRAGMENT).
GN KIAA0561.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE=96290545; PubMed=9628581;
RA Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,
RA Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. IX.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 5:31-39(1998).
RN [2]
RP SEQUENCE OF 1-593 FROM N.A.
RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J.,
RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Attix C., Andreise T., Frankheim M., Amico-Keller G., Coefield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
RA Arellano A., Saunders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carrano A.V.;
RT "Sequence analysis of an ~600 kb region in 19p13.1 between JAK3 and
RT pDE4C.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB011133; BAA25487.1; -;
DR EMBL; AC005793; AAC62830.1; -;
DR HSSP; P05132; ICTP.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00595; PDZ; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PF00109; TYRKINASE.
DR SMART; SM00228; PDZ; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TKc; 1.
DR PROSITE; PS50106; PDZ; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
FT NON_TER
SQ SEQUENCE 1308 AA; 143004 MW; 9B3A23C528EF47A6 CRC64;

Query Match 41.2%; Score 51.5; DB 4; Length 1308;
Best Local Similarity 54.2%; Pred. No. 34;
Matches 13; Conservative 1; Mismatches 5; Indels 5; Gaps 1;

QY 1 LDTMPKFAFSSDEGVGGPGAPK 19

Db 782 LDTMPKFAFSSDEGVGGPGAPK 805

RESULT 6
ID O57795 PRELIMINARY; PRT; 153 AA.
AC O57795;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE HYPOTHETICAL 17.0 KDA PROTEIN PH0068.
GN PH0068.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OC NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudo H., Yamazaki J., Kishida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
DR EMBL; AF000001; BAA29137.1; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 153 AA; 16966 MW; 9063F41B6DA9255B CRC64;

Query Match 40.8%; Score 51; DB 17; Length 153;
Best Local Similarity 60.0%; Pred. No. 4.5;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 LDTMPKFAFSSDEGVGGPGAPK 15
Db 121 LDTMPKFAFSSDEGVGGPGAPK 135

RESULT 7
ID Q95S26 PRELIMINARY; PRT; 297 AA.
AC Q95S26;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE LD33666P.
GN ANTP.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, CN BW SP;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., R.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY060407; AAL25446.1; -;
SQ SEQUENCE 297 AA; 32845 MW; A88C5435ABD619H3 CRC64;

Query Match 40.8%; Score 51; DB 5; Length 297;
Best Local Similarity 45.0%; Pred. No. 9;
Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 4 MVKEQKGGKGGGAPPKDLMY 23
 | : | | | | : | : | : | : | : | : | :
 Db 230 MYQQSGVPPVPGAPPQGNMH 249

RESULT 8

Q30097
 ID Q30097 PRELIMINARY; PRT; 237 AA.
 AC Q30097;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC CLASS II HLA-DO-BETA-1 (FRAGMENT).
 GN HLA-DOB1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yasunaga S.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; L40180; AAA92331.1; --
 DR HSSP; P13760; 2SEB.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00969; MHC_II_beta.
 DR ProDom; PD000328; MHC_II_beta; 1.
 DR SMART; SM00407; IGcl; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1
 SQ SEQUENCE 237 AA; 27038 MW; 460B63ABCA7BC8EA CRC64;

Query Match 40.0%; Score 50; DB 7; Length 237;
 Best Local Similarity 34.8%; Pred. No. 10;
 Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 LDTMVKEQKGGKGGGAPPKDLMY 23
 | : | | | | : | : | : | : | : | : | :
 Db 215 LGLIIRSRKGGQPPGAPGLLH 237

RESULT 9

Q30098
 ID Q30098 PRELIMINARY; PRT; 237 AA.
 AC Q30098;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC CLASS II HLA-DO-BETA-1 (FRAGMENT).
 GN HLA-DOB1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yasunaga S.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; L40181; AAA92332.1; --
 DR HSSP; P13760; 2SEB.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 DR SMART; SM00407; IGcl; 1.

DR PROSITE; PS00290; IG_MHC; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1
 SQ SEQUENCE 237 AA; 27179 MW; 75C1B91440C0D5DF CRC64;

Query Match 40.0%; Score 50; DB 7; Length 237;
 Best Local Similarity 34.8%; Pred. No. 10;
 Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 LDTMVKEQKGGKGGGAPPKDLMY 23
 | : | | | | : | : | : | : | : | : | :
 Db 215 LGLIIRSRKGGQPPGAPGLLH 237

RESULT 10

Q29970
 ID Q29970 PRELIMINARY; PRT; 264 AA.
 AC Q29970;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE CELL SURFACE GLYCOPROTEIN (FRAGMENT).
 GN HLA-DWI2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88226367; PubMed=3371836;
 RA Yasunami M.;
 RT "Structural analysis of human major histocompatibility complex class II genes".
 RL Fukuoka Igaku Zasshi 79:153-167(1988).
 DR EMBL; M57649; AAA63217.1; --
 DR HSSP; P13760; 2SEB.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 DR SMART; SM00407; IGcl; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1
 SQ SEQUENCE 264 AA; 29871 MW; BB6A4A9054F3CB75 CRC64;

Query Match 40.0%; Score 50; DB 7; Length 264;
 Best Local Similarity 34.8%; Pred. No. 11;
 Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 LDTMVKEQKGGKGGGAPPKDLMY 23
 | : | | | | : | : | : | : | : | : | :
 Db 242 LGLIIRSRKGGQPPGAPGLLH 264

RESULT 11

Q30155
 ID Q30155 PRELIMINARY; PRT; 269 AA.
 AC Q30155;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE HLA-DRB2 PROTEIN.
 GN HLA-DRB2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

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```

RP SEQUENCE FROM N.A.
RX MEDLINE=87192945; PubMed=3494674;
RA Tsukamoto K., Yasunuki M., Kimura A., Inoko H., Ando A., Hirose T.,
RA Inayama S., Sasazuki T.;
RT "DQW1 beta gene from HLA-DP2-DW12 consists of six exons and expresses
RT multiple DQW1 beta polypeptides through alternative splicing.";
RL Immunogenetics 25:343-346(1987).
DR EMBL: M16276; AAA59823.1; -.
DR HSSP: P13760; 2SEP.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR000353; MHC_II_beta.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF00969; MHC_II_beta; 1.
DR ProDom: PD000328; MHC_II_beta; 1.
DR SMART: SM00407; IGc1; 1.
DR SMART: PS00290; IG_MHC; 1.
DR PROSITE: PS00290; IG_MHC; 1.
KW Glycoprotein; MHC II; Transmembrane.
KW SEQUENCE 269 AA; 30532 MW; 4FF81EC5AD92A6EA CRC64;

Query Match 40.0%; Score 50; DB 7; Length 269;
Best Local Similarity 34.8%; Pred. No. 12;
Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 LDTMVKEQKGKGGCGAPPKDMY 23
DB 247 LGLIIRQSRKQGGQGGPPAGLLH 269

RESULT 12
Q9N893 PRELIMINARY; PRT; 611 AA.
AC Q9N893;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE VIR12 PROTEIN.
GN VIR12.
OS Plasmodium vivax.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5855;
RN [1]
RP SEQUENCE FROM N.A.
RA Oliver K., Bowman S., Hall N., Quail M., Rajandream M.A., Harris D.,
RA del Portillo H.A., Lanzar M., Barrell B.G.;
RA Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AL360354; CAB96702.1; -.
DR EMBL: AL360354; CAB96702.1; -.
SQ SEQUENCE 611 AA; 68442 MW; A642D1893D7DD8F4 CRC64;

Query Match 40.0%; Score 50; DB 5; Length 611;
Best Local Similarity 56.2%; Pred. No. 27;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 MVKEQKGKGGCGAPPK 19
DB 366 ITKQKGVSPAGSPSK 381

RESULT 13
O74299 PRELIMINARY; PRT; 191 AA.
AC O74299;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE ORF15 PROTEIN PRECURSOR.
OS Schizophyllum commune [Bracket fungus].
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Stereales; Schizophyllaceae; Schizophyllum.
OX NCBI_TaxID=5334;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=4-40 (CBS 340.81);
RA Lugones L.G.;
RL Thesis (1998); University of Groningen.
DR EMBL: AJ007543; CAA07544.1; -.
RT Signal. 1 22 POTENTIAL.
FT SIGNAL
SQ SEQUENCE 191 AA; 19973 MW; 778518EF0D830179 CRC64;

Query Match 39.2%; Score 49; DB 3; Length 191;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 VKEQKGKGGCGAPPK 19
DB 90 IEELKGGKPGAGHPK 104

RESULT 14
Q9HNP6 PRELIMINARY; PRT; 266 AA.
AC Q9HNP6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PSEUDOURIDYLATE SYNTHASE I.
GN TRUA OR VNG2003G.
OS Halobacterium sp. (strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
OC Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Shroogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithausen B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Eberhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
RA "Genome sequence of Halobacterium species NRC-1.";
RT Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
RL EMBL: AE005094; AAG20174.1; -.
DR InterPro: IPR001406; PseudoU synth_1.
DR Pfam: PF01416; PseudoU synth_1; 1.
KW Complete proteome.
SQ SEQUENCE 266 AA; 28863 MW; FD2D3373A9E98037 CRC64;

Query Match 39.2%; Score 49; DB 17; Length 266;
Best Local Similarity 40.0%; Pred. No. 16;
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 LDTMVKEQKGKGGCGAPPK 20
DB 197 IDTVLGDEPVAGDGVPPAD 216

RESULT 15
Q16509 PRELIMINARY; PRT; 331 AA.
AC Q16509;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE TAL-1.
GN TAL-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

```

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91360285; PubMed=1886719;
 RA Bernard O., Lecoq N., Jonveaux P., Souyri M., Mauchauffe M.,
 RT Berger R., Larsen C.J., Mathieu-Mahul D.;
 RL "Two site-specific deletions and t(1;14) translocation restricted to
 human T-cell acute leukemias disrupt the 5' part of the tal-1 gene.";
 DR Oncogene 6:1477-1488(1991).
 DR EMBL; S53245; AAB19683.1; -;
 DR InterPro; IPR001092; HLH_dim.
 DR Pfam; PF00010; HLH; 1.
 DR SMART; SM00353; HLH; 1.
 DR PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN 1.
 SQ SEQUENCE 331 AA; 34284 MW; 58D0E31589DB396 CRC64;

Query Match 39.2%; Score 49; DB 4; Length 331;
 Best Local Similarity 69.2%; Pred. No. 20;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 10 KGPGGGAPPKDL 22
 Db 269 GGGGGAPPDDL 281

Search completed: September 4, 2002, 17:01:33
 Job time: 1154 sec

Thu Sep 5 11:23:43 2002

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 17:05:06 : Search time 34.18 Seconds
(without alignments)
21.523 Million cell updates/sec

Title: US-09-821-726-5

Perfect score: 90

Sequence: 1 KKEVMPISQSLDALVREKK 19

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	94.4	199	1	C11P_HUMAN
2	62	68.9	184	1	C11P_MOUSE
3	43	47.8	633	1	TOPL_THEMA
4	43	47.8	734	1	METE_THEMA
5	42.5	47.2	715	1	ERF2_CANAL
6	42	46.7	203	1	NAHD_PSEPU
7	42	46.7	212	1	NAHD_PSESP
8	41	45.6	292	1	SPAN_SHIFL
9	41	45.6	334	1	RL3_METVA
10	41	45.6	361	1	PDA6_ARATH
11	41	45.6	669	1	PRIA_CHLTR
12	41	45.6	753	1	GYRA_CAMFE
13	41	45.6	862	1	GIYA_ARCFU
14	40.5	45.0	451	1	SMC1_YEAST
15	40.5	45.0	1225	1	RL10_MYCGE
16	40	44.4	162	1	RT15_MOUSE
17	40	44.4	258	1	LPXB_HAEIN
18	40	44.4	390	1	FTSY_HAEIN
19	40	44.4	414	1	BENK_ACICA
20	40	44.4	466	1	GRAA_BACSU
21	40	44.4	482	1	YN35_YEAST
22	40	44.4	524	1	ANDS_EMENI
23	40	44.4	548	1	UVRE_AQUAE
24	40	44.4	663	1	GRPE_THEAC
25	39	43.3	175	1	YCX6_YEAST
26	39	43.3	190	1	P8BQ_VOLCA
27	39	43.3	202	1	COAT_CYMW
28	39	43.3	212	1	Y227_AQUAE
29	39	43.3	259	1	C256_MOUSE
30	39	43.3	342	1	SUCA_ARATH
31	39	43.3	347	1	TRPB_BACSU
32	39	43.3	400	1	MIQ1_KLUMA
33	39	43.3	543	1	MIQ1_KLUMA

RESULT 1
CLIP_HUMAN
ID C11P_HUMAN STANDARD; PRT; 199 AA.
AC Q9NS71; 657 1 HUTH_HUMAN
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE CALL protein.
GN CALL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RX MEDLINE=20296773; PubMed=10835488;
RA Yoshikawa Y., Mukai H., Hino F., Asada K., Kato I.;
RT "Isolation of two novel genes, down-regulated in gastric cancer.";
RL Jpn. J. Cancer Res. 91:459-463(2000).
CC -I- TISSUE SPECIFICITY: Expressed in stomach. No expression is
CC detected in cancer tissue or gastric cancer cell lines.
CC -----
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CC -----
CC EMBL; AB039886; BAA92433.1; -
DR MIM; 606402; -
SQ SEQUENCE 199 AA; 21999 MW; C099B8B9A1338D7A CRC64;
Query Match 94.4%; Score 85; DB 1; Length 199;
Best Local Similarity 100.0%; Pred. No. 6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 KEVMPISQSLDALVREKK 19
Db 102 KEVMPISQSLDALVREKK 119
RESULT 2
CLIP_MOUSE
ID C11P_MOUSE STANDARD; PRT; 184 AA.
AC Q9CR36; Q9D7K7; Q9CTZ5;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE CALL protein homolog.
GN CALL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

P42357 homo sapien
Q02208 saccharomyc
Q08236 saccharomyc
Q9V108 pyrococcus
P39373 sulfolobus
O97513 orcinus orc
O9ZMW8 helicobacte
O24931 helicobacte
O9K998 bacillus ha
P21911 schizosacch
P34454 caenorhabdi
P44000 haemophilus

ALIGNMENTS

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Stomach, and Tongue;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Hono H., Kasukawa T., Saio R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga K., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -----
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CC -----
DR EMBL; AK008990; BAB26010.1; -
DR EMBL; AK008622; BAB25784.1; -
DR EMBL; AK008641; BAB25801.1; -
DR EMBL; AK008647; BAB25805.1; -
DR EMBL; AK008722; BAB25856.1; -
DR EMBL; AK008745; BAB25872.1; -
DR EMBL; AK008933; BAB25975.1; -
DR EMBL; AK008956; BAB25988.1; -
DR EMBL; AK009145; BAB26103.1; -
DR EMBL; AK019050; BAB31525.1; -
FT CONFLICT 113 113 P -> L (IN REF. 1; BAB26103).
SQ SEQUENCE 184 AA; 20134 MW; 288982F0404FFA8B CRC64;

Query Match 68.9%; Score 62; DB 1; Length 184;
Best Local Similarity 61.1%; Pred. No. 0.0037;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 KEVMSIQSLDALVKEKK 19
Db 88 KDAMPSQLDLTWVEQK 105
I: |||:| | :|||:|
: |||:| | :|||:|

RESULT 3
TOP1_THEME
ID TOP1_THEME STANDARD; PRT; 633 AA.
AC P46799;
DC 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA topoisomerase I (EC 5.99.1.2) (Omega-protein) (Relaxing enzyme)
DE (Untwisting enzyme) (Swivelase).
GN TOPA OR TM0258.
OS Thermotoga maritima
OC Bacteria; Thermotogales; Thermotoga.
OX NCBI_TaxID=23336;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=96138548; PubMed=8547314;
RA Bouthier de la Tour C., Kaltoum H., Portemer C., Confalonieri F.,
RA Huber R., Duquet M.;
RT "Cloning and sequencing of the gene coding for topoisomerase I from
RT the extremely thermophilic eubacterium, Thermotoga maritima.";
RL Biochim. Biophys. Acta 1264:279-283(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
CC -----
CC -1- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE
CC CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.
CC -1- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded
CC DNA, followed by passage and rejoining.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA
CC BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN
CC WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS
CC AT ONE END OF THE ENZYME-SEVERED DNA STRAND.
CC -1- SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U27841; AAA68949.1; -
DR EMBL; AE001708; AAD35346.1; -
DR HSSP; P06612; IECL.
DR TIGR; TM0258; -
DR InterPro; IPR003601; DNATopI_ATP_bind.
DR InterPro; IPR003602; DNATopI_DNA_bind.
DR InterPro; IPR000380; Pro_topoisomerase.
DR InterPro; IPR002936; Toprim.
DR Pfam; PF01131; Topoisom_bac; 1.
DR Pfam; PF01751; Toprim; 1.
DR PRINTS; PR00417; PRTPISMRASEI.
DR SMART; SM00437; TOPIAC; 1.
DR SMART; SM00436; TOPIBC; 1.
DR SMART; SM00493; TOPRIM; 1.
DR PROSITE; PS00396; TOPOISOMERASE_I_PROK; 1.
KW Isomerase; Topoisomerase; DNA-binding; Zinc-finger; Metal-binding;
FT ACT_SITE 559 580 C4-TYPE.
FT ZN_FING 288 288 DNA CLEAVAGE (BY SIMILARITY).
SQ SEQUENCE 633 AA; 72694 MW; F7262A044060CFE9 CRC64;

Query Match 47.8%; Score 43; DB 1; Length 633;
Best Local Similarity 52.9%; Pred. No. 19;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 EVMPISQSLDALVKEKK 19
Db 216 ETLKEIQSIDLVVEEK 232
I: |||:| | :|||:|
: |||:| | :|||:|

RESULT 4
METE_THEME

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ID METE_THEME STANDARD; PRT; 734 AA.
AC Q9X112;
DC 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 5-methyltetrahydropteroyl-L-glutamate--homocysteine methyltransferase
DE (EC 2.1.1.14) (Methionine synthase, vitamin-B12 independent isozyme)
DE (Cobalamin-independent methionine synthase).
GN METE OR TM1286.
OS Thermotoga maritima.
OC Bacteria; Thermotogales; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A. 3109;
RC STRAIN=MSBB / DSM 3109;
RA MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
CC -|- FUNCTION: CATALYZES THE TRANSFER OF A METHYL GROUP FROM 5-
METHYLTETRAHYDROPTEROLATE TO HOMOCYSTEINE RESULTING IN METHIONINE
FORMATION (BY SIMILARITY).
CC -|- CATALYTIC ACTIVITY: 5-methyltetrahydropteroyl-L-glutamate + L-
homocysteine = tetrahydropteroyl-L-glutamate + L-methionine.
CC -|- COFACTOR: ZINC; BINDS ONE ION PER SUBUNIT (BY SIMILARITY).
CC -|- PATHWAY: TERMINAL STEP IN THE DE NOVO BIOSYNTHESIS OF METHIONINE.
CC -|- SIMILARITY: BELONGS TO THE VITAMIN-B12 INDEPENDENT METHIONINE
SYNTHASE FAMILY.
CC -----
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CC -----
CC EMBL; AE001784; AAD36360.1; -.
CC TIGR; TM1286; -.
CC InterPro: IPR002629; Methionine_synth.
CC Pfam: PF01171; Methionine_synth; 1.
CC Transfaser: Methyltransferase; Methionine biosynthesis; Zinc; Repeat;
KW Complete proteome. 618 ZINC (BY SIMILARITY).
FT METAL 618 620 ZINC (BY SIMILARITY).
FT METAL 620 620 ZINC (BY SIMILARITY).
FT METAL 704 704 ZINC (BY SIMILARITY).
FT SEQUENCE 734 AA; 85570 MW; 34B19187480D443B CRC64;
Query Match 47.8%; Score 43; DB 1; Length 734;
Best Local Similarity 47.1%; Pred. No. 23;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
OY 3 EYMPSTQSLDALVKEKK 19
DB 713 EVIPSLRNHVALAKEMR 729
RESULT 5
ERF2_CANAL STANDARD; PRT; 715 AA.
AC OI3354;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Eukaryotic peptide chain release factor GTP-binding subunit (ERF2)
DE (translation release factor 3) (ERF3) (ERF-3).
GN
OS
OG
OC
OC Pseudomonas.
OC NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=G7 / ATCC 17485;
RX MEDLINE=95095951; PubMed=8002605;
RA Eaton R.W.;
RT "Organization and evolution of naphthalene catabolic pathways:

```

sequence of the DNA encoding 2-hydroxychromene-2-carboxylate isomerase and trans-o-hydroxybenzylidenepyrivate hydratase-aldolase from the NAH7 plasmid.";
 J. Bacteriol. 176:7757-7762(1994).
 [2]
 CHARACTERIZATION.
 STRAIN-G7 / ATCC 17485;
 MEDLINE-93077433; PubMed-1447127;
 Eaton R.W., Chapman P.J.;
 "Bacterial metabolism of naphthalene: construction and use of recombinant bacteria to study ring cleavage of 1,2-dihydroxynaphthalene and subsequent reactions.";
 J. Bacteriol. 174:7542-7554(1992).
 CC -!- FUNCTION: CATALYZES THE ISOMERIZATION OF 2-HYDROXYCHROMENE-2-CARBOXYLATE (HCCA) TO TRANS-O-HYDROXYBENZYLIDENEPYRIVATE (THBPA).
 CC THE OPTIMUM PH FOR THE ENZYME IS 10. THE REACTION IS REVERSIBLE.
 CC -!- COFACTOR: GLUTATHIONE SEEMS TO STABILIZE THE ENZYME, WHICH LOSES ACTIVITY RAPIDLY IN THE ABSENCE OF THIS COMPOUND.
 CC -!- PATHWAY: UPPER NAPHTHALENE CATABOLIC PATHWAY WHICH INVOLVES CONVERSION OF NAPHTHALENE TO SALICYLATE.
 CC -----
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 CC -----
 DR EMBL; U09057; AAA66358.1; .
 DR InterPro; IPR004287; HCCA_isomerase.
 DR Pfam; PF03046; HCCA_isomerase; 1.
 KW Isomerase; Plasmid; Aromatic hydrocarbons catabolism.
 SQ SEQUENCE 203 AA; 23061 MW; E84B56F21C604945 CRC64;
 CC -----
 Query Match 46.7%; Score 42; DB 1; Length 203;
 Best Local Similarity 53.3%; Pred. No. 8.6;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 4 VMPSTQSLDALVKEK 18
 : | : | | | | | |
 Db 118 IAPDLESIPALVSEK 132

 RESULT 7
 NAHD_PSESP
 ID NAHD_PSESP STANDARD; PRT; 212 AA.
 AC Q52462;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 2-hydroxychromene-2-carboxylate isomerase (HCCA isomerase).
 GN DOXJ.
 OS Pseudomonas sp. (strain C18).
 OG Plasmid.
 OC Bacteria; Proteobacteria.
 OX NCBI_TaxID=306;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-94042852; PubMed-8226631;
 RA Denome S.A., Stanley D.C., Olson E.S., Young K.D.;
 RT "Metabolism of dibenzothioephene and naphthalene in Pseudomonas strains: complete DNA sequence of an upper naphthalene catabolic pathway.";
 RL J. Bacteriol. 175:6890-6901(1993).
 CC -!- FUNCTION: CATALYZES THE ISOMERIZATION OF 2-HYDROXYCHROMENE-2-CARBOXYLATE (HCCA) TO TRANS-O-HYDROXYBENZYLIDENEPYRIVATE (THBPA).
 CC THE OPTIMUM PH FOR THE ENZYME IS 10. THE REACTION IS REVERSIBLE.
 CC -!- PATHWAY: UPPER NAPHTHALENE CATABOLIC PATHWAY WHICH INVOLVES CONVERSION OF NAPHTHALENE TO SALICYLATE, AND CATABOLISM OF DIBENZOTHIOEPHENE (DBT) AND PHENANTHRENE. CONVERTS PHENANTHRENE TO 1-HYDROXY-2-NAPHTHOIC ACID AND THE METABOLISM OF DBT IS LIMITED TO

OXIDATION OF THE AROMATIC RING.
 -!- MISCELLANEOUS: DOXH AND DOXJ ENCODE DIFFERENT ENZYMES THAT MAY HAVE INTERCHANGEABLE FUNCTIONS.
 CC -----
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 CC -----
 DR EMBL; M60405; AAA16133.2; ALT_SEQ.
 DR InterPro; IPR004287; HCCA_isomerase.
 DR Pfam; PF03046; HCCA_isomerase; 1.
 KW Isomerase; Plasmid; Aromatic hydrocarbons catabolism.
 SQ SEQUENCE 212 AA; 24039 MW; 5EF96A619913DB4F CRC64;
 CC -----
 Query Match 46.7%; Score 42; DB 1; Length 212;
 Best Local Similarity 53.3%; Pred. No. 9;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 4 VMPSTQSLDALVKEK 18
 : | : | | | | | |
 Db 131 IAPDLESIPALVSEK 145

 RESULT 8
 SPAN_SHIFL
 ID SPAN_SHIFL STANDARD; PRT; 292 AA.
 AC P35532;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 13-JUL-1999 (Rel. 38, Last annotation update)
 DE Surface presentation of antigens protein span (Spa32 protein).
 GN SPAN OR SPA32.
 OS Shigella flexneri, and
 OS Shigella sonnei.
 OG Plasmid 210 kb invasion pWR100, and plasmid 230 kb pMYSH6000.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Shigella.
 OX NCBI_TaxID=623, 624;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES-S.flexneri; STRAIN=M90T; PLASMID=210 kb invasion pWR100;
 RX MEDLINE-92193289; PubMed-1312536;
 RA Venkatesan M.M., Buysse J.M., Oaks E.V.;
 RT "Surface presentation of Shigella flexneri invasion plasmid antigens requires the products of the spa locus.";
 RL J. Bacteriol. 174:1990-2001(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES-S.flexneri; STRAIN=2A; PLASMID=230 kb pMYSH6000;
 RX MEDLINE-93224456; PubMed-8385666;
 RA Sasakawa C., Komatsu K., Tobe T., Suzuki T., Yoshikawa M.;
 RT "Eight genes in region 5 that form an operon are essential for invasion of epithelial cells by Shigella flexneri 2a.";
 RL J. Bacteriol. 175:2334-2346(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES-S.sonnei; STRAIN=HW383;
 RX Arakawa E., Kato J.I., Ito K.I., Watanabe H.;
 RT Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP DISULFIDE BOND, AND MUTAGENESIS.
 RC SPECIES-S.flexneri;
 RX MEDLINE-95281569; PubMed-7761426;
 RA Watarai M., Tobe T., Yoshikawa M., Sasakawa C.;
 RT "Disulfide oxidoreductase activity of Shigella flexneri is required for release of Ipa proteins and invasion of epithelial cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:4927-4931(1995).
 CC -!- FUNCTION: REQUIRED FOR SURFACE PRESENTATION OF INVASION PLASMID

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CC ANTIGENS. COULD PLAY A ROLE IN PRESERVING THE TRANSLOCATION
CC COMPETENCE OF IPAB AND IPAD PROTEINS.
CC SECRETION OF IPAB AND IPAD PROTEINS.
CC -1- SUBCELLULAR LOCATION: Outer membrane (Potential).
CC -1- SIMILARITY: BELONGS TO THE SPAN FAMILY.
CC -----
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CC -----
CC EMBL; M81458; AAA26542.1; -
CC EMBL; D13663; BAA02827.1; -
CC EMBL; D50601; BAA09160.1; -
CC PIR; D42284; D42284.
CC PIR; S27681; S27681.
CC PIR; E49846; E49846.
CC Plasmid; Virulence; Outer membrane.
CC KW DISULFID 19 BY SIMILARITY
CC FT SEQUENCE 292 AA; 32977 MW; 78A112B3D24AB63C CRC64;
CC SEQUENCE 292 AA; 32977 MW; 78A112B3D24AB63C CRC64;
CC -----
Query Match 45.6%; Score 41; DB 1; Length 292;
Best Local Similarity 47.4%; Pred. No. 19;
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 KKEVMPISIOSLDALVKEK 19
DB 18 KCEKLSIDNIDSLVLK 36
-----
RESULT 9
RL3_METVA STANDARD; PRT; 334 AA.
AC Q9UWG2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 50S ribosomal protein L3P.
GN RPL3P.
OS Methanococcus vannielii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2187;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92283262; PubMed=1597181;
RA Graack H.-R., Grohmann L., Kitakawa M., Schaefer K.L., Kruft V.;
RT "Yml9, a nucleus-encoded mitochondrial ribosomal protein of yeast, is
RT homologous to L3 ribosomal proteins from all natural kingdoms and
RT photosynthetic organelles."
RL Eur. J. Biochem. 206:373-380(1992).
CC -1- SIMILARITY: BELONGS TO THE L3P FAMILY OF RIBOSOMAL PROTEINS.
CC InterPro; IPR000597; Ribosomal_L3.
CC Pfam; PF00297; Ribosomal_L3; 1.
CC ProDom; PD001374; Ribosomal_L3; 1.
CC PROSITE; PS00474; RIBOSOMAL_L3; 1.
CC Ribosomal protein.
KW Ribosomal protein.
SQ SEQUENCE 334 AA; 36728 MW; 963996FD1FDCB48F CRC64;
-----
Query Match 45.6%; Score 41; DB 1; Length 334;
Best Local Similarity 41.2%; Pred. No. 21;
Matches 7; Conservative 8; Mismatches 2; Indels 0; Gaps 0;
QY 1 KKEVMPISIOSLDALVKE 17
DB 118 KKEIKTVESLDALVLEK 134
-----
RESULT 11
SYMM_NEUCR STANDARD; PRT; 669 AA.
ID SYMM_NEUCR
AC F12663;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Created)
-----
RESULT 10
PDA6_ARATH STANDARD; PRT; 361 AA.
ID PDA6_ARATH
AC O22263;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable protein disulfide isomerase A6 precursor (EC 5.3.4.1) (P5).
GN AT2G47470 OR T30B22.23.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLOMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Renning C.M., Koo H.L.,
RA Morfat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Coppenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana".
RL Nature 402:761-768(1999).
CC -1- CATALYTIC ACTIVITY: Rearrangement of both intrachain and
CC interchain disulfide bonds in proteins to form the native
CC structures.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
CC -1- SIMILARITY: CONTAINS 2 THIOREDOXIN DOMAINS.
CC -----
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CC -----
CC EMBL; AC002535; AAC62863.1; -
CC HSP; P07237; IMEK.
CC SWISS-2DPAGE; O22263; ARATH.
CC Mendel; 26293; Arath;2433;26293.
CC InterPro; IPR000063; Thioredoxin.
CC Pfam; PF00085; thiore; 2.
CC PRINTS; PR00421; THIOREDOXIN.
CC PROSITE; PS00194; THIOREDOXIN; 2.
CC Redox-active center; Isomerase; Endoplasmic reticulum; Repeat; Signal.
KW SIGNAL
FT CHAIN 1 22 POTENTIAL
FT CHAIN 23 361 PROBABLE PROTEIN DISULFIDE ISOMERASE A6.
FT DISULFID 52 55 REDOX-ACTIVE (BY SIMILARITY).
FT DISULFID 171 174 REDOX-ACTIVE (BY SIMILARITY).
FT SEQUENCE 361 AA; 39497 MW; 9F4C7A07B0209DB5 CRC64;
-----
Query Match 45.6%; Score 41; DB 1; Length 361;
Best Local Similarity 80.0%; Pred. No. 23;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 8 IOSLDALVKE 17
DB 266 VESLDALVKE 275
-----
RESULT 11
SYMM_NEUCR STANDARD; PRT; 669 AA.
ID SYMM_NEUCR
AC F12663;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Created)

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DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Tyrosyl-tRNA synthetase, mitochondrial precursor (EC 6.1.1.1)
 DE (Tyrosine--tRNA ligase) (TVRRS).
 GN CVT-18.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Sordariaceae; Neurospora.
 OC NCB1_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87273496; PubMed=3607872;
 RA Akins R.A., Lambowitz A.M.;
 RT "A protein required for splicing group I introns in Neurospora
 RT mitochondria is mitochondrial tyrosyl-tRNA synthetase or a derivative
 RT thereof.";
 RL Cell 50:331-345(1987).
 RN [2]
 RP REVISIONS.
 RA Lambowitz A.M.;
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP FUNCTIONS.
 RX MEDLINE=90352708; PubMed=2143700;
 RA Cherniack A.D., Garriga G., Kittle J.D. Jr., Akins R.A.,
 RA Lambowitz A.M.;
 RT "Function of Neurospora mitochondrial tyrosyl-tRNA synthetase in RNA
 RT splicing requires an idiosyncratic domain not found in other
 RT synthetases.";
 RL Cell 62:745-755(1990).
 CC -1- FUNCTION: HAS BOTH A AMINOACYL-TRNA SYNTHETASE ACTIVITY AND IS
 CC INVOLVED IN THE SPLICING OF GROUP I INTRONS. IT ACTS IN INTRON
 CC SPLICING BY STABILIZING THE CATALYTICALLY ACTIVE STRUCTURE OF THE
 CC INTRON.
 CC -1- CATALYTIC ACTIVITY: ATP + L-tyrosine + tRNA(Tyr) = AMP +
 CC diphosphate + L-tyrosyl-tRNA(Tyr).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; M17118; AAA33620.1;
 DR PIR; A27158; SYNCYT.
 DR HSSP; P00952; 2TSL.
 DR InterPro; IPR002305; trna-synt_lb.
 DR InterPro; IPR001412; trna-synt_I.
 DR InterPro; IPR002307; trna-synt_tyr.
 DR Pfam; PF00579; trna-synt_lb; 1.
 DR PRINTS; PR01040; TRNASYNTHYR.
 DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
 DR Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 DR Mitochondrion; transist peptide; mRNA processing.
 FT TRANSIT 1 32 MITOCHONDRION.
 FT CHAIN 33 669 TYROSYL-TRNA SYNTHETASE.
 FT SITE 104 113 "HIGH" REGION.
 FT SITE 324 328 "KMSKS" REGION.
 FT BINDING 327 327 ATP (BY SIMILARITY).
 FT DOMAIN 33 75 INVOLVED IN SPLICING (PROBABLE).
 FT MUTAGEN 127 127 G->E: SPLICING AND AMINOACYLATION
 FT DEFECTS (MUTANTS C-18-1 AND C-18-2).
 SQ SEQUENCE 669 AA; 75422 MW; DD136CAC9AD1BEB5 CRC64;
 Query Match 45.6%; Score 41; DB 1; Length 669;
 Best Local Similarity 33.3%; Pred. No. 44;
 Matches 6; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

OY 1 KKEVMPSTQSLDALVKEK 18
 |:::|:::|:::|:::|:::|
 DB 631 KQEMIASVTKTIDGMDEK 648

RESULT 12

PRIA_CHLTR PRIA_CHLTR STANDARD; PRT; 753 AA.
 AC 084783;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Primosomal protein N' (Replication factor Y).
 GN PRIA OR Cn778.
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OC NCB1_TaxID=813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D/OW-3/CX;
 RX MEDLINE=99000809; PubMed=97841136;
 RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
 RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
 RA Davis R.W.;
 RT "Genome sequence of an obligate intracellular pathogen of humans:
 RT Chlamydia trachomatis.";
 RL Science 282:754-759(1998).
 CC -1- FUNCTION: RECOGNIZES A SPECIFIC HAIRPIN SEQUENCE ON PHIX SSDNA.
 CC THIS STRUCTURE IS THEN RECOGNIZED AND BOUND BY PROTEINS PRIA AND
 CC PRIC. FORMATION OF THE PRIMOSOME PROCEEDS WITH THE SUBSEQUENT
 CC ACTIONS OF DNAB, DNAC, DNAT AND PRIMASE. PRIA THEN FUNCTIONS AS A
 CC HELICASE WITHIN THE PRIMOSOME (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HELICASE FAMILY. PRIA SUBFAMILY.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch)
 CC -----
 DR EMBL; AE001350; AAC68373.1;
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR001650; Helicase_C.
 DR Pfam; PF00271; helicase_C; 1.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELICC; 1.
 DR DNA replication; DNA-binding; ATP-binding; Helicase; Primosome;
 DR Zinc-finger; Complete proteome.
 FT NP_BIND 241 248 ATP (POTENTIAL).
 FT SITE 337 340 DEEH BOX.
 FT ZN_FING 458 470 C4-TYPE (POTENTIAL).
 FT ZN_FING 485 501 C4-TYPE (POTENTIAL).
 SQ SEQUENCE 753 AA; 84831 MW; C91861B4385C5E35 CRC64;

Query Match 45.6%; Score 41; DB 1; Length 753;
 Best Local Similarity 61.1%; Pred. No. 50;
 Matches 11; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

OY 1 KKEVMPSTQSLDALVKEK 18
 |:::|:::|:::|:::|:::|
 DB 172 KTEV--SAKTLDALVKOK 187

RESULT 13

GYRA_CAMEE
 ID GYRA_CAMEE STANDARD; PRT; 862 AA.
 AC P47235;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE DNA gyrase subunit A (EC 5.99.1.3).

GN GYRA.

OS Campylobacter fetus.

OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;

OC Campylobacter.

OX NCBI_TaxID=196;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 27374 / UA50;

RX MEDLINE=97209069; PubMed=9056011;

RA Taylor D.E., Chau A.S.;

RT "Cloning and nucleotide sequence of the gyrA gene from Campylobacter fetus subsp. fetus ATCC 27374 and characterization of ciprofloxacin-resistant laboratory and clinical isolates."

RT Antimicrob. Agents Chemother. 41:665-671(1997).

RL Antimicrob. Agents Chemother. 41:665-671(1997).

CC -!- FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED DNA RINGS, INCLUDING CATENANES AND KNOTTED RINGS.

CC -!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.

CC -!- SUBUNIT: MADE UP OF TWO CHAINS, THE A CHAIN IS RESPONSIBLE FOR DNA BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE ENZYME FORMS AN A2B2 TETRAMER.

CC -----

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CC -----

CC EMBL: U25640; AAA67068.1; -

DR HSPF; P03097; IAB4.

DR InterPro: IPR002205; DNA_topoisomIV.

DR Pfam: PF00521; DNA_topoisomIV; 1.

DR SMART: SM00434; TOP4c; 1.

DR Topoisomerase; Isomerase; ATP-binding; Antibiotic resistance.

KW ACT_SITE 126 126 DNA_CLEAVAGE (BY SIMILARITY).

FT ACT_SITE 126 126

SQ SEQUENCE 862 AA; 95820 MW; E450D81809A10C35 CRC64;

Query Match 45.68; Score 41; DB 1; Length 862;

Best Local Similarity 41.28; Pred. No. 58;

Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

OY 2 KEVMPSTIOSLDALVKEK 18

DB 447 KEILELKEKLDLAKSE 463

|||||:|:|:|:|:

RESULT 14

GLYA_ARCFU STANDARD; PRT; 451 AA.

ID GLYA_ARCFU STANDARD; PRT; 1225 AA.

AC P32908;

DT 01-OCT-1993 (Rel. 27, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Serine hydroxymethyltransferase (EC 2.1.2.1) (Serine methylase) (SHMT).

GN GLYA OR AF0852.

OS Archaeoglobus fulgidus.

OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;

OC Archaeoglobus.

OX NCBI_TaxID=2234;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;

RX MEDLINE=98049343; PubMed=9389475;

RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kierlavage A.R., Graham D.E., Kyrpides N.C.,

RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., Mckenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glöck A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.P., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

RA "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus."

RL Nature 390:364-370(1997).

CC -!- FUNCTION: INTERCONVERSION OF SERINE AND GLYCINE + H(2)O = tetrahydrofolate + L-serine.

CC -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).

CC -!- PATHWAY: KEY ENZYME IN THE BIOSYNTHESIS OF PURINES, LIPIDS, HORMONES AND OTHER COMPONENTS.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).

CC -!- SIMILARITY: BELONGS TO THE SHMT FAMILY.

CC -----

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CC -----

CC EMBL: A5001045; AAB90386.1; -

DR HSPF; P07511; 1CJ0.

DR TIGR; AF0852; -

DR InterPro: IPR001085; SHMT.

DR Pfam: PF00464; SHMT; 1.

DR PROSITE: PS00096; SHMT; FALSE_NEG.

KW Transferase; Pyridoxal phosphate; One-carbon metabolism;

KW COMPLETE PROTEOME. 252 PYRIDOXAL PHOSPHATE (BY SIMILARITY).

FT BINDING 252 252

SQ SEQUENCE 451 AA; 50411 MW; 5329CA21149FEF58 CRC64;

Query Match 45.0%; Score 40.5; DB 1; Length 451;

Best Local Similarity 50.0%; Pred. No. 36;

Matches 10; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

OY 1 KKEVPSTIOSLDALVKEK 19

DB 397 KEEMRAIAEIMDAAIKEK 416

|||||:|:|:|:|:

RESULT 15

SMCL_YEAST STANDARD; PRT; 1225 AA.

ID SMCL_YEAST STANDARD; PRT; 1225 AA.

AC P32908;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Chromosome segregation protein SMCL (DA-box protein SMCL).

GN SMCL OR CHL10 OR YFL008W.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94103320; PubMed=8276886;

RA Strunnikov A.V., Iarionov V.L., Koshland D.;

RT "SMCL: an essential yeast gene encoding a putative head-rod-tail protein is required for nuclear division and defines a new ubiquitous protein family."

RT J. Cell Biol. 123:1635-1648(1993).

RL [2]

RN SEQUENCE FROM N.A.

RP SEQUENCE=5288C / AB972;

RC STRAIN=5288C / AB972;

Search completed: September 4, 2002, 17:05:07
Job time: 1133 sec

RESULT 2
US-09-720-533-49
; Sequence 49, Application US/09720533
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: LAL, Preeti
; APPLICANT: TANG, Y. Tom
; APPLICANT: GORGONE, Gina A.
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AKERBLOM, Ingrid E.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: YUE, Henry
; APPLICANT: PATTERSON, Chandra
; APPLICANT: REDDY, Roopa
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: BANDMAN, Olga
; TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
; FILE REFERENCE: PP-0541 PCT
; CURRENT APPLICATION NUMBER: US/09/720,533
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/090,762; 60/094,983; 60/102,686; 60/112,129
; PRIOR FILING DATE: 1998-06-26; 1998-07-31; 1998-10-01; 1998-12-11
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PERL Program
; SEQ ID NO 49
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte Clone No: 2593853
US-09-720-533-49

Query Match 94.4%; Score 85; DB 5; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 KEVMPISQSLDALVKEKK 19
Db 88 KEVMPISQSLDALVKEKK 105

RESULT 3
US-10-119-480-148
; Sequence 148, Application US/10119480
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C1
; CURRENT APPLICATION NUMBER: US/10/119,480
; CURRENT FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 246
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-119-480-148

Query Match 94.4%; Score 85; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 KEVMPISQSLDALVKEKK 19
Db 88 KEVMPISQSLDALVKEKK 105

RESULT 4
US-10-216-159A-148
; Sequence 148, Application US/10216159A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C6
; CURRENT APPLICATION NUMBER: US/10/216,159A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-159A-148

Query Match 94.4%; Score 85; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 KEVMPISQSLDALVKEKK 19
Db 88 KEVMPISQSLDALVKEKK 105

RESULT 5
US-10-216-162-148
; Sequence 148, Application US/10216162
; GENERAL INFORMATION:

us-09-821-726-5.rapn

Thu Sep 5 11:23:42 2002

```

; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC2
; CURRENT APPLICATION NUMBER: US/10/216,162
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-162-148

Query Match          94.4%; Score 85; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 KEVMPSTQSLDALVKEKK 19
    |||||
Db  88 KEVMPSTQSLDALVKEKK 105

RESULT 7
US-10-216-164-148
; Sequence 148, Application US/10216164
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC5
; CURRENT APPLICATION NUMBER: US/10/216,164
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20

Query Match          94.4%; Score 85; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 KEVMPSTQSLDALVKEKK 19
    |||||
Db  88 KEVMPSTQSLDALVKEKK 105

RESULT 6
US-10-216-163-148
; Sequence 148, Application US/10216163
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC3
; CURRENT APPLICATION NUMBER: US/10/216,163

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; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079656
 ; PRIOR FILING DATE: 1998-03-26
 ; PRIOR APPLICATION NUMBER: 60/079728
 ; PRIOR FILING DATE: 1998-03-27
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 148
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-216-164-148

Query Match 94.4%; Score 85; DB 6; Length 185;
 Best Local Similarity 100.0%; Pred. No. 3.6e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 KEVMPISQSLDALVKEKK 19
 Db 88 KEVMPISQSLDALVKEKK 105

RESULT 8
 US-10-216-165-148
 ; Sequence 148, Application US/10216165
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530P1C7
 ; CURRENT APPLICATION NUMBER: US/10/216,165
 ; PRIOR FILING DATE: 2002-08-09
 ; PRIOR APPLICATION NUMBER: 10/119,480
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/062287
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063549
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/064103
 ; PRIOR FILING DATE: 1997-10-31
 ; PRIOR APPLICATION NUMBER: 60/069873
 ; PRIOR FILING DATE: 1997-12-17
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079656
 ; PRIOR FILING DATE: 1998-03-26
 ; PRIOR APPLICATION NUMBER: 60/079728
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 148
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-216-165-148

Query Match 94.4%; Score 85; DB 6; Length 185;
 Best Local Similarity 100.0%; Pred. No. 3.6e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 KEVMPISQSLDALVKEKK 19
 Db 88 KEVMPISQSLDALVKEKK 105

RESULT 9
 US-10-216-166-148
 ; Sequence 148, Application US/10216166
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530P1C9
 ; CURRENT APPLICATION NUMBER: US/10/216,166
 ; PRIOR FILING DATE: 2002-08-09
 ; PRIOR APPLICATION NUMBER: 10/119,480
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/062287
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063549
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/064103
 ; PRIOR FILING DATE: 1997-10-31
 ; PRIOR APPLICATION NUMBER: 60/069873
 ; PRIOR FILING DATE: 1997-12-17
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079656
 ; PRIOR FILING DATE: 1998-03-26
 ; PRIOR APPLICATION NUMBER: 60/079728
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 148
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-216-166-148

Query Match 94.4%; Score 85; DB 6; Length 185;
 Best Local Similarity 100.0%; Pred. No. 3.6e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 KEVMPISQSLDALVKEKK 19
 Db 88 KEVMPISQSLDALVKEKK 105

RESULT 10
 US-10-216-167-148
 ; Sequence 148, Application US/10216167
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc

us-09-821-726-5.rapn

Thu Sep 5 11:23:42 2002

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; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C4
; CURRENT APPLICATION NUMBER: US/10/216,167
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-167-148

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEVMPSTQSLDALVKEKK 19
Db 88 KEVMPSTQSLDALVKEKK 105

RESULT 11
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; Sequence 148, Application US/10216168
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C10
; CURRENT APPLICATION NUMBER: US/10/216,168
; CURRENT FILING DATE: 2002-08-09
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; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-167-148

Query Match          94.4%; Score 85; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEVMPSTQSLDALVKEKK 19
Db 88 KEVMPSTQSLDALVKEKK 105

RESULT 12
US-10-216-160-148
; Sequence 148, Application US/10216160
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C8
; CURRENT APPLICATION NUMBER: US/10/216,160
; CURRENT FILING DATE: 2002-08-09
; Prior Application removed - See File Wrapper or PALM
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-160-148

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Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEVMPSTQSLDALVKEKK 19
Db 88 KEVMPSTQSLDALVKEKK 105

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RESULT 13
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 ; Sequence 148, Application US/10218849
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530PIC11
 ; CURRENT APPLICATION NUMBER: US/10/218,849
 ; CURRENT FILING DATE: 2002-08-12
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 148
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-218-849-148

Query Match 94.4%; Score 85; DB 6; Length 185;
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QY 2 KEVMPSTQSLDALVKEKK 19
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 Db 88 KEVMPSTQSLDALVKEKK 105

RESULT 14
 US-10-218-930-148
 ; Sequence 148, Application US/10218930
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530PIC13
 ; CURRENT APPLICATION NUMBER: US/10/218,930
 ; CURRENT FILING DATE: 2002-08-12
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 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 88 KEVMPSTQSLDALVKEKK 105

RESULT 15
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 ; Sequence 148, Application US/10219003
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530PIC12
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 ; CURRENT FILING DATE: 2002-08-12
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 ; Prior Filing Date: 1997-10-17
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 ; Prior Filing Date: 1997-10-28
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 ; Prior Filing Date: 1997-10-31
 ; Prior Application Number: 60/069873
 ; Prior Filing Date: 1997-12-17
 ; Prior Application Number: 60/078910
 ; Prior Filing Date: 1998-03-20
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 ; Prior Filing Date: 1998-06-25
 ; Prior Application Number: 60/090695
 ; Prior Filing Date: 1998-06-25

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94.4%; Score 85; DB 6; Length 185;
Query Match
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 18; Conservative 0; Mismatches 0; Indels

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88 KEVMPSIQSLDALVKEK 105

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Thu Sep 5 11:23:42 2002

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Title: US-09-821-726-5

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	90	100.0	185	22	US-09-821-726-13
4	85	94.4	150	13	US-08-906-708-24
5	85	94.4	182	20	US-09-684-524-212
6	85	94.4	182	24	US-10-050-704-212
7	85	94.4	185	1	PCT-US98-16318-18
					Sequence 5, Appli
					Sequence 6, Appli
					Sequence 13, Appl
					Sequence 24, Appl
					Sequence 212, App
					Sequence 18, Appl

8	85	94.4	185	15	US-09-130-189-18	Sequence 18, Appl
9	85	94.4	185	20	US-09-684-524-105	Sequence 105, App
10	85	94.4	185	21	US-09-709-238-211	Sequence 211, App
11	85	94.4	185	21	US-09-746-783-146	Sequence 146, App
12	85	94.4	185	23	US-09-941-992-211	Sequence 211, App
13	85	94.4	185	23	US-09-989-279-211	Sequence 211, App
14	85	94.4	185	23	US-09-989-293A-211	Sequence 211, App
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ALIGNMENTS

RESULT 1
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; Sequence 5, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
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; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-821-726-5

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; Sequence 212, Application US/10050704
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: PZ039P1
; CURRENT APPLICATION NUMBER: US/10/050,704
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 09/684,524
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 212
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-704-212

Query Match 94.4%; Score 85; DB 24; Length 182;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 KEVMPISQSLDALVKEKK 19
Db 88 KEVMPISQSLDALVKEKK 105

RESULT 7
PCT-US98-16318-18
; Sequence 18, Application PC/TUS9816318
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: G16051A
; CURRENT APPLICATION NUMBER: PCT/US98/16318
; CURRENT FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US98-16318-18

Query Match 94.4%; Score 85; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 KEVMPISQSLDALVKEKK 19
Db 88 KEVMPISQSLDALVKEKK 105

RESULT 8
US-09-130-189-18
; Sequence 18, Application US/09130189
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: G16051A
; CURRENT APPLICATION NUMBER: US/09/130,189
; CURRENT FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-130-189-18

Query Match 94.4%; Score 85; DB 15; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 KEVMPISQSLDALVKEKK 19
Db 88 KEVMPISQSLDALVKEKK 105

RESULT 9
US-09-684-524-105
; Sequence 105, Application US/09684524
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: PZ039P1
; CURRENT APPLICATION NUMBER: US/09/684,524
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-684-524-105

Query Match 94.4%; Score 85; DB 20; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 KEVMPISQSLDALVKEKK 19
Db 88 KEVMPISQSLDALVKEKK 105

RESULT 10
US-09-709-238-211
; Sequence 211, Application US/09709238
; GENERAL INFORMATION:

APPLICANT: Baker, Kevin
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Gunney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Yuan, Jean
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding the Same
FILE REFERENCE: P2730R1C1
CURRENT APPLICATION NUMBER: US/09/709,238
CURRENT FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: US 60/087,607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: US 60/087,609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: US 60/087,759
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: US 60/087,827
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,326
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: US 60/088,167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: US 60/088,202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: US 60/088,212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: US 60/088,217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: US 60/088,655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: US 60/088,722
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: US 60/088,730
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: US 60/088,734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: US 60/088,738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: US 60/088,740
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: US 60/088,741
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: US 60/088,742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: US 60/088,810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: US 60/088,811
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: US 60/088,824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: US 60/088,825
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: US 60/088,826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: US 60/088,858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: US 60/088,861
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PRIOR FILING DATE: 1998-06-11
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PRIOR APPLICATION NUMBER: US 60/089,105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: US 60/089,440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: US 60/089,512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: US 60/089,514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: US 60/089,532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US 60/089,538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US 60/089,598
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PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: US 60/089,908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: US 60/089,947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: US 60/089,948
PRIOR FILING DATE: 1998-06-19
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PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: US 60/090,246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: US 60/090,252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: US 60/090,254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: US 60/090,355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: US 60/090,429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: US 60/090,444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,461
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,538
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,676
PRIOR FILING DATE: 1998-06-25

Howes, Steven H.
Fechtel, Kim
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
ENCODING THEM
NUMBER OF SEQUENCES: 231
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/746,783
FILING DATE: 21-Dec-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Milasincic, Debra J.
REGISTRATION NUMBER: 46,931
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 146:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 146:
US-09-746-783-146

Query Match 94.4%; Score 85; DB 21; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEVMPISQSLDALVKEKK 19
Db 88 KEVMPISQSLDALVKEKK 105

RESULT 12
US-09-941-992-211
Sequence 211, Application US/09941992
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey

PRIOR APPLICATION NUMBER: US 60/090,678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 60/090,688
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 60/090,690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 60/090,691
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 60/090,694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 60/090,695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 60/090,696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 60/090,862
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 60/090,863
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 60/091,358
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: US 60/091,360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: US 60/091,478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/091,486
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/091,519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/091,544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: US 60/091,626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/091,628
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/091,633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/091,646
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/091,673
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/091,978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: US 60/091,982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: US 60/092,182
PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: US 60/092,472
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: US 60/093,339
PRIOR FILING DATE: 1998-07-20
PRIOR APPLICATION NUMBER: US 60/094,651
PRIOR FILING DATE: 1998-07-30

Query Match 94.4%; Score 85; DB 21; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEVMPISQSLDALVKEKK 19
Db 88 KEVMPISQSLDALVKEKK 105

RESULT 11
US-09-746-783-146
Sequence 146, Application US/09746783
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Racie, Lisa A.
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Agostino, Michael J.

APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C1
CURRENT APPLICATION NUMBER: US/09/941,992
CURRENT FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
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PRIOR FILING DATE: 1998-06-02
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PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
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PRIOR FILING DATE: 1998-06-12
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PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
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PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
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PRIOR FILING DATE: 1998-06-19
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690

;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090694
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090862
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
;; PRIOR APPLICATION NUMBER: 60/092472

Query Match 94.4%; Score 85; DB 23; Length 185;

Best Local Similarity 100.0%; Pred. No. 1.7e-05;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEVMSIQSLDALVREKK 19

|||||

Db 88 KEVMSIQSLDALVREKK 105

RESULT 13

US-09-989-279-211

; Sequence 211, Application US/0989279

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730PIC56

; CURRENT APPLICATION NUMBER: US/09/989,279

; CURRENT FILING DATE: 2001-11-19

;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/065186
;; PRIOR FILING DATE: 1997-11-12
;; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR FILING DATE: 1998-07-07
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472

Query Match 94.4%; Score 85; DB 23; Length 185;
Best Local Similarity: 100.0%; Pred. No. 1.7e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEVMPISQSLDALVKKK 19
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Db 88 KEVMPISQSLDALVKKK 105

RESULT 14

US-09-989-293A-211
; Sequence 211, Application US/09989293A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC66
; CURRENT APPLICATION NUMBER: US/09/989,293A
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311

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5	PRIOR FILING DATE: 1998-02-25	6	PRIOR APPLICATION NUMBER: 60/089598
6	PRIOR APPLICATION NUMBER: 60/078910	7	PRIOR FILING DATE: 1998-06-17
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11	PRIOR FILING DATE: 1998-05-07	12	PRIOR APPLICATION NUMBER: 60/089653
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15	PRIOR FILING DATE: 1998-06-02	16	PRIOR APPLICATION NUMBER: 60/089907
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17	PRIOR FILING DATE: 1998-06-02	18	PRIOR APPLICATION NUMBER: 60/089908
18	PRIOR APPLICATION NUMBER: 60/087759	19	PRIOR FILING DATE: 1998-06-18
19	PRIOR FILING DATE: 1998-06-02	20	PRIOR APPLICATION NUMBER: 60/089944
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23	PRIOR FILING DATE: 1998-06-04	24	PRIOR APPLICATION NUMBER: 60/089952
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14	PRIOR APPLICATION NUMBER:	60/092182
15	PRIOR FILING DATE:	1998-07-09
16	PRIOR APPLICATION NUMBER:	60/092472

Query Match 94.4%; Score 85; DB 23; Length 185;

QY 2 KEVPSIQSLDALVKEK 19
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 Db 88 KEVPSIOSLDALVKEK 105

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; GENERAL INFORMATION:	
; APPLICANT: Ashkenazi, Avi J.	
; APPLICANT: Baker, Kevin P.	
; APPLICANT: Botstein, David	
; APPLICANT: Desnovers, Luc	
; APPLICANT: Eaton, Dan L.	
; APPLICANT: Ferrara, Napoleone	
; APPLICANT: Fong, Sherman	
; APPLICANT: Gerber, Hanspeter	
; APPLICANT: Gerritsen, Mary E.	
; APPLICANT: Goddard, Audrey	
; APPLICANT: Godowski, Paul J.	
; APPLICANT: Grimaldi, J. Christopher	
; APPLICANT: Gurney, Austin L.	
; APPLICANT: Kljavin, Ivar J.	
; APPLICANT: Napier, Mary A.	
; APPLICANT: Pan, James	
; APPLICANT: Paoni, Nicholas F.	
; APPLICANT: Roy, Margaret Ann	
; APPLICANT: Stewart, Timothy A.	
; APPLICANT: Tumas, Daniel	
; APPLICANT: Watanabe, Colin K.	
; APPLICANT: Williams, P. Mickey	
; APPLICANT: Wood, William I.	
; APPLICANT: Zhang, Zemin	
TITLE OF INVENTION: Secreted and Transferred	
FILE REFERENCE: P2730P1C55	
CURRENT APPLICATION NUMBER: US/09/989721-211	
CURRENT FILING DATE: 2001-11-19	
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PRIOR APPLICATION NUMBER: 60/065186	
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PRIOR FILING DATE: 1998-03-20	

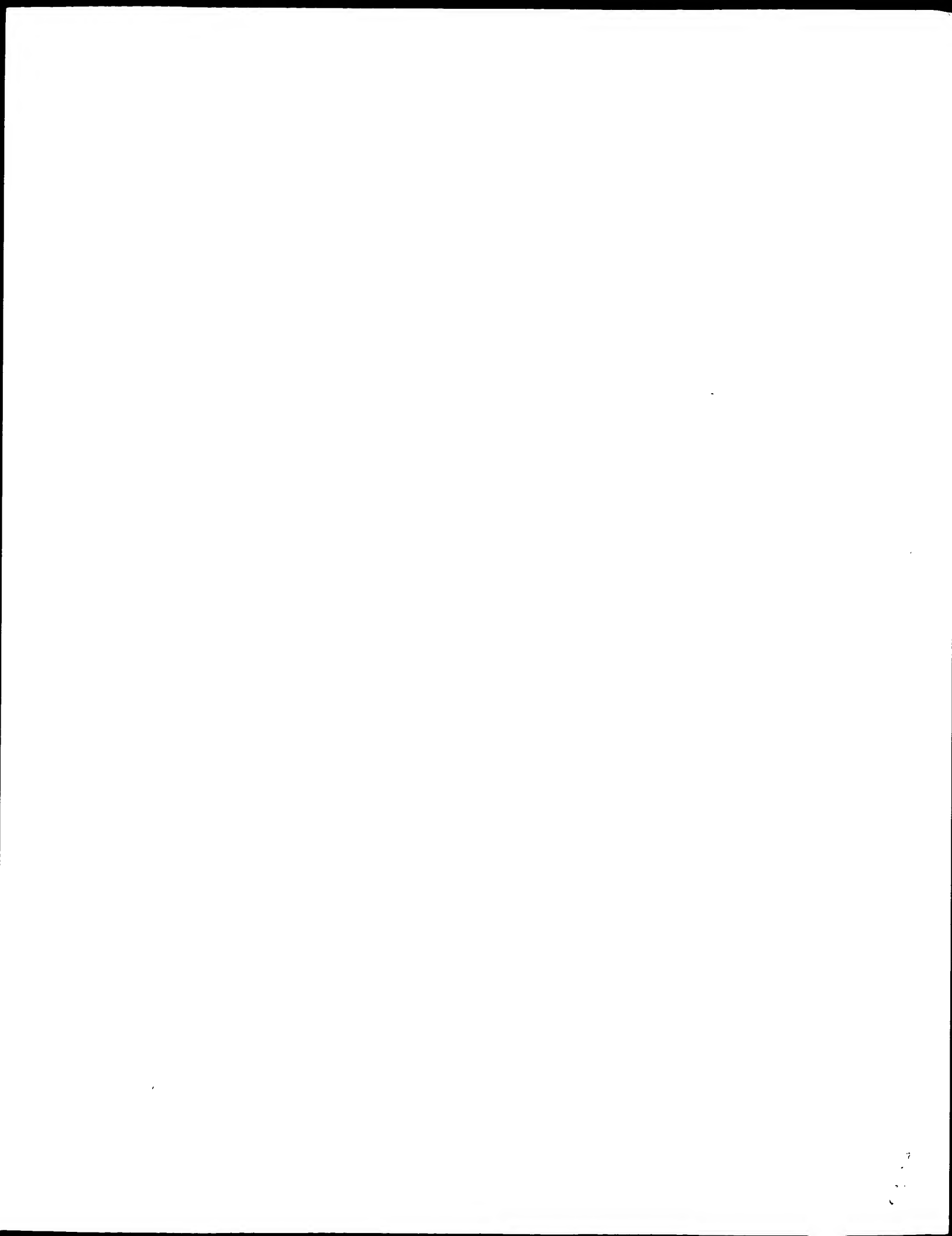
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472

Query Match 94.4%; Score 85; DB 23; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 KEVMPISQSLDALVKEKK 19
Db 88 KEVMPISQSLDALVKEKK 105
|||||

Search completed: September 4, 2002, 16:59:20
Job time: 1041 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model
Run on: September 4, 2002, 17:04:23 ; Search time 166.13 Seconds
(without alignments)
273.874 Million cell updates/sec

Title: US-09-821-726-13
Perfect score: 994
Sequence: 1 MKFTIVFAGLLGVFLAPALA.....YTTSVLWIVDISFCGDTVEN 185

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 763338 seqs, 245939087 residues

Total number of hits satisfying chosen parameters: 763338

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pcp.*
 - 2: /cgn2_6/ptodata/2/paa/US05_NEW_COMB.pcp.*
 - 3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pcp.*
 - 4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pcp.*
 - 5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pcp.*
 - 6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pcp.*
 - 7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	984	99.0	185	5	US-09-991-150-211
2	984	99.0	185	5	US-09-720-533-49
3	984	99.0	185	6	US-10-119-480-148
4	984	99.0	185	6	US-10-216-159A-148
5	984	99.0	185	6	US-10-216-162-148
6	984	99.0	185	6	US-10-216-163-148
7	984	99.0	185	6	US-10-216-164-148
8	984	99.0	185	6	US-10-216-165-148
9	984	99.0	185	6	US-10-216-166-148
10	984	99.0	185	6	US-10-216-167-148
11	984	99.0	185	6	US-10-216-168-148
12	984	99.0	185	6	US-10-216-160-148
13	984	99.0	185	6	US-10-218-849-148
14	984	99.0	185	6	US-10-218-930-148
15	984	99.0	185	6	US-10-219-003-148
16	984	99.0	185	6	US-10-218-612-148
17	984	99.0	185	6	US-10-218-956-148
18	984	99.0	185	6	US-10-219-010-148
19	984	99.0	185	6	US-10-218-765-148
20	984	99.0	185	6	US-10-218-784-148
21	984	99.0	185	6	US-10-219-061-148
22	984	99.0	185	6	US-10-219-062-148
23	984	99.0	185	6	US-10-219-063-148
24	984	99.0	185	6	US-10-219-064-148
25	984	99.0	185	6	US-10-219-065-148
26	984	99.0	185	6	US-10-219-066-148

ALIGNMENTS

RESULT 1

US-09-991-150-211
; Sequence 211, Application US/09991150

; GENERAL INFORMATION:

- ; APPLICANT: Ashkenazi, Avi J.
- ; APPLICANT: Baker, Kevin P.
- ; APPLICANT: Botstein, David
- ; APPLICANT: Desnoyers, Luc
- ; APPLICANT: Eaton, Dan L.
- ; APPLICANT: Ferrara, Napoleone
- ; APPLICANT: Fong, Sherman
- ; APPLICANT: Gerber, Hanspeter
- ; APPLICANT: Gieritsen, Mary E.
- ; APPLICANT: Goddard, Audrey
- ; APPLICANT: Godowski, Paul J.
- ; APPLICANT: Grimaldi, J. Christopher
- ; APPLICANT: Gurney, Austin L.
- ; APPLICANT: Kljavin, Ivar J.
- ; APPLICANT: Napier, Mary A.
- ; APPLICANT: Pan, James
- ; APPLICANT: Paoni, Nicholas F.
- ; APPLICANT: Roy, Margaret Ann
- ; APPLICANT: Stewart, Timothy A.
- ; APPLICANT: Tumas, Daniel
- ; APPLICANT: Watanabe, Colin K.
- ; APPLICANT: Williams, P. Mickey
- ; APPLICANT: Wood, William I.
- ; APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same
FILE REFERENCE: P2730PIC48
CURRENT APPLICATION NUMBER: US/09/991,150
CURRENT FILING DATE: 2001-11-16
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 532

SEQ ID NO 211

LENGTH: 185

TYPE: PRT

ORGANISM: Homo sapiens

US-09-991-150-211

Query Match 99.0%; Score 984; DB 5; Length 185;
Best Local Similarity 98.9%; Pred. No. 1.6e-95;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKFTIVFAGLLGVFLAPALANYINDNDNNAGSQSQSVSVNNEHNVANVDNNNGWDSW 60
Db 1 MKFTIVFAGLLGVFLAPALANYINDNDNNAGSQSQSVSVNNEHNVANVDNNNGWDSW 60

QY 61 NSIWDYNGNGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPPKGLM 120
Db 61 NSIWDYNGNGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPPKGLM 120
QY 121 YSVNPNKVDLDSKFGKNIANMCRGIPITYMAEEMQASLFFYSGTCTTTSVLWIVDISFCG 180
Db 121 YSVNPNKVDLDSKFGKNIANMCRGIPITYMAEEMQASLFFYSGTCTTTSVLWIVDISFCG 180
QY 181 DTVEN 185
Db 181 DTVEN 185

RESULT 2

US-09-720-533-49
; Sequence 49, Application US/09720533
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: LAL, Preeti
; APPLICANT: TANG, Y. Tom
; APPLICANT: GORGONE, Gina A.
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: BAUGHN, Mariah B.
; APPLICANT: AKERBLOM, Ingrid E.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: YUE, Henry
; APPLICANT: PATTERSON, Chandra
; APPLICANT: REDDY, Roopa
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: BANDMAN, Olga
; TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
; FILE REFERENCE: PF-0541 PCT
; CURRENT APPLICATION NUMBER: US/09/720,533
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/090,762; 60/094,983; 60/102,686; 60/112,129
; PRIOR FILING DATE: 1998-06-26; 1998-07-31; 1998-10-01; 1998-12-11
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PERL Program
; SEQ ID NO 49
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte Clone No: 2593853
US-09-720-533-49

Query Match 99.0%; Score 984; DB 5; Length 185;
Best Local Similarity 98.9%; Pred. No. 1.6e-95;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKFTIVFAGLLGVFLAPALANYINVDNNDNAGSQSQSVSVNNEHNVANVDNNGWDSW 60
Db 1 MKFTIVFAGLLGVFLAPALANYINVDNNDNAGSQSQSVSVNNEHNVANVDNNGWDSW 60
QY 61 NSIWDYNGNGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPPKGLM 120
Db 61 NSIWDYNGNGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPPKGLM 120
QY 121 YSVNPNKVDLDSKFGKNIANMCRGIPITYMAEEMQASLFFYSGTCTTTSVLWIVDISFCG 180
Db 121 YSVNPNKVDLDSKFGKNIANMCRGIPITYMAEEMQASLFFYSGTCTTTSVLWIVDISFCG 180
QY 181 DTVEN 185
Db 181 DTVEN 185

RESULT 3

US-10-119-480-148

; Sequence 148, Application US/10119480
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C1
; CURRENT APPLICATION NUMBER: US/10/119,480
; CURRENT FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 246
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-119-480-148

Query Match 99.0%; Score 984; DB 6; Length 185;
Best Local Similarity 98.9%; Pred. No. 1.6e-95;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKFTIVFAGLLGVFLAPALANYINVDNNDNAGSQSQSVSVNNEHNVANVDNNGWDSW 60
Db 1 MKFTIVFAGLLGVFLAPALANYINVDNNDNAGSQSQSVSVNNEHNVANVDNNGWDSW 60
QY 61 NSIWDYNGNGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPPKGLM 120
Db 61 NSIWDYNGNGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPPKGLM 120
QY 121 YSVNPNKVDLDSKFGKNIANMCRGIPITYMAEEMQASLFFYSGTCTTTSVLWIVDISFCG 180
Db 121 YSVNPNKVDLDSKFGKNIANMCRGIPITYMAEEMQASLFFYSGTCTTTSVLWIVDISFCG 180
QY 181 DTVEN 185
Db 181 DTVEN 185

RESULT 4

US-10-216-159A-148
; Sequence 148, Application US/10216159A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C6
; CURRENT APPLICATION NUMBER: US/10/216,159A
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17

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; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-216-159A-148

Query Match          99.0%; Score 984; DB 6; Length 185;
Best Local Similarity 98.9%; Pred No. 1.6e-95;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKFTIVFAGLLGVFLAPALANYNIDVDDNNAGSQQSVSVNNEHNVANVDNNNGWDSW 60
Db 1 MKFTIVFAGLLGVFLAPALANYNINVDNNAGSQQSVSVNNEHNVANVDNNNGWDSW 60
Qy 61 NSIWDYNGFAATRLFOKKTCTIVHKMKKEVMPISQSLDALVKEKKLOGKPGGPPKGLM 120
Db 61 NSIWDYNGFAATRLFOKKTCTIVHKMKKEVMPISQSLDALVKEKKLOGKPGGPPKGLM 120
Qy 121 YSVNPNKVDLLSKFGKNIANMCRGIPTYMAEEMOEASLFFYSCTCTTTSVLWIVDISFCG 180
Db 121 YSVNPNKVDLLSKFGKNIANMCRGIPTYMAEEMOEASLFFYSCTCTTTSVLWIVDISFCG 180
Qy 181 DTVEN 185
Db 181 DTVEN 185

RESULT 5
US-10-216-162-148
; Sequence 148, Application US/10216162
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Victoria
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C2
; CURRENT APPLICATION NUMBER: US/10/216,162
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17

Query Match          99.0%; Score 984; DB 6; Length 185;
Best Local Similarity 98.9%; Pred No. 1.6e-95;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKFTIVFAGLLGVFLAPALANYNIDVDDNNAGSQQSVSVNNEHNVANVDNNNGWDSW 60
Db 1 MKFTIVFAGLLGVFLAPALANYNINVDNNAGSQQSVSVNNEHNVANVDNNNGWDSW 60
Qy 61 NSIWDYNGFAATRLFOKKTCTIVHKMKKEVMPISQSLDALVKEKKLOGKPGGPPKGLM 120
Db 61 NSIWDYNGFAATRLFOKKTCTIVHKMKKEVMPISQSLDALVKEKKLOGKPGGPPKGLM 120
Qy 121 YSVNPNKVDLLSKFGKNIANMCRGIPTYMAEEMOEASLFFYSCTCTTTSVLWIVDISFCG 180
Db 121 YSVNPNKVDLLSKFGKNIANMCRGIPTYMAEEMOEASLFFYSCTCTTTSVLWIVDISFCG 180
Qy 181 DTVEN 185
Db 181 DTVEN 185

RESULT 6
US-10-216-163-148
; Sequence 148, Application US/10216163
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Victoria
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C3
; CURRENT APPLICATION NUMBER: US/10/216,163
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17

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; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-163-148

Query Match          99.0%; Score 984; DB 6; Length 185;
Best Local Similarity 98.9%; Pred. No. 1.6e-95;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYINVDNNDNAGSGGQSVSVNNEHNVANVDNNGWDSW 60
   |||||
Db 1 MKFTIVFAGLLGVFLAPALANYINVDNNDNAGSGGQSVSVNNEHNVANVDNNGWDSW 60
   |||||
QY 61 NSIWDYGNCGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKKEKLGKGGPPPKGLM 120
   |||||
Db 61 NSIWDYGNCGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKKEKLGKGGPPPKGLM 120
   |||||
QY 121 YSNPNKVVDDLSKFGKNIANMCRGPTTYMAEMQASLFFSYGTCYTTSVLWIVDISFCG 180
   |||||
Db 121 YSNPNKVVDDLSKFGKNIANMCRGPTTYMAEMQASLFFSYGTCYTTSVLWIVDISFCG 180
   |||||
QY 181 DTVEN 185
   |||||
Db 181 DTVEN 185

RESULT 7
US-10-216-164-148
; Sequence 148, Application US/10216164
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C5
; CURRENT APPLICATION NUMBER: US/10/216,164
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
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; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-164-148

Query Match          99.0%; Score 984; DB 6; Length 185;
Best Local Similarity 98.9%; Pred. No. 1.6e-95;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYINVDNNDNAGSGGQSVSVNNEHNVANVDNNGWDSW 60
   |||||
Db 1 MKFTIVFAGLLGVFLAPALANYINVDNNDNAGSGGQSVSVNNEHNVANVDNNGWDSW 60
   |||||
QY 61 NSIWDYGNCGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKKEKLGKGGPPPKGLM 120
   |||||
Db 61 NSIWDYGNCGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKKEKLGKGGPPPKGLM 120
   |||||
QY 121 YSNPNKVVDDLSKFGKNIANMCRGPTTYMAEMQASLFFSYGTCYTTSVLWIVDISFCG 180
   |||||
Db 121 YSNPNKVVDDLSKFGKNIANMCRGPTTYMAEMQASLFFSYGTCYTTSVLWIVDISFCG 180
   |||||
QY 181 DTVEN 185
   |||||
Db 181 DTVEN 185

RESULT 8
US-10-216-165-148
; Sequence 148, Application US/10216165
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C7
; CURRENT APPLICATION NUMBER: US/10/216,165
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
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; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-165-148

Query Match          99.0%; Score 984; DB 6; Length 185;
Best Local Similarity 98.9%; Pred. No. 1.6e-95;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYINVDNDNNAGSGQSVSVNNEHNVANVDNNNGWDSW 60
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MKFTIVFAGLLGVFLAPALANYINVDNDNNAGSGQSVSVNNEHNVANVDNNNGWDSW 60
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 NSIWDYNGGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPKGLM 120
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 NSIWDYNGGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPKGLM 120
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 YSNPNKVVDDLSKFGKNIANMCRGIPITYMAEEMQEAASLFFYSGTCYTTSVLWIVDISFCG 180
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 YSNPNKVVDDLSKFGKNIANMCRGIPITYMAEEMQEAASLFFYSGTCYTTSVLWIVDISFCG 180
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 181 DTVEN 185
   |||||
Db 181 DTVEN 185
   |||||

RESULT 9
US-10-216-166-148
; Sequence 148, Application US/10216166
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin I.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C9
; CURRENT APPLICATION NUMBER: US/10/216,166
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
```

```
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-166-148

Query Match          99.0%; Score 984; DB 6; Length 185;
Best Local Similarity 98.9%; Pred. No. 1.6e-95;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYINVDNDNNAGSGQSVSVNNEHNVANVDNNNGWDSW 60
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MKFTIVFAGLLGVFLAPALANYINVDNDNNAGSGQSVSVNNEHNVANVDNNNGWDSW 60
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 NSIWDYNGGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPKGLM 120
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 NSIWDYNGGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPKGLM 120
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 YSNPNKVVDDLSKFGKNIANMCRGIPITYMAEEMQEAASLFFYSGTCYTTSVLWIVDISFCG 180
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 YSNPNKVVDDLSKFGKNIANMCRGIPITYMAEEMQEAASLFFYSGTCYTTSVLWIVDISFCG 180
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 181 DTVEN 185
   |||||
Db 181 DTVEN 185
   |||||

RESULT 10
US-10-216-167-148
; Sequence 148, Application US/10216167
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin I.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C4
; CURRENT APPLICATION NUMBER: US/10/216,167
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-167-148

Query Match 99.0%; Score 984; DB 6; Length 185;
Best Local Similarity 98.9%; Pred. No. 1.6e-95;

Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYNDVNDNNAGSGQSVSVNNEHNVANVYDNNNGWDSW 60
|||||
Db 1 MKFTIVFAGLLGVFLAPALANYNDVNDNNAGSGQSVSVNNEHNVANVYDNNNGWDSW 60
QY 61 NSWDYNGNGFAATRLFKKTCIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120
|||||
Db 61 NSWDYNGNGFAATRLFKKTCIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120
QY 121 YSNPNKVDLDSKFGKNIANMCRGIPTVMAEMOEASLFFYSGTCYTTSVLWIVDISFCG 180
|||||
Db 121 YSNPNKVDLDSKFGKNIANMCRGIPTVMAEMOEASLFFYSGTCYTTSVLWIVDISFCG 180
QY 181 DTVEN 185
|||||
Db 181 DTVEN 185

RESULT 11

US-10-216-168-148

; Sequence 148, Application US/10216168

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Desnoyers, Luc

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Smith, Victoria

; APPLICANT: Stephan, Jean-Philippe F.

; APPLICANT: Watanabe, Colin L.

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3530P1C10

; CURRENT APPLICATION NUMBER: US/10/216,168

; CURRENT FILING DATE: 2002-08-09

; PRIOR APPLICATION NUMBER: 10/119,480

; PRIOR FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/062287

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063549

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/064103

; PRIOR FILING DATE: 1997-10-31

; PRIOR APPLICATION NUMBER: 60/069873

; PRIOR FILING DATE: 1997-12-17

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/079294

; PRIOR FILING DATE: 1998-03-25

; PRIOR APPLICATION NUMBER: 60/079656

; PRIOR FILING DATE: 1998-03-26

; PRIOR APPLICATION NUMBER: 60/079728

; PRIOR FILING DATE: 1998-03-27

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 246

; SEQ ID NO 148

; LENGTH: 185

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-216-168-148

Query Match 99.0%; Score 984; DB 6; Length 185;

Best Local Similarity 98.9%; Pred. No. 1.6e-95;

Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYNDVNDNNAGSGQSVSVNNEHNVANVYDNNNGWDSW 60
|||||
Db 1 MKFTIVFAGLLGVFLAPALANYNDVNDNNAGSGQSVSVNNEHNVANVYDNNNGWDSW 60
QY 61 NSWDYNGNGFAATRLFKKTCIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120
|||||
Db 61 NSWDYNGNGFAATRLFKKTCIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120
QY 121 YSNPNKVDLDSKFGKNIANMCRGIPTVMAEMOEASLFFYSGTCYTTSVLWIVDISFCG 180
|||||
Db 121 YSNPNKVDLDSKFGKNIANMCRGIPTVMAEMOEASLFFYSGTCYTTSVLWIVDISFCG 180
QY 181 DTVEN 185
|||||
Db 181 DTVEN 185

RESULT 12

US-10-216-160-148

; Sequence 148, Application US/10216160

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Desnoyers, Luc

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Smith, Victoria

; APPLICANT: Stephan, Jean-Philippe F.

; APPLICANT: Watanabe, Colin L.

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3530P1C8

; CURRENT APPLICATION NUMBER: US/10/216,160

; CURRENT FILING DATE: 2002-08-09

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 246

; SEQ ID NO 148

; LENGTH: 185

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-216-160-148

Query Match 99.0%; Score 984; DB 6; Length 185;

Best Local Similarity 98.9%; Pred. No. 1.6e-95;

Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYNDVNDNNAGSGQSVSVNNEHNVANVYDNNNGWDSW 60
|||||
Db 1 MKFTIVFAGLLGVFLAPALANYNDVNDNNAGSGQSVSVNNEHNVANVYDNNNGWDSW 60
QY 61 NSWDYNGNGFAATRLFKKTCIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120
|||||
Db 61 NSWDYNGNGFAATRLFKKTCIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120
QY 121 YSNPNKVDLDSKFGKNIANMCRGIPTVMAEMOEASLFFYSGTCYTTSVLWIVDISFCG 180
|||||
Db 121 YSNPNKVDLDSKFGKNIANMCRGIPTVMAEMOEASLFFYSGTCYTTSVLWIVDISFCG 180
QY 181 DTVEN 185
|||||
Db 181 DTVEN 185

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; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-930-148

Query Match          99.0%; Score 984; DB 6; Length 185;
Best Local Similarity 98.9%; Pred. No. 1.6e-95;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYNDVDDNNAGSQGQSVSVNNEHNVANVDNNNGWDSW 60
   |||||
DB 1 MKFTIVFAGLLGVFLAPALANYINVDNNAGSQGQSVSVNNEHNVANVDNNNGWDSW 60
   |||||
QY 61 NSIWDYNGGFAATRLFOKTCIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPPKGLM 120
   |||||
DB 61 NSIWDYNGGFAATRLFOKTCIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPPKGLM 120
   |||||
QY 121 YSVNPNKVDLDSKFGKNIANMCRGIPTYMAEEMQEAASLFFYSGTCYTTSVLWIVDISFCG 180
   |||||
DB 121 YSVNPNKVDLDSKFGKNIANMCRGIPTYMAEEMQEAASLFFYSGTCYTTSVLWIVDISFCG 180
   |||||
QY 181 DTVEN 185
   |||||
DB 181 DTVEN 185
   |||||

RESULT 15
US-10-219-003-148
; Sequence 148, Application US/10219003
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC12
; CURRENT APPLICATION NUMBER: US/10/219,003
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22

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; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-849-148

Query Match          99.0%; Score 984; DB 6; Length 185;
Best Local Similarity 98.9%; Pred. No. 1.6e-95;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYNDVDDNNAGSQGQSVSVNNEHNVANVDNNNGWDSW 60
   |||||
DB 1 MKFTIVFAGLLGVFLAPALANYINVDNNAGSQGQSVSVNNEHNVANVDNNNGWDSW 60
   |||||
QY 61 NSIWDYNGGFAATRLFOKTCIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPPKGLM 120
   |||||
DB 61 NSIWDYNGGFAATRLFOKTCIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPPKGLM 120
   |||||
QY 121 YSVNPNKVDLDSKFGKNIANMCRGIPTYMAEEMQEAASLFFYSGTCYTTSVLWIVDISFCG 180
   |||||
DB 121 YSVNPNKVDLDSKFGKNIANMCRGIPTYMAEEMQEAASLFFYSGTCYTTSVLWIVDISFCG 180
   |||||
QY 181 DTVEN 185
   |||||
DB 181 DTVEN 185
   |||||

RESULT 14
US-10-218-930-148
; Sequence 148, Application US/10218930
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC13
; CURRENT APPLICATION NUMBER: US/10/218,930
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148

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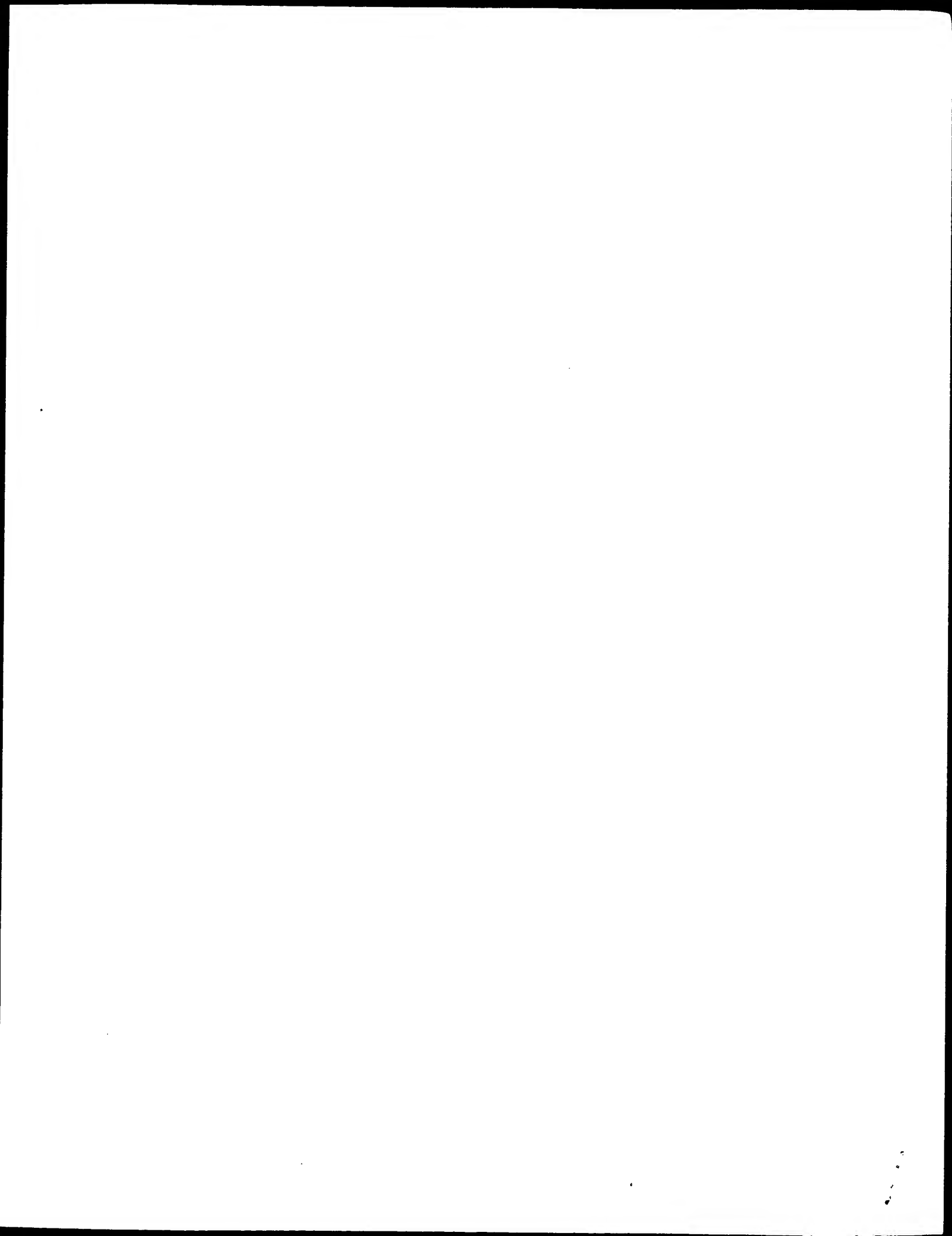
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;	PRIOR APPLICATION NUMBER:	60/119549
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;	PRIOR APPLICATION NUMBER:	60/123618
;	PRIOR FILING DATE:	1999-03-10
;	PRIOR APPLICATION NUMBER:	60/125259
;	PRIOR FILING DATE:	1999-03-19
;	PRIOR APPLICATION NUMBER:	60/125775
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;	PRIOR APPLICATION NUMBER:	60/126773
;	PRIOR FILING DATE:	1999-03-29
;	PRIOR APPLICATION NUMBER:	60/127887
;	PRIOR FILING DATE:	1999-04-05
;	PRIOR APPLICATION NUMBER:	60/130232
;	PRIOR FILING DATE:	1999-04-21
;	PRIOR APPLICATION NUMBER:	60/131022
;	PRIOR FILING DATE:	1999-04-26
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;	PRIOR FILING DATE:	1999-04-27
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;	PRIOR APPLICATION NUMBER:	60/140650
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;	PRIOR APPLICATION NUMBER:	60/140723
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;	PRIOR FILING DATE:	1999-06-23
;	PRIOR APPLICATION NUMBER:	60/144758
;	PRIOR FILING DATE:	1999-07-20
;	PRIOR APPLICATION NUMBER:	60/145698
;	PRIOR FILING DATE:	1999-07-26
;	PRIOR APPLICATION NUMBER:	60/146222
;	PRIOR FILING DATE:	1999-07-28
;	PRIOR APPLICATION NUMBER:	60/146963
;	PRIOR FILING DATE:	1999-08-03
;	PRIOR APPLICATION NUMBER:	60/149320
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;	PRIOR APPLICATION NUMBER:	60/149638
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;	PRIOR APPLICATION NUMBER:	60/151733
;	PRIOR FILING DATE:	1999-08-31

; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835
; PRIOR FILING DATE: 1999-12-07

Query Match 99.0%; Score 984; DB 6; Length 185;
Best Local Similarity 98.9%; Pred. No. 1.6e-95;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYNDVNDNNAGSQSQSVSVNNEHNVANVDNNNGWDSW 60
Db 1 MKFTIVFAGLLGVFLAPALANYNDVNDNNAGSQSQSVSVNNEHNVANVDNNNGWDSW 60
QY 61 NSIWDYGNNGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPPKGLM 120
Db 61 NSIWDYGNNGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPPKGLM 120
QY 121 YSVNPNKVDLDSKFGKNIANMCRGIPTYMAEEMQEAASLFFYSGTCYTTSVLWIVDISFCG 180
Db 121 YSVNPNKVDLDSKFGKNIANMCRGIPTYMAEEMQEAASLFFYSGTCYTTSVLWIVDISFCG 180
QY 181 DTVEN 185
Db 181 DTVEN 185

Search completed: September 4, 2002, 17:04:24
Job time: 1155 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2002, 16:59:20 ; Search time 704.77 Seconds
(without alignments)
92.394 Million cell updates/sec

Title: US-09-821-726-13
Perfect score: 994
Sequence: 1 MKFTIVFAGLLGVFLAPALA.....YTTSVLWIVDISFGDTVEN 185

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA_Main:*

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26: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	994	100.0	185	22	US-09-821-726-13
2	984	99.0	185	1	PCT-US98-16318-18
3	984	99.0	185	15	US-09-130-189-18
4	984	99.0	185	20	US-09-684-524-105
5	984	99.0	185	21	US-09-709-238-211
6	984	99.0	185	21	US-09-746-783-146
7	984	99.0	185	23	US-09-941-992-211

8	984	99.0	185	23	US-09-989-279-211	Sequence 211, App
9	984	99.0	185	23	US-09-989-293A-211	Sequence 211, App
10	984	99.0	185	23	US-09-989-721-211	Sequence 211, App
11	984	99.0	185	23	US-09-989-722-211	Sequence 211, App
12	984	99.0	185	23	US-09-989-723-211	Sequence 211, App
13	984	99.0	185	23	US-09-989-724-211	Sequence 211, App
14	984	99.0	185	23	US-09-989-725-211	Sequence 211, App
15	984	99.0	185	23	US-09-989-726-211	Sequence 211, App
16	984	99.0	185	23	US-09-989-727-211	Sequence 211, App
17	984	99.0	185	23	US-09-989-728-211	Sequence 211, App
18	984	99.0	185	23	US-09-989-729A-211	Sequence 211, App
19	984	99.0	185	23	US-09-989-730-211	Sequence 211, App
20	984	99.0	185	23	US-09-989-731-211	Sequence 211, App
21	984	99.0	185	23	US-09-989-732-211	Sequence 211, App
22	984	99.0	185	23	US-09-989-734-211	Sequence 211, App
23	984	99.0	185	23	US-09-989-735-211	Sequence 211, App
24	984	99.0	185	23	US-09-989-862-211	Sequence 211, App
25	984	99.0	185	23	US-09-990-427-211	Sequence 211, App
26	984	99.0	185	23	US-09-990-436-211	Sequence 211, App
27	984	99.0	185	23	US-09-990-437-211	Sequence 211, App
28	984	99.0	185	23	US-09-990-438-211	Sequence 211, App
29	984	99.0	185	23	US-09-990-439-211	Sequence 211, App
30	984	99.0	185	23	US-09-990-440-211	Sequence 211, App
31	984	99.0	185	23	US-09-990-441-211	Sequence 211, App
32	984	99.0	185	23	US-09-990-442-211	Sequence 211, App
33	984	99.0	185	23	US-09-990-443-211	Sequence 211, App
34	984	99.0	185	23	US-09-990-444-211	Sequence 211, App
35	984	99.0	185	23	US-09-990-456-211	Sequence 211, App
36	984	99.0	185	23	US-09-990-562-211	Sequence 211, App
37	984	99.0	185	23	US-09-990-711-211	Sequence 211, App
38	984	99.0	185	23	US-09-990-726-211	Sequence 211, App
39	984	99.0	185	23	US-09-991-073-211	Sequence 211, App
40	984	99.0	185	23	US-09-991-157-211	Sequence 211, App
41	984	99.0	185	23	US-09-991-163-211	Sequence 211, App
42	984	99.0	185	23	US-09-991-172-211	Sequence 211, App
43	984	99.0	185	23	US-09-991-181-211	Sequence 211, App
44	984	99.0	185	23	US-09-991-854-211	Sequence 211, App
45	984	99.0	185	23	US-09-992-521-211	Sequence 211, App

ALIGNMENTS

RESULT 1

US-09-821-726-13

; Sequence 13, Application US/09821726

; GENERAL INFORMATION:

; APPLICANT: MARTIN, TERENCE E.

; APPLICANT: TOBACK, F. GARY

; APPLICANT: POWELL, C. THOMAS

; APPLICANT: AGARWAL, KAN

; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS

; FILE REFERENCE: 21459/90913

; CURRENT APPLICATION NUMBER: US/09/821,726

; CURRENT FILING DATE: 2001-03-29

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 13

; LENGTH: 185

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-821-726-13

Query Match 100.0%; Score 994; DB 22; Length 185;
Best Local Similarity 100.0%; Pred. No. 4.4e-103;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKFTIVFAGLLGVFLAPALANYINDVNDNNAGSGQGSVSVNNEHNVAVDNNNGWDSW 60

Db 1 MKFTIVFAGLLGVFLAPALANYINDVNDNNAGSGQGSVSVNNEHNVAVDNNNGWDSW 60

Qy 61 NSIWDYNGNGFAATRLFOKKTCTVHKMKKEVMPSTQSLDALVKEKLOGKGGPPPKGLM 120

Db 61 NSIWDYNGGFAATRLFKKTCIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPPKGLM 120
QY 121 YSVNPNKVDLDSKFGKNIANNMCRGIPTTYMAEMOEASLFFYSGTCYTTSVLWIVDISFCG 180
Db 121 YSVNPNKVDLDSKFGKNIANNMCRGIPTTYMAEMOEASLFFYSGTCYTTSVLWIVDISFCG 180
QY 181 DTVEN 185
Db 181 DTVEN 185

RESULT 2

PCT-US98-16318-18
; Sequence 18, Application PC/TUS9816318
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: G16051A
; CURRENT APPLICATION NUMBER: PCT/US98/16318
; CURRENT FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US98-16318-18

Query Match 99.0%; Score 984; DB 1; Length 185;
Best Local Similarity 98.9%; Pred. No. 5.8e-102;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYNDVNDNNAGSGQGSVSVNNEHNVANVDNNNGWDSW 60
Db 1 MKFTIVFAGLLGVFLAPALANYNDVNDNNAGSGQGSVSVNNEHNVANVDNNNGWDSW 60
QY 61 NSIWDYNGGFAATRLFKKTCIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPPKGLM 120
Db 61 NSIWDYNGGFAATRLFKKTCIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPPKGLM 120
QY 121 YSVNPNKVDLDSKFGKNIANNMCRGIPTTYMAEMOEASLFFYSGTCYTTSVLWIVDISFCG 180
Db 121 YSVNPNKVDLDSKFGKNIANNMCRGIPTTYMAEMOEASLFFYSGTCYTTSVLWIVDISFCG 180
QY 181 DTVEN 185
Db 181 DTVEN 185

RESULT 3

US-09-130-189-18
; Sequence 18, Application US/09130189
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.

; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: G16051A
; CURRENT APPLICATION NUMBER: US/09/130,189
; CURRENT FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-130-189-18

Query Match 99.0%; Score 984; DB 15; Length 185;
Best Local Similarity 98.9%; Pred. No. 5.8e-102;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYNDVNDNNAGSGQGSVSVNNEHNVANVDNNNGWDSW 60
Db 1 MKFTIVFAGLLGVFLAPALANYNDVNDNNAGSGQGSVSVNNEHNVANVDNNNGWDSW 60
QY 61 NSIWDYNGGFAATRLFKKTCIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPPKGLM 120
Db 61 NSIWDYNGGFAATRLFKKTCIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPPKGLM 120
QY 121 YSVNPNKVDLDSKFGKNIANNMCRGIPTTYMAEMOEASLFFYSGTCYTTSVLWIVDISFCG 180
Db 121 YSVNPNKVDLDSKFGKNIANNMCRGIPTTYMAEMOEASLFFYSGTCYTTSVLWIVDISFCG 180
QY 181 DTVEN 185
Db 181 DTVEN 185

RESULT 4

US-09-684-524-105
; Sequence 105, Application US/09684524
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/09/684,524
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-684-524-105

Query Match 99.0%; Score 984; DB 20; Length 185;
Best Local Similarity 98.9%; Pred. No. 5.8e-102;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYNDVNDNNAGSGQGSVSVNNEHNVANVDNNNGWDSW 60
Db 1 MKFTIVFAGLLGVFLAPALANYNDVNDNNAGSGQGSVSVNNEHNVANVDNNNGWDSW 60
QY 61 NSIWDYNGGFAATRLFKKTCIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPPKGLM 120
Db 61 NSIWDYNGGFAATRLFKKTCIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPPKGLM 120
QY 121 YSVNPNKVDLDSKFGKNIANNMCRGIPTTYMAEMOEASLFFYSGTCYTTSVLWIVDISFCG 180

Db 121 YSNPNKVDLSKFGKNIAMCRGIPTTYMAEEMQENSLFFYSGTCYTTSVLWIVDSFCG 180

QY 181 DTVEN 185

|||||

Db 181 DTVEN 185

RESULT 5

US-09-709-238-211

; Sequence 211, Application US/09709238

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Chen, Jian

; APPLICANT: Goddard, Audrey

; APPLICANT: Gurney, Austin

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Collin K.

; APPLICANT: Wood, William I.

; APPLICANT: Yuan, Jean

; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding the Same

; FILE REFERENCE: P2730R1C1

; CURRENT APPLICATION NUMBER: US/09/709,238

; CURRENT FILING DATE: 2000-11-08

; PRIOR APPLICATION NUMBER: PCT/US99/12252

; PRIOR FILING DATE: 1999-06-02

; PRIOR APPLICATION NUMBER: US 60/087,607

; PRIOR FILING DATE: 1998-06-02

; PRIOR APPLICATION NUMBER: US 60/087,609

; PRIOR FILING DATE: 1998-06-02

; PRIOR APPLICATION NUMBER: US 60/087,759

; PRIOR FILING DATE: 1998-06-03

; PRIOR APPLICATION NUMBER: US 60/087,827

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: US 60/088,021

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: US 60/088,025

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: US 60/088,028

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: US 60/088,029

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: US 60/088,030

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: US 60/088,033

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: US 60/088,326

; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: US 60/088,167

; PRIOR FILING DATE: 1988-06-05

; PRIOR APPLICATION NUMBER: US 60/088,202

; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: US 60/088,212

; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: US 60/088,217

; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: US 60/088,655

; PRIOR FILING DATE: 1998-06-09

; PRIOR APPLICATION NUMBER: US 60/088,722

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,730

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,734

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,738

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,740

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,741

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,742

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,810

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,810

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,811

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,824

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,825

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,826

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,858

; PRIOR FILING DATE: 1998-06-11

; PRIOR APPLICATION NUMBER: US 60/088,861

; PRIOR FILING DATE: 1998-06-11

; PRIOR APPLICATION NUMBER: US 60/088,863

; PRIOR FILING DATE: 1998-06-11

; PRIOR APPLICATION NUMBER: US 60/088,876

; PRIOR FILING DATE: 1998-06-11

; PRIOR APPLICATION NUMBER: US 60/089,090

; PRIOR FILING DATE: 1998-06-12

; PRIOR APPLICATION NUMBER: US 60/089,105

; PRIOR FILING DATE: 1998-06-12

; PRIOR APPLICATION NUMBER: US 60/089,440

; PRIOR FILING DATE: 1998-06-16

; PRIOR APPLICATION NUMBER: US 60/089,512

; PRIOR FILING DATE: 1998-06-16

; PRIOR APPLICATION NUMBER: US 60/089,514

; PRIOR FILING DATE: 1998-06-16

; PRIOR APPLICATION NUMBER: US 60/089,532

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: US 60/089,538

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: US 60/089,598

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: US 60/089,599

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: US 60/089,600

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: US 60/089,653

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: US 60/089,801

; PRIOR FILING DATE: 1998-06-18

; PRIOR APPLICATION NUMBER: US 60/089,907

; PRIOR FILING DATE: 1998-06-18

; PRIOR APPLICATION NUMBER: US 60/089,908

; PRIOR FILING DATE: 1998-06-18

; PRIOR APPLICATION NUMBER: US 60/089,947

; PRIOR FILING DATE: 1998-06-19

; PRIOR APPLICATION NUMBER: US 60/089,948

; PRIOR FILING DATE: 1998-06-19

; PRIOR APPLICATION NUMBER: US 60/089,952

; PRIOR FILING DATE: 1998-06-19

; PRIOR APPLICATION NUMBER: US 60/090,246

; PRIOR FILING DATE: 1998-06-22

; PRIOR APPLICATION NUMBER: US 60/090,252

; PRIOR FILING DATE: 1998-06-22

; PRIOR APPLICATION NUMBER: US 60/090,254

; PRIOR FILING DATE: 1998-06-22

; PRIOR APPLICATION NUMBER: US 60/090,355

; PRIOR FILING DATE: 1998-06-23

; PRIOR APPLICATION NUMBER: US 60/090,429

; PRIOR FILING DATE: 1998-06-24

; PRIOR APPLICATION NUMBER: US 60/090,431

; PRIOR FILING DATE: 1998-06-24

; PRIOR APPLICATION NUMBER: US 60/090,435

; PRIOR FILING DATE: 1998-06-24

; PRIOR APPLICATION NUMBER: US 60/090,349

; PRIOR FILING DATE: 1998-06-23

; PRIOR APPLICATION NUMBER: US 60/090,444

; PRIOR FILING DATE: 1998-06-24

; PRIOR APPLICATION NUMBER: US 60/090,445

; PRIOR FILING DATE: 1998-06-24

; PRIOR APPLICATION NUMBER: US 60/090,461

; PRIOR FILING DATE: 1998-06-24

; PRIOR APPLICATION NUMBER: US 60/090,472

PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,538
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 60/090,678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 60/090,688
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 60/090,690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 60/090,691
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 60/090,694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 60/090,695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 60/090,696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 60/090,862
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 60/090,863
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 60/091,358
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: US 60/091,360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: US 60/091,478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/091,486
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/091,519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/091,544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: US 60/091,626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/091,628
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/091,633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/091,646
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/091,673
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/091,978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: US 60/091,982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: US 60/092,182
PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: US 60/092,472
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: US 60/093,339
PRIOR FILING DATE: 1998-07-20
PRIOR APPLICATION NUMBER: US 60/094,651
PRIOR FILING DATE: 1998-07-30

Query Match 99.0%; Score 984; DB 21; Length 185;
Best Local Similarity 98.9%; Pred. No. 5.8e-102;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYNDVNDNNAGSQSQSVSVNNEHNVANVNDNNNGWDSW 60
DB 1 MKFTIVFAGLLGVFLAPALANYNDVNDNNAGSQSQSVSVNNEHNVANVNDNNNGWDSW 60
QY 61 NSIWDYNGGFAATRLFKKTCIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120

DB 61 NSIWDYNGGFAATRLFKKTCIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120
QY 121 YSVNPNKVDLSKFGKNIANMCRGIPTIYMAEEMQESLFFYSCTCTTSLVLTIVDISFCG 180
DB 121 YSVNPNKVDLSKFGKNIANMCRGIPTIYMAEEMQESLFFYSCTCTTSLVLTIVDISFCG 180
QY 181 DTVEN 185
DB 181 DTVEN 185

RESULT 6

US-09-746-783-146
Sequence 146, Application US/09746783

GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth
McCoy, John M.
LaVallie, Edward R.
Racie, Lisa A.
Treach, Maurice
Spaulding, Vikki
Agostino, Michael J.
Howes, Steven H.
Fechtel, Kim

TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
ENCODING THEM

NUMBER OF SEQUENCES: 231

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/746,783

FILING DATE: 21-Dec-2000

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Milasincic, Debra J.

REGISTRATION NUMBER: 46,931

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 742-4214

INFORMATION FOR SEQ ID NO: 146:

SEQUENCE CHARACTERISTICS:

LENGTH: 185 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 146:

US-09-746-783-146

Query Match 99.0%; Score 984; DB 21; Length 185;
Best Local Similarity 98.9%; Pred. No. 5.8e-102;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYNDVNDNNAGSQSQSVSVNNEHNVANVNDNNNGWDSW 60

DB 1 MKFTIVFAGLLGVFLAPALANYNDVNDNNAGSQSQSVSVNNEHNVANVNDNNNGWDSW 60

QY 61 NSIWDYNGGFAATRLFKKTCIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120

DB 61 NSIWDYNGGFAATRLFKKTCIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120

;; PRIOR APPLICATION NUMBER: 60/090246
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090252
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090254
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090349
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090355
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090429
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090431
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090435
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090444
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090472
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090535
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090540
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090542
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090676
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090678
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090690
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090694
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090862
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
;; PRIOR APPLICATION NUMBER: 60/092472

Query Match 99.0%; Score 984; DB 23; Length 185;

Best Local Similarity 98.9%; Pred. No. 5.8e-102;

Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVPAGLLGVFLAPALANYINVDNNNAGSGQSVSVNNEHNVANVDNNNGWDSW 60
|||||
Db 1 MKFTIVPAGLLGVFLAPALANYINVDNNNAGSGQSVSVNNEHNVANVDNNNGWDSW 60
|||||

QY 61 NSIWYNGNGFAATRLFKKTCIVHKKMKKEVMPSTQSLDALVKEKKLQKGGPGPPKGLM 120
|||||
Db 61 NSIWYNGNGFAATRLFKKTCIVHKKMKKEVMPSTQSLDALVKEKKLQKGGPGPPKGLM 120
|||||
QY 121 YSVNPNKVDDLSKFGKNTANMCRGIPTYNMDEMQRASLFFYSGTCYTTSVLWIVDISFCG 180
|||||
Db 121 YSVNPNKVDDLSKFGKNTANMCRGIPTYNMDEMQRASLFFYSGTCYTTSVLWIVDISFCG 180
|||||
QY 181 DTVEN 185
|||||
Db 181 DTVEN 185
|||||
RESULT 8
US-09-989-279-211
; Sequence 211, Application US/09989279
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC56
; CURRENT APPLICATION NUMBER: US/09/989,279
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02


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Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKFTIVFAGLLGVFLPALANYINVDNDNNAGSGQSVSVNNEHNVANVDNNGWDSW 60
      |||||
Db 1 MKFTIVFAGLLGVFLPALANYINVDNDNNAGSGQSVSVNNEHNVANVDNNGWDSW 60
      |||||
QY 61 NSIWDYNGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKEKKLQKGGPPPKGLM 120
      |||||
Db 61 NSIWDYNGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKEKKLQKGGPPPKGLM 120
      |||||
QY 121 YSNPNKVDLDSFGKNIANMCRGIPTIYMAEEMQEAFLFFYSGTCYTTSVLWIVDISFCG 180
      |||||
Db 121 YSNPNKVDLDSFGKNIANMCRGIPTIYMAEEMQEAFLFFYSGTCYTTSVLWIVDISFCG 180
      |||||
QY 181 DTVEN 185
      |||||
Db 181 DTVEN 185
      |||||
RESULT 9
US-09-989-293A-211
; Sequence 211, Application US/09989293A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301C66
; CURRENT APPLICATION NUMBER: US/09/989,293A
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088742
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; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
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; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
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;; PRIOR APPLICATION NUMBER: 60/089907
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089908
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089947
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089948
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089952
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/090246
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090252
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090254
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090349
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090355
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090429
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090431
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090435
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090444
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090472
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090535
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090540
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090542
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
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;; PRIOR APPLICATION NUMBER: 60/090694
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090862
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182

;; PRIOR FILING DATE: 1998-07-09
;; PRIOR APPLICATION NUMBER: 60/092472

Query Match 99.0%; Score 984; DB 23; Length 185;
Best Local Similarity 98.9%; Pred. No. 5.8e-102;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKFTIVFAGLLGVFLAPALANYINDVDDNNNAGSGQGSVSVNNEHNVYVNDNNNGWDSW 60
Db 1 MKFTIVFAGLLGVFLAPALANYINDVDDNNNAGSGQGSVSVNNEHNVYVNDNNNGWDSW 60
Qy 61 NSIWDYGNCFATRLFKKTCIVHKMKKEVMPSTOSLDALVKEKKLOKGGPPPKGLM 120
Db 61 NSIWDYGNCFATRLFKKTCIVHKMKKEVMPSTOSLDALVKEKKLOKGGPPPKGLM 120
Qy 121 YSVNPNKVDDLSKFGKNIANMCRGIPTYMAEEMQESLFFYSGTCYTTSVLWIVDIFSCG 180
Db 121 YSVNPNKVDDLSKFGKNIANMCRGIPTYMAEEMQESLFFYSGTCYTTSVLWIVDIFSCG 180
Qy 181 DTVEN 185
Db 181 DTVEN 185

RESULT 10
US-09-989-721-211
;; Sequence 211, Application US/09989721
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kijavini, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P2730PIC55
;; CURRENT APPLICATION NUMBER: US/09/989,721
;; CURRENT FILING DATE: 2001-11-19
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/065186
;; PRIOR FILING DATE: 1997-11-12
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/066770
;; PRIOR FILING DATE: 1997-11-24
;; PRIOR APPLICATION NUMBER: 60/075945
;; PRIOR FILING DATE: 1998-02-25
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28


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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472

Query Match          99.0%; Score 984; DB 23; Length 185;
Best Local Similarity 98.9%; Pred. No. 5.8e-102;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYINVDNNNAGSGQSQSVSNNEHNVANVDNNNGWDSW 60
   |||||
Db 1 MKFTIVFAGLLGVFLAPALANYINVDNNNAGSGQSQSVSNNEHNVANVDNNNGWDSW 60
   |||||
QY 61 NSIWDYNGGFAATRLFOKKTCTIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120
   |||||
Db 61 NSIWDYNGGFAATRLFOKKTCTIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120
   |||||
QY 121 YSNPNKVDLDSKFGKNTANMCRGIPTYMAEPMQEQASLFFYSGTCTYTSVLWIVDISFCG 180
   |||||
Db 121 YSNPNKVDLDSKFGKNTANMCRGIPTYMAEPMQEQASLFFYSGTCTYTSVLWIVDISFCG 180
   |||||
QY 181 DTVEN 185
   |||||
Db 181 DTVEN 185

RESULT 11
US-09-989-722-211
; Sequence 211, Application US/09989722
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC63
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
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; PRIOR APPLICATION NUMBER: 60/088555
; PRIOR FILING DATE: 1998-06-09
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; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
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; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
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; PRIOR APPLICATION NUMBER: 60/089514
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; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
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; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089948
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089952
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090246
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; PRIOR APPLICATION NUMBER: 60/090252
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090254
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
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; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR APPLICATION NUMBER: 60/090676
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; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519

; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472

Query Match 99.0%; Score 984; DB 23; Length 185;
Best Local Similarity 98.9%; Pred. No. 5.8e-102;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKFTIVFAGLLGVFLAPALANYINVDNDNNAGSQGSVSVNNEHNVYVNDNNNGWDSW 60
Db 1 MKFTIVFAGLLGVFLAPALANYINVDNDNNAGSQGSVSVNNEHNVYVNDNNNGWDSW 60

Qy 61 NSIWDYGNCGFAATRLFOKKTCTIVHKMKKEVMPISQSLDALVKELKQKGGPGPPKGLM 120
Db 61 NSIWDYGNCGFAATRLFOKKTCTIVHKMKKEVMPISQSLDALVKELKQKGGPGPPKGLM 120

Qy 121 YSVNPNKYVDDLKSKFGKNIANMCRGIPTYMAEEMQEAFLFFYSGTCYTTSLVLIWIVDISFCG 180
Db 121 YSVNPNKYVDDLKSKFGKNIANMCRGIPTYMAEEMQEAFLFFYSGTCYTTSLVLIWIVDISFCG 180

Qy 181 DTVEN 185
Db 181 DTVEN 185

RESULT 12

US-09-989-723-211
; Sequence 211, Application US/09989723
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C62
; CURRENT APPLICATION NUMBER: US/09/989,723
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12


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; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472

Query Match          99.0%; Score 984; DB 23; Length 185;
Best Local Similarity 98.9%; Pred. No. 5.8e-102;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYNDVNDNNAGSGQSVSVNNEHNVANVDNNNGWDSW 60
Db 1 MKFTIVFAGLLGVFLAPALANYINVDNDNNAGSGQSVSVNNEHNVANVDNNNGWDSW 60

QY 61 NSIWDYNGFAATRLFOKKTICVHKMKKEVMPSTIQSLDALVKEKKLOGKPGGPPKGLM 120
Db 61 NSIWDYNGFAATRLFOKKTICVHKMKKEVMPSTIQSLDALVKEKKLOGKPGGPPKGLM 120

QY 121 YSNPNKVDLSKFGKNIANMCRGIPTIYMAEEMQASLFFYSTCTYTSVLWIVDISFCG 180
Db 121 YSNPNKVDLSKFGKNIANMCRGIPTIYMAEEMQASLFFYSTCTYTSVLWIVDISFCG 180

QY 181 DTVEN 185
Db 181 DTVEN 185

RESULT 13
US-09-989-724-211
; SEQUENCE 211, Application US/09989724
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC67
; CURRENT APPLICATION NUMBER: US/09/989,724
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089948
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089952
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090246
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090252
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090254
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
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; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
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; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862

; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472

Query Match 99.0%; Score 984; DB 23; Length 185;

Best Local Similarity 98.9%; Pred. No. 5.8e-102;

Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYINDVNDNNAGSQSQSVSVNNEHNVANVDNNNGDSW 60
DB 1 MKFTIVFAGLLGVFLAPALANYINDVNDNNAGSQSQSVSVNNEHNVANVDNNNGDSW 60
QY 61 NSIWDYNGNGFAATRLFQKTCIVHKMKKEVMPISQISLDALVKEKLOGKGGPPPKGLM 120
DB 61 NSIWDYNGNGFAATRLFQKTCIVHKMKKEVMPISQISLDALVKEKLOGKGGPPPKGLM 120
QY 121 YSVNPNKVVDDLSKFGKNIANMCRGIPTYMAEEMQEAFLFFYSGTCYTTSVLWIVDISFCG 180
DB 121 YSVNPNKVVDDLSKFGKNIANMCRGIPTYMAEEMQEAFLFFYSGTCYTTSVLWIVDISFCG 180
QY 181 DTVEN 185
DB 181 DTVEN 185

RESULT 14

US-09-989-725-211

; Sequence 211, Application US/09989725

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

1	PRIOR FILING DATE: 1998-06-11	60/08876
2	PRIOR APPLICATION NUMBER: 60/08876	60/08876
3	PRIOR FILING DATE: 1998-06-11	60/089105
4	PRIOR APPLICATION NUMBER: 60/089105	60/089105
5	PRIOR FILING DATE: 1998-06-12	60/089440
6	PRIOR APPLICATION NUMBER: 60/089440	60/089440
7	PRIOR FILING DATE: 1998-06-16	60/089512
8	PRIOR APPLICATION NUMBER: 60/089512	60/089512
9	PRIOR FILING DATE: 1998-06-16	60/089514
10	PRIOR APPLICATION NUMBER: 60/089514	60/089514
11	PRIOR FILING DATE: 1998-06-16	60/089532
12	PRIOR APPLICATION NUMBER: 60/089532	60/089532
13	PRIOR FILING DATE: 1998-06-17	60/089538
14	PRIOR APPLICATION NUMBER: 60/089538	60/089538
15	PRIOR FILING DATE: 1998-06-17	60/089598
16	PRIOR APPLICATION NUMBER: 60/089598	60/089598
17	PRIOR FILING DATE: 1998-06-17	60/089599
18	PRIOR APPLICATION NUMBER: 60/089599	60/089599
19	PRIOR FILING DATE: 1998-06-17	60/089600
20	PRIOR APPLICATION NUMBER: 60/089600	60/089600
21	PRIOR FILING DATE: 1998-06-17	60/089653
22	PRIOR APPLICATION NUMBER: 60/089653	60/089653
23	PRIOR FILING DATE: 1998-06-17	60/089801
24	PRIOR APPLICATION NUMBER: 60/089801	60/089801
25	PRIOR FILING DATE: 1998-06-18	60/089907
26	PRIOR APPLICATION NUMBER: 60/089907	60/089907
27	PRIOR FILING DATE: 1998-06-18	60/089908
28	PRIOR APPLICATION NUMBER: 60/089908	60/089908
29	PRIOR FILING DATE: 1998-06-18	60/089947
30	PRIOR APPLICATION NUMBER: 60/089947	60/089947
31	PRIOR FILING DATE: 1998-06-19	60/089948
32	PRIOR APPLICATION NUMBER: 60/089948	60/089948
33	PRIOR FILING DATE: 1998-06-19	60/089952
34	PRIOR APPLICATION NUMBER: 60/089952	60/089952
35	PRIOR FILING DATE: 1998-06-19	60/090246
36	PRIOR APPLICATION NUMBER: 60/090246	60/090246
37	PRIOR FILING DATE: 1998-06-22	60/090252
38	PRIOR APPLICATION NUMBER: 60/090252	60/090252
39	PRIOR FILING DATE: 1998-06-22	60/090254
40	PRIOR APPLICATION NUMBER: 60/090254	60/090254
41	PRIOR FILING DATE: 1998-06-22	60/090349
42	PRIOR APPLICATION NUMBER: 60/090349	60/090349
43	PRIOR FILING DATE: 1998-06-23	60/090355
44	PRIOR APPLICATION NUMBER: 60/090355	60/090355
45	PRIOR FILING DATE: 1998-06-23	60/090429
46	PRIOR APPLICATION NUMBER: 60/090429	60/090429
47	PRIOR FILING DATE: 1998-06-24	60/090431
48	PRIOR APPLICATION NUMBER: 60/090431	60/090431
49	PRIOR FILING DATE: 1998-06-24	60/090435
50	PRIOR APPLICATION NUMBER: 60/090435	60/090435
51	PRIOR FILING DATE: 1998-06-24	60/090444
52	PRIOR APPLICATION NUMBER: 60/090444	60/090444
53	PRIOR FILING DATE: 1998-06-24	60/090445
54	PRIOR APPLICATION NUMBER: 60/090445	60/090445
55	PRIOR FILING DATE: 1998-06-24	60/090472
56	PRIOR APPLICATION NUMBER: 60/090472	60/090472
57	PRIOR FILING DATE: 1998-06-24	60/090535
58	PRIOR APPLICATION NUMBER: 60/090535	60/090535
59	PRIOR FILING DATE: 1998-06-24	60/090540
60	PRIOR APPLICATION NUMBER: 60/090540	60/090540
61	PRIOR FILING DATE: 1998-06-24	60/090542
62	PRIOR APPLICATION NUMBER: 60/090542	60/090542
63	PRIOR FILING DATE: 1998-06-24	60/090557
64	PRIOR APPLICATION NUMBER: 60/090557	60/090557
65	PRIOR FILING DATE: 1998-06-24	60/090676
66	PRIOR APPLICATION NUMBER: 60/090676	60/090676
67	PRIOR FILING DATE: 1998-06-25	60/090678
68	PRIOR APPLICATION NUMBER: 60/090678	60/090678
69	PRIOR FILING DATE: 1998-06-25	60/090690
70	PRIOR APPLICATION NUMBER: 60/090690	60/090690
71	PRIOR FILING DATE: 1998-06-25	60/090694
72	PRIOR APPLICATION NUMBER: 60/090694	60/090694
73	PRIOR FILING DATE: 1998-06-25	60/090696
74	PRIOR APPLICATION NUMBER: 60/090696	60/090696

; PRIOR APPLICATION NUMBER: 60/090695
 ; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/090696
 ; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/090862
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: 60/090863
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: 60/091360
 ; PRIOR FILING DATE: 1998-07-01
 ; PRIOR APPLICATION NUMBER: 60/091478
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091544
 ; PRIOR FILING DATE: 1998-07-01
 ; PRIOR APPLICATION NUMBER: 60/091519
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091626
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091633
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091978
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09
 ; PRIOR APPLICATION NUMBER: 60/092472

Query Match 99.0%; Score 984; DB 23; Length 185;
 Best Local Similarity 98.9%; Pred. No. 5.8e-102;
 Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKFTIVFAGLGVFLPALANYNVDVNDNNAGSGQSVVNNHNVANVDNNGWDSW 60
 Db 1 MKFTIVFAGLGVFLPALANYNVDVNDNNAGSGQSVVNNHNVANVDNNGWDSW 60
 Qy 61 NSIWDYNGFAATRLFOKTKCIVHKMKKEVMPISQISLDALVKELKQGGPGPPKGLM 120
 Db 61 NSIWDYNGFAATRLFOKTKCIVHKMKKEVMPISQISLDALVKELKQGGPGPPKGLM 120
 Qy 121 YSVNPNKVDLSKFGKNIANCMRGIPITYMAEEMOEASLFFYSGTCTYTSVLWIVDISFCG 180
 Db 121 YSVNPNKVDLSKFGKNIANCMRGIPITYMAEEMOEASLFFYSGTCTYTSVLWIVDISFCG 180
 Qy 181 DTVEN 185
 Db 181 DTVEN 185

RESULT 15
 US-09-989-726-211
 ; Sequence 211, Application US/09989726
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730PIC60
 ; CURRENT APPLICATION NUMBER: US/09/989,726
 ; CURRENT FILING DATE: 2001-11-19
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/065186
 ; PRIOR FILING DATE: 1997-11-12
 ; PRIOR APPLICATION NUMBER: 60/065311
 ; PRIOR FILING DATE: 1997-11-13
 ; PRIOR APPLICATION NUMBER: 60/066770
 ; PRIOR FILING DATE: 1997-11-24
 ; PRIOR APPLICATION NUMBER: 60/075945
 ; PRIOR FILING DATE: 1998-02-25
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/083322
 ; PRIOR FILING DATE: 1998-04-28
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 ; PRIOR FILING DATE: 1998-06-10
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 ; PRIOR FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: 60/088824
 ; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: 60/088826
 ; PRIOR FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: 60/088858
 ; PRIOR FILING DATE: 1998-06-11
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 ; PRIOR APPLICATION NUMBER: 60/089514
 ; PRIOR FILING DATE: 1998-06-16
 ; PRIOR APPLICATION NUMBER: 60/089532
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089538
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089598
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089599
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089600
 ; PRIOR FILING DATE: 1998-06-17
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 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: 60/089907
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: 60/089908
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 ; PRIOR FILING DATE: 1998-06-19
 ; PRIOR APPLICATION NUMBER: 60/089952
 ; PRIOR FILING DATE: 1998-06-19
 ; PRIOR APPLICATION NUMBER: 60/090246
 ; PRIOR FILING DATE: 1998-06-22
 ; PRIOR APPLICATION NUMBER: 60/090252
 ; PRIOR FILING DATE: 1998-06-22
 ; PRIOR APPLICATION NUMBER: 60/090254
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 ; PRIOR APPLICATION NUMBER: 60/090349
 ; PRIOR FILING DATE: 1998-06-23
 ; PRIOR APPLICATION NUMBER: 60/090355
 ; PRIOR FILING DATE: 1998-06-23
 ; PRIOR APPLICATION NUMBER: 60/090429
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090431
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090435
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090444
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090445
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090472
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090535
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090540
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090542
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090557
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090676
 ; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/090678

; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/090690
 ; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/090694
 ; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/090695
 ; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/090696
 ; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/090862
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: 60/090863
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: 60/091360
 ; PRIOR FILING DATE: 1998-07-01
 ; PRIOR APPLICATION NUMBER: 60/091478
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091544
 ; PRIOR FILING DATE: 1998-07-01
 ; PRIOR APPLICATION NUMBER: 60/091519
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091626
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091633
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091978
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09
 ; PRIOR APPLICATION NUMBER: 60/092472

Query Match 99.0%; Score 984; DB 23; Length 185;
 Best Local Similarity 98.9%; Pred. No. 5.8e-102;
 Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	MKFTIVFAGLLGVFLAPALANYNIDVNDNNAGSQSQSVSVNNEHNVANVDNNNGWDSW	60
Db	1	MKFTIVFAGLLGVFLAPALANYNINVDNNAGSQSQSVSVNNEHNVANVDNNNGWDSW	60
QY	61	NSIDYGNCGFAATRLFKKTCIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM	120
Db	61	NSIDYGNCGFAATRLFKKTCIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM	120
QY	121	YSVNPKNKVDLDSKFGKNIANMCRGPTTYMAEEMQASLFFYSCTCTTSLVLIWVDSFCG	180
Db	121	YSVNPKNKVDLDSKFGKNIANMCRGPTTYMAEEMQASLFFYSCTCTTSLVLIWVDSFCG	180
QY	181	DTVEN 185	
Db	181	DTVEN 185	

Search completed: September 4, 2002, 16:59:21
 Job time: 1042 sec


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PR 12-JUN-1998; 98US-0089105.
PR 16-JUN-1998; 98US-0089440.
PR 16-JUN-1998; 98US-0089512.
PR 16-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089653.
PR 17-JUN-1998; 98US-0089801.
PR 18-JUN-1998; 98US-0089801.
PR 18-JUN-1998; 98US-0089907.
PR 18-JUN-1998; 98US-0089908.
PR 19-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089948.
PR 19-JUN-1998; 98US-0089952.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090461.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 10-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 12-AUG-1998; 98US-0096146.
PR 17-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.

PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 99US-0115565.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX
XX WPI; 2000-072883/06.
XX N-PSDB; AAZ65023.
XX
XX Membrane-bound proteins and related nucleotide sequences
XX claim 12; Fig 139; 822pp; English.
XX
XX The invention provides membrane-bound PRO polypeptides and
XX polynucleotides encoding them. The PRO sequences of the invention were
XX identified based on extracellular domain homology screening. The PRO
XX sequences have homology with proteins including LDL receptors, TIE
XX ligands and various enzymes. The membrane-bound proteins and receptor
XX molecules are useful as pharmaceutical and diagnostic agents. Receptor
XX immunoadhesins, for instance, can be used as therapeutic agents to block
XX receptor-ligand interactions. The membrane-bound proteins can also be
XX employed for screening of potential peptide or small molecule inhibitors
XX of the relevant receptor/ligand interaction. The PRO encoding sequences
XX are useful as hybridization probes, in chromosome and gene mapping and in
XX the generation of antisense RNA and DNA. PRO nucleic acid sequences
XX will also be useful for the preparation of PRO polypeptides, especially
XX by recombinant techniques.
XX
XX Sequence 185 AA;

Query Match 64.5%; Score 640; DB 21; Length 185;
Best Local Similarity 63.8%; Pred. No. 1.7e-60;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

Qy 1 MKLTMFVVLGLLAAAGFA-YTVNINCNDGVDSGQSVSINGVHNVANIDNNNGWDS 59
Db 1 mkftivfagllgvlapalanvnnv-dnnnngsgqsvsvnnhvanvndnngwds 59
Qy 60 WNSLWDYENSFAATRLFSKSKSCIVHRMKNKAMPISLDLDTMYKEQK--GKPGGAPPKDL 117
Db 60 wnsiwdyngngfaatrllqkktcihvknnkempsiqslaldalvkekklqgkpggppkgl 119
```

QY 118 MYSVNPTRVEDLNTFGPKIAGMCRGPIPTVVAEEIPGNOPLYSKKCYTADILWILRMSFC 177
 ||||| :|||: || || |||||:|||| : || ||| :|||: :|||
 Db 120 mysnpnkvdlskfgknianmrgiptymaeemqasiffysgtcttsvliwivdisfc 179
 ||||| :|||: || || |||||:|||| : || ||| :|||: :|||
 QY 178 GTSVE 182
 | :||
 Db 180 gdtve 184
 | :||

RESULT 5
 AAB65209
 ID AAB65209 standard; Protein; 185 AA.
 XX
 AC AAB65209;
 XX
 DT 02-APR-2001 (first entry)
 XX
 DE Human PRO1005 (UNQ489) protein sequence SEQ ID NO:211.
 XX
 KW Human; secreted and transmembrane protein; PRO; cytostatic;
 KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
 KW diagnostic assay.
 XX
 OS Homo sapiens.
 XX
 PN WO200073454-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 30-MAR-2000; 2000WO-US08439.
 XX
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 27-JUL-1999; 99US-0143048.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 28-JUL-1999; 99US-0146222.
 PR 17-AUG-1999; 99US-0149396.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 08-OCT-1999; 99US-0158663.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;
 XX
 DR WPI; 2001-032160/04.
 DR N-PSDB; AAF44169.
 XX
 XX PRO polynucleotides used to produce polypeptides used to target
 PT bioactive molecules such as toxins, radiolabels or antibodies, to
 PT specific cells, to cause targeted cell death -
 XX
 PS Claim 12; Fig 139; 935pp; English.
 XX

CC The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
 CC can be used for targeted delivery of bioactive molecules, such as
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA
 CC and DNA. They may also be used to produce transgenic animals which are
 CC used to develop and screen therapeutically useful reagents. The PRO
 CC nucleotide and protein sequence can be used for tissue typing and in
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
 CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.

XX Sequence 185 AA:

Query Match 64.5%; Score 640; DB 22; Length 185;
 Best Local Similarity 63.8%; Pred. NO. 1.7e-60;
 Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;
 QY 1 MKLTMEVVCLLGLLAAPGFA-YTVNINGNVGVGSGQSVSINGVHNVANIDNNNGWDS 59
 ||||| :|||: || || |||||:|||| : || ||| :|||: :|||
 Db 1 mkftivfagllgflapalanyninv-odnnnagsgqsvsnvnhnvanvnnngwds 59
 ||||| :|||: || || |||||:|||| : || ||| :|||: :|||
 QY 60 WNSLWDYENSFAATRLFSKSCIVHRMKNKDAMPSQLQDLDTMYKEQ--CKGPGGAPPKDL 117
 ||||| :|||: || || |||||:|||| : || ||| :|||: :|||
 Db 60 wnsiwdyngngfaatrllfqkctcihkmknevmpsiqsdalvkekklqkgpgpppgkgl 119
 ||||| :|||: || || |||||:|||| : || ||| :|||: :|||
 QY 118 MYSVNPTRVEDLNTFGPKIAGMCRGPIPTVVAEEIPGNOPLYSKKCYTADILWILRMSFC 177
 ||||| :|||: || || |||||:|||| : || ||| :|||: :|||
 Db 120 mysnpnkvdlskfgknianmrgiptymaeemqasiffysgtcttsvliwivdisfc 179
 ||||| :|||: || || |||||:|||| : || ||| :|||: :|||
 QY 178 GTSVE 182
 | :||
 Db 180 gdtve 184
 | :||

RESULT 6

AAB50957
 ID AAB50957 standard; Protein; 185 AA.

XX
 AC AAB50957;

DT 21-MAR-2001 (first entry)

XX
 DE Human PRO1005 protein.

XX Human; PRO; cytostatic; nootropic; neuroprotective; respiratory general;
 KW antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
 KW PRO agonist; cancer; inflammatory disorder; immunological disorder.

OS Homo sapiens.

XX
 PN WO200073348-A2.

XX
 PD 07-DEC-2000.

XX
 PF 30-MAY-2000; 2000WO-US14941.

XX
 PR 02-JUN-1999; 99WO-US12252.

PR 22-JUN-1999; 99US-0140650.

PR 23-JUN-1999; 99US-0141037.

PR 20-JUL-1999; 99US-0144758.

PR 01-SEP-1999; 99WO-US20111.

PR 08-SEP-1999; 99WO-US20594.

PR 29-OCT-1999; 99US-0162506.

PR 30-NOV-1999; 99WO-US28313.

PR 01-DEC-1999; 99WO-US28634.

PR 02-DEC-1999; 99WO-US28551.

PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30999.


```

RESULT 10
AAM23556
ID AAM23556 standard; Protein; 184 AA.
XX
AC AAM23556;
XX
DT 12-OCT-2001 (first entry)
XX
DE Human EST encoded protein SEQ ID NO: 1081.
XX
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition.
XX
OS Homo sapiens.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US02687.
XX
PR 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617746.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
DR WPI; 2001-476164/51.
DR N-PSDB; AAF98215.
XX
XX
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
XX antibodies and research use -
XX
XX Claim 20; Page 814-815; 1275pp; English.
XX
XX The present invention provides the protein and coding sequences of novel
XX proteins from a variety of organisms, including human, dog, cat, horse,
XX cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
XX urchin and tomato. These were derived from expressed sequence tags (ESTs)
XX from the organism of interest. They can be used in diagnostics,
XX forensics, gene mapping, identification of mutations, to assess
XX biodiversity and for nutritional purposes. The present sequence is a
XX protein of the invention.
XX
XX Sequence 184 AA;
XX
Query Match 16.2%; Score 161; DB 22; Length 184;
Best Local Similarity 26.6%; Pred. No. 4.1e-09;
Matches 51; Conservative 45; Mismatches 68; Indels 28; Gaps 8;
QY 1 MKLTFFVGLLGLAAGFAYTV-NI---NGNDGNVDGSGQSQSVISGVHNVANIDNNNG 56
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 1 mkilvafivlitfiglshgyevfnliispsnngnv----qetvtdnektalinihag 56
QY 57 WDSWNSLWDYENSAATRLFSKSCIVIRNMKNKDAMPSLODLDTMVKQKGGPGGAPPKD 116
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 57 scscttidykhgylaarvlsrracfilkmhqnpplnnlqwyiekqa-----ld 108
QY 117 LMYS-----VNP--TRVEDLNTF--GPKIAGMCRGIPTYVAEEIPGPNOLYSKKCYT 165
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 109 nmfsskytwkynpleslikdvdvfillgspiekckhpiykgeventhn-vgaggcak 167
QY 166 ADILWILRMSPC 177
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 168 agligligisic 179

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RESULT 11
AAE04211
ID AAE04211 standard; Protein; 184 AA.
XX
AC AAE04211;
XX
DT 09-AUG-2001 (first entry)
XX
DE Human gene 14 encoded secreted protein HNSAA27, SEQ ID NO:66.
XX
KW Human; secreted protein; proliferative disorder; cancer; tumour;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW inflammation; allergy; neurological disorder; Alzheimer's disease;
KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW cardiovascular disorder; angiogenic disorder; kidney disorder;
KW gastrointestinal disorder; pregnancy-related disorder; gene therapy;
KW endocrine disorder; infection; wound healing; vulnery;
KW cell culture; chemotaxis; food additive; chromosome 2;
KW binding partner identification.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..20
XX FT /label= signal_peptide
XX FT 21..184
XX FT /note= "Mature secreted protein"
XX PN WO200136432-A2.
XX
XX 25-MAY-2001.
XX
XX 15-NOV-2000; 2000WO-US31162.
XX
XX 19-NOV-1999; 99US-0166415.
XX 30-JUN-2000; 2000US-0215136.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Komatsoulis GA, Baker KP, Young PE;
XX WPI: 2001-343793/36.
XX N-PSDB; AAD08501.
XX
XX Isolated nucleic acid molecule encoding a human secreted protein is
XX used in preventing, treating or ameliorating a medical condition -
XX
XX Claim 11; Page 444; 509pp; English.
XX
XX AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted
XX protein genes, and AAE04199-AAE04239 represent the proteins they encode.
XX AAE04240-AAE04297 represent human secreted protein fragments or variants.
XX The secreted proteins and their genes are useful for preventing,
XX treating or ameliorating medical conditions, e.g., by protein or gene
XX therapy. Pathological conditions can be diagnosed by determining the
XX amount of the new protein in a sample or by determining the presence of
XX mutations in the new genes. Specific uses are described for each of the
XX 18 genes, based on the tissues in which they are most highly expressed,
XX and include developing products for the diagnosis or treatment of
XX proliferative disorders, cancer, tumours, foetal and developmental
XX abnormalities, haematopoietic disorders, diseases of the immune system,
XX AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
XX allergies, neurological disorders (e.g., Alzheimer's disease,
XX Parkinson's disease), cognitive disorders, schizophrenia, asthma,
XX skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
XX cardiovascular disorders, angiogenic disorders, kidney disorders,
XX gastrointestinal disorders, pregnancy-related disorders, endocrine
XX disorders, and infections. The proteins can also be used to aid wound
XX healing and epithelial cell proliferation, to prevent skin ageing due to

```

CC sunburn, to maintain organs before transplantation, for supporting cell
 CC culture of primary tissues, to regenerate tissues, to identify their
 CC cognate ligands or binding partners, and in chemotaxis, and can be used
 CC as a food additive or preservative to modify storage properties.
 CC Antibodies specific for a protein of the invention can be used in
 CC alleviating symptoms associated with the disorders mentioned above, and
 CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
 CC immunoassay (ELISA). The present sequence represents a human
 CC secreted protein of the invention.
 XX
 XX Sequence 184 AA;
 SQ
 Query Match 16.2%; Score 161; DB 22; Length 184;
 Best Local Similarity 26.6%; Pred. No. 4.1e-09;
 Matches 51; Conservative 45; Mismatches 68; Indels 28; Gaps 8;
 QY 1 MKLTMFVVGILLGLAAGPAYTV-NI---NGNDGNVDGSGQOSVSIINGVHVNVANIDNNNG 56
 Db 1 mkilvavlvltifglsghyevfnlispnngnv----qetvtdidnektainihag 56
 QY 57 WDSWNSLWDYENSFAATRLFSKSCIVHRMKNKDAMPSLQDLDTMVKQKGGPGGAPPKD 116
 Db 57 scssttfdykhgyiasrvlsrracfilkmhqnplnlqwyiyekqa-----ld 108
 QY 117 LMYS-----VNP--TRVEDLNTF--GPKIAGMCRGIPTYVAEETPGNPOLYSKKCYT 165
 Db 109 nmfsskytwkynpleslikdvdfllgspieklckhiplkygevvventhn-vgaggcak 167
 QY 166 ADILWILRMSFC 177
 Db 168 agllgilgisic 179
 RESULT 12
 ID AAE04233 standard; Protein; 184 AA.
 AC AAE04233;
 XX
 XX 09-AUG-2001 (first entry)
 XX Human gene 14 encoded secreted protein HNSAA27, SEQ ID NO:88.
 XX Human; secreted protein; proliferative disorder; cancer; tumour;
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
 KW cardiovascular disorder; angiogenic disorder; kidney disorder;
 KW gastrointestinal disorder; pregnancy-related disorder; gene therapy;
 KW endocrine disorder; infection; wound healing; vulnerability;
 KW cell culture; chemotaxis; food additive; chromosome 2;
 KW binding partner identification.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX Peptide 1..20
 XX /label= signal_peptide
 XX Protein 21..184
 XX /note= "Mature secreted protein"
 XX
 XX WO200136432-A2.
 XX
 XX 25-MAY-2001.
 XX
 XX 15-NOV-2000; 2000WO-US31162.
 XX
 XX 19-NOV-1999; 99US-0166415.
 XX
 XX 30-JUN-2000; 2000US-0215136.
 XX

(HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Ruben SM, Komatsoulis GA, Baker KP, Young PE;
 XX WPI; 2001-343793/36.
 DR N-PSDB; AAD08523.
 XX
 PT Isolated nucleic acid molecule encoding a human secreted protein is
 PT used in preventing, treating or ameliorating a medical condition -
 XX
 XX Claim 11: Page 463-464; 509pp; English.
 XX
 CC AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted
 CC protein genes, and AAE04199-AAE04239 represent the proteins they encode.
 CC AAE04240-AAE04297 represent human secreted protein fragments or variants.
 CC The secreted proteins and their genes are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Pathological conditions can be diagnosed by determining the
 CC amount of the new protein in a sample or by determining the presence of
 CC mutations in the new genes. Specific uses are described for each of the
 CC 18 genes, based on the tissues in which they are most highly expressed,
 CC and include developing products for the diagnosis or treatment of
 CC proliferative disorders, cancer, tumours, foetal and developmental
 CC abnormalities, haematopoietic disorders, diseases of the immune system,
 CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
 CC allergies, neurological disorders (e.g., Alzheimer's disease,
 CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,
 CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
 CC cardiovascular disorders, angiogenic disorders, kidney disorders,
 CC gastrointestinal disorders, pregnancy-related disorders, endocrine
 CC disorders, and infections. The proteins can also be used to aid wound
 CC healing and epithelial cell proliferation, to prevent skin ageing due to
 CC sunburn, to maintain organs before transplantation, for supporting cell
 CC culture of primary tissues, to regenerate tissues, to identify their
 CC cognate ligands or binding partners, and in chemotaxis, and can be used
 CC as a food additive or preservative to modify storage properties.
 CC Antibodies specific for a protein of the invention can be used in
 CC alleviating symptoms associated with the disorders mentioned above, and
 CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
 CC immunoassay (ELISA). The present sequence represents a human
 CC secreted protein of the invention.
 XX
 XX Sequence 184 AA;
 SQ
 Query Match 16.2%; Score 161; DB 22; Length 184;
 Best Local Similarity 26.6%; Pred. No. 4.1e-09;
 Matches 51; Conservative 45; Mismatches 68; Indels 28; Gaps 8;
 QY 1 MKLTMFVVGILLGLAAGPAYTV-NI---NGNDGNVDGSGQOSVSIINGVHVNVANIDNNNG 56
 Db 1 mkilvavlvltifglsghyevfnlispnngnv----qetvtdidnektainihag 56
 QY 57 WDSWNSLWDYENSFAATRLFSKSCIVHRMKNKDAMPSLQDLDTMVKQKGGPGGAPPKD 116
 Db 57 scssttfdykhgyiasrvlsrracfilkmhqnplnlqwyiyekqa-----ld 108
 QY 117 LMYS-----VNP--TRVEDLNTF--GPKIAGMCRGIPTYVAEETPGNPOLYSKKCYT 165
 Db 109 nmfsskytwkynpleslikdvdfllgspieklckhiplkygevvventhn-vgaggcak 167
 QY 166 ADILWILRMSFC 177
 Db 168 agllgilgisic 179
 RESULT 13
 ID AAY66690
 XX AAY66690 standard; protein; 184 AA.
 AC AAY66690;
 XX
 XX 05-APR-2000 (first entry)
 XX

XX DE Membrane-bound protein PRO813.
XX DE
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping.
XX OS
XX OS Homo sapiens.
PN WO9963088-A2.
XX PD
XX PD 09-DEC-1999.
PF 02-JUN-1999; 99WO-US12252.
XX 02-JUN-1998; 98US-0087607.
PR 02-JUN-1998; 98US-0087609.
PR 02-JUN-1998; 98US-0087759.
PR 03-JUN-1998; 98US-0087827.
PR 04-JUN-1998; 98US-0088021.
PR 04-JUN-1998; 98US-0088025.
PR 04-JUN-1998; 98US-0088028.
PR 04-JUN-1998; 98US-0088029.
PR 04-JUN-1998; 98US-0088030.
PR 04-JUN-1998; 98US-0088033.
PR 04-JUN-1998; 98US-0088326.
PR 05-JUN-1998; 98US-0088167.
PR 05-JUN-1998; 98US-0088202.
PR 05-JUN-1998; 98US-0088212.
PR 09-JUN-1998; 98US-0088217.
PR 09-JUN-1998; 98US-0088655.
PR 10-JUN-1998; 98US-0088722.
PR 10-JUN-1998; 98US-0088730.
PR 10-JUN-1998; 98US-0088734.
PR 10-JUN-1998; 98US-0088738.
PR 10-JUN-1998; 98US-0088740.
PR 10-JUN-1998; 98US-0088741.
PR 10-JUN-1998; 98US-0088742.
PR 10-JUN-1998; 98US-0088810.
PR 10-JUN-1998; 98US-0088811.
PR 10-JUN-1998; 98US-0088824.
PR 10-JUN-1998; 98US-0088825.
PR 11-JUN-1998; 98US-0088826.
PR 11-JUN-1998; 98US-0088858.
PR 11-JUN-1998; 98US-0088861.
PR 11-JUN-1998; 98US-0088863.
PR 11-JUN-1998; 98US-0088876.
PR 12-JUN-1998; 98US-0089090.
PR 16-JUN-1998; 98US-0089105.
PR 16-JUN-1998; 98US-0089440.
PR 16-JUN-1998; 98US-0089512.
PR 16-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089653.
PR 18-JUN-1998; 98US-0089601.
PR 18-JUN-1998; 98US-0089907.
PR 18-JUN-1998; 98US-0089908.
PR 19-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089948.
PR 19-JUN-1998; 98US-0089952.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090461.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 04-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
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PR 17-AUG-1998; 98US-0096891.
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PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.

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PR 26-AUG-1998: 98US-0098014.
PR 31-AUG-1998: 98US-0098525.
PR 16-SEP-1998: 98US-0100634.
PR 12-JAN-1999: 99US-0115565.
XX
XX (GETH ) GENENTECH INC.
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX
XX WPI: 2000-072883/06.
DR N-PSDB; AAB65029.
XX
XX Membrane-bound proteins and related nucleotide sequences
XX
XX Claim 12; Fig 149; 822pp; English.
XX
XX The invention provides membrane-bound PRO polypeptides and
XX polynucleotides encoding them. The PRO sequences of the invention were
XX identified based on extracellular domain homology screening. The PRO
XX sequences have homology with proteins including LDL receptors, TIE
XX ligands and various enzymes. The membrane-bound proteins and receptor
XX molecules are useful as pharmaceutical and diagnostic agents. Receptor
XX immunoadhesins, for instance, can be used as therapeutic agents to block
XX receptor-ligand interactions. The membrane-bound proteins can also be
XX employed for screening of potential peptide or small molecule inhibitors
XX of the relevant receptor/ligand interaction. The PRO encoding sequences
XX are useful as hybridization probes, in chromosome and gene mapping and in
XX the generation of antisense RNA and DNA. PRO nucleic acid sequences
XX will also be useful for the preparation of PRO polypeptides, especially
XX by recombinant techniques.
XX
XX Sequence 184 AA;
XX
XX Query Match 16.1%; Score 160; DB 21; Length 184;
XX Best Local Similarity 26.0%; Pred. No. 5.3e-09;
XX Matches 50; Conservative 46; Mismatches 68; Indels 28; Gaps 8;
XX
Qy 1 MKLTFMVVGLGLLAAPGFAYTV-NI---NGNDGNVDSGQQSVSINGVHINVANIDNNNG 56
Db 1 mklilvafvlvltfignqshgyevfniispsnngnv----getvtdnektaihviahg 56
Qy 57 WDSWNSLWDYENSFAATRLFSKSCIVHRMKNKDAMPISLOLDTMVKBQKCGKPGGAPPKD 116
Db 57 scsattifdykhygyiaasrvlsrracfcikmdhqnlpplnnlqwyiyekga-----ld 108
Qy 117 LMYS-----VNP--TRVEDLNTF--GPKTAGMCRGIPTYVAEEIPGNQPLYSKCYT 165
Db 109 nmfsnktytwkynpleslikdvdfllgspkleickhiplykgevventhn-vgaggcak 167
Qy 166 ADILWILRMSFC 177
Db 168 agllgilgisic 179
XX
RESULT 14
AAB65213
ID AAB65213 standard; Protein; 184 AA.
XX
XX AAB65213;
XX
XX 02-APR-2001 (first entry)
XX
XX Human PRO813 (UNQ465) protein sequence SEQ ID NO:221.
XX
XX Human; secreted and transmembrane protein; PRO; cytostatic;
XX cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
XX diagnostic assay.
XX
XX Homo sapiens.
XX
XX WO200073454-A1.
XX

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XX
XX 07-DEC-2000.
XX
XX 30-MAR-2000; 2000WO-US08439.
XX
XX 02-JUN-1999; 99WO-US12252.
XX 23-JUN-1999; 99US-0141037.
XX 07-JUL-1999; 99US-0143048.
XX 20-JUL-1999; 99US-0144758.
XX 26-JUL-1999; 99US-0145698.
XX 28-JUL-1999; 99US-0146222.
XX 17-AUG-1999; 99US-0149396.
XX 15-SEP-1999; 99WO-US21090.
XX 08-OCT-1999; 99WO-US21547.
XX 30-NOV-1999; 99US-0158663.
XX 01-DEC-1999; 99WO-US28313.
XX 16-DEC-1999; 99WO-US28301.
XX 20-DEC-1999; 99WO-US30095.
XX 05-JAN-2000; 99WO-US30911.
XX 06-JAN-2000; 2000WO-US00219.
XX 11-FEB-2000; 2000WO-US00376.
XX 18-FEB-2000; 2000WO-US03565.
XX 22-FEB-2000; 2000WO-US04341.
XX 24-FEB-2000; 2000WO-US04914.
XX 24-FEB-2000; 2000WO-US05004.
XX 02-MAR-2000; 2000WO-US05841.
XX 15-MAR-2000; 2000WO-US06884.
XX 20-MAR-2000; 2000WO-US07377.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi CU, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF;
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
XX Zhang Z;
XX
XX WPI: 2001-032160/04.
XX N-PSDB; AAF44175.
XX
XX PRO polynucleotides used to produce polypeptides used to target
XX bioactive molecules such as toxins, radiolabels or antibodies, to
XX specific cells, to cause targeted cell death -
XX
XX Claim 12; Fig 149; 935pp; English.
XX
XX The present invention describes human secreted and transmembrane PRO
XX proteins. The PRO proteins have cytostatic activity. The PRO proteins
XX can be used for targeted delivery of bioactive molecules, such as
XX toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
XX sequences, and their fragments, can be used as hybridisation probes, in
XX chromosomal and gene mapping, and in the generation of anti-sense RNA
XX and DNA. They may also be used to produce transgenic animals which are
XX used to develop and screen therapeutically useful reagents. The PRO
XX nucleotide and protein sequence can be used for tissue typing and in
XX treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
XX AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
XX in the isolation of human PRO sequences. AAF44087 to AAF44269 and
XX AAB65154 to AAB65300 represent human PRO polynucleotide and protein
XX sequences given in the exemplification of the present invention.
XX
XX Sequence 184 AA;
XX

```

```

Query Match 16.1%; Score 160; DB 22; Length 184;
Best Local Similarity 26.0%; Pred. No. 5.3e-09;
Matches 50; Conservative 46; Mismatches 68; Indels 28; Gaps 8;
Qy 1 MKLTFMVVGLGLLAAPGFAYTV-NI---NGNDGNVDSGQQSVSINGVHINVANIDNNNG 56
Db 1 mklilvafvlvltfignqshgyevfniispsnngnv----getvtdnektaihviahg 56

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CC CC -!- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC CC modified and this statement is not removed. Usage by and for commercial
CC CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC DR EMBL: AF048693; AAC18081.1; -.
CC DR EMBL: AF078096; AAC72915.1; -.
CC DR EMBL: AL034344; CAB81658.1; -.
CC DR EMBL: L12143; AAK13575.1; -.
CC DR EMBL: U13221; AAA92038.1; -.
CC DR HSSP: O63245; 2HPH.
CC DR TRANSFAC: T02471; -.
CC DR MIM: 601090; -.
CC DR MIM: 601631; -.
CC DR InterPro: IPR001766; Fork_head.
CC DR Pfam: PF00250; Fork_head; 1.
CC DR PRINTS: PR00053; FORKHEAD.
CC DR SMART: SM00339; FH; 1.
CC DR PROSITE: PS00657; FORK_HEAD_1; 1.
CC DR PROSITE: PS00658; FORK_HEAD_2; 1.
CC DR PROSITE: PS00339; FORK_HEAD_3; 1.
CC DR DNA-binding: Nuclear protein; Transcription regulation;
CC KW Disease mutation.
CC FT DNA_BIND 77 168 FORK-HEAD.
CC FT DOMAIN 28 33 POLY-ALA.
CC FT DOMAIN 169 173 POLY-ARG.
CC FT DOMAIN 194 197 POLY-PRO.
CC FT DOMAIN 262 272 POLY-SER.
CC FT DOMAIN 292 297 POLY-PRO.
CC FT DOMAIN 375 382 POLY-GLY.
CC FT DOMAIN 438 445 POLY-SER.
CC FT DOMAIN 447 456 POLY-GLY.
CC FT DOMAIN 486 495 POLY-ALA.
CC FT VARIANT 82 82 S -> T (IN ARS).
CC FT VARIANT 87 87 /FTID=VAR_007944.
CC FT VARIANT 112 112 I -> M (IN ARS).
CC FT VARIANT 126 126 F -> S (IN IGDA).
CC FT VARIANT 126 126 /FTID=VAR_007815.
CC FT VARIANT 131 131 I -> M (IN ARS).
CC FT VARIANT 131 131 S -> L (IN ARS).
CC FT CONFLICT 70 77 /FTID=VAR_007817.
CC FT CONFLICT 101 101 Q -> P (IN REF. 4).
CC FT CONFLICT 180 180 L -> Q (IN REF. 4).
CC FT CONFLICT 199 202 V -> L (IN REF. 2).
CC FT CONFLICT 426 426 RQPP -> ASPP (IN REF. 2).
CC FT CONFLICT 426 426 D -> N (IN REF. 1).
CC FT CONFLICT 553 AA; 56788 MW; 59C6FB94303ED59A CRC64;
CC SQ SEQUENCE 553 AA; 56788 MW; 59C6FB94303ED59A CRC64;

Query Match 9.28; Score 91; DB 1; Length 553;
Best Local Similarity 19.68; Pred. No. 0.39; 57; Indels 78; Gaps 9;
Matches 38; Conservative 21; Mismatches 78; Gaps 9;

QY 14 LAAPGFAYTVNTNGNDGNDGSGQGSVINGVHVA-----NIDNNNGW----- 57
DB 76 WKVPYSYALIT---MAIQNAPDKKITLNGIYQFIMDRFPFYRDKNQGNSTIRHLSL 132
QY 58 -----DSNLSLWDYENS--FAATRLFSKSKSVIHRMKNKDM 91
DB 133 NECFVKVPRDDKKPGKGSYVTLDPDSYNW---FENGSLRRRRRFRKKKDAVKKEKDR 169
QY 92 -----PSQLDLTVMVEQKCGKGGAPPKDLMYVSNPTREVDLTFGPKIACRGIP 144
DB 190 HKLEPPPPGPPPPAPPEADGNAPCPQPP-----PVLQIDIKTEN---GTC---- 233
QY 145 TYVAEEIPGNQPL 158

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DB 234 -----PSPQPL 240
RESULT 4
ID EFBI_MOUSE STANDARD; PRT; 345 AA.
AC P52795;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ephrin-B1 precursor (EPH-related receptor tyrosine kinase ligand 2)
DE (LERK-2) (ELK ligand) (ELK-L) (STRA1 protein) (CEK5 receptor ligand)
DE (CEK5-L).
GN EFNB1 OR EPLG2 OR LERK2 OR STRA1 OR EPL2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV.
RX MEDLINE=95203867; PubMed=7896266;
RA Fletcher F.A., Renshaw B., Hollingsworth T., Baum P., Lyman S.D.,
RA Jenkins N.A., Gilbert D.J., Copeland N.G., Davidson B.L.;
RT "Genomic organization and chromosomal localization of mouse Eplg2, a
RT gene encoding a binding protein for the receptor tyrosine kinase
RT elk.";
RL Genomics 24:127-132(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95377533; PubMed=7649373;
RA Bouillet P., Oulad-Abdelghani M., Vicaire S., Garnier J.M.,
RA Schaubaur B., Dollé P., Chambon P.;
RT "Efficient cloning of cDNAs of retinolic acid-responsive genes in Pl9
RT embryonal carcinoma cells and characterization of a novel mouse gene,
RT Stral (mouse LERK-2/Eplg2).";
RL Dev. Biol. 170:420-433(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95014510; PubMed=7929389;
RA Shao H., Lou L., Pandey A., Pasquale E.B., Dixit V.M.;
RT "cDNA cloning and characterization of a ligand for the Cek5 receptor
RT protein-tyrosine kinase.";
RL J. Biol. Chem. 269:26606-26609(1994).
RN [4]
RP FUNCTION
RX MEDLINE=20171264; PubMed=10704386;
RA Imondi R., Wideman C., Kaprielian Z.;
RT "Complementary expression of transmembrane ephrins and their receptors
RT in the mouse spinal cord: a possible role in constraining the
RT orientation of longitudinally projecting axons.";
RL Development 127:1397-1410(2000).
CC -!- FUNCTION: BINDS TO, AND INDUCE THE COLLAPSE OF, COMMISSURAL
CC AXONS/GROWTH CONES IN VITRO. MAY PLAY A ROLE IN CONSTRAINING THE
CC ORIENTATION OF LONGITUDINALLY PROJECTING AXONS.
CC -!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHB1 AND EPHA1.
CC -!- SUBCELLULAR LOCATION: TYPE I membrane protein.
CC -!- TISSUE SPECIFICITY: EXPRESSED ON LATERAL FLOOR PLATE CELLS,
CC SPECIFICALLY ON COMMISSURAL AXON SEGMENTS THAT HAVE PASSED THROUGH
CC THE FLOOR PLATE. EXPRESSED IN CELLS OF THE RETINAL GANGLION CELL
CC LAYER DURING RETINAL AXON GUIDANCE TO THE OPTIC DISC.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE FLOOR PLATE THROUGHOUT THE
CC PERIOD OF COMMISSURAL AXON PATHFINDING.
CC -!- PTM: INDUCIBLE PHOSPHORYLATION OF TYROSINE RESIDUES IN THE
CC CYTOPLASMIC DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

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CHM1_BOVIN
ID CHM1_BOVIN STANDARD; PRT; 335 AA.
AC P17404: P23590;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Chondromodulin-I precursor (CHM-I) (Small cartilage-derived glycoprotein) (SCGP) [Contains: Chondrosurfactant protein (CH-SP)].
DE glycoprotein)
GN CHM1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
OX
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 215-241 AND 297-317.
RX TISSUE=Fetal epiphyseal cartilage;
RX MEDLINE=9122210; PubMed=1709014;
RA Hiraki Y., Tanaka H., Inoue H., Kondo J., Kamizono A., Suzuki F.;
RT "Molecular cloning of a new class of cartilage-specific matrix, chondromodulin-I, which stimulates growth of cultured chondrocytes.";
RL Biochem. Biophys. Res. Commun. 175:971-977(1991).
RN [2]
RP SEQUENCE OF 215-335, VARIANT MFT-221, AND GLYCOSYLATION.
RC TISSUE=Nasal cartilage;
RX MEDLINE=9027643; PubMed=2351661;
RA Neame P.J., Treep J.T., Young C.N.;
RT "An 18-kDa glycoprotein from bovine nasal cartilage. Isolation and primary structure of small, cartilage-derived glycoprotein.";
RN J. Biol. Chem. 265:9628-9633(1990).
RN [3]
RP ERRATUM.
RA Neame P.J., Treep J.T., Young C.N.;
RN J. Biol. Chem. 265:22056-22056(1990).
RN [4]
RP POST-TRANSLATIONAL PROCESSING.
RX MEDLINE=21316541; PubMed=11323410;
RA Azizan A., Holaday N., Neame P.J.;
RT "Post-translational processing of bovine chondromodulin-I.";
RN J. Biol. Chem. 276:23632-23638(2001).
RN [5]
RP REVIEW.
RX MEDLINE=20367654; PubMed=10912526;
RA Hiraki Y., Shukunami C.;
RT "Chondromodulin-I as a novel cartilage-specific growth-modulating factor.";
RN Pediatr. Nephrol. 14:602-605(2000).
CC -!- FUNCTION: Bifunctional growth regulator that stimulates the growth of cultured chondrocytes in the presence of basic fibroblast growth factor (FGF) but inhibits the growth of cultured vascular endothelial cells. May contribute to the rapid growth of cartilage and vascular invasion prior to the replacement of cartilage by bone during endochondral bone development.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and secreted. Accumulated in the inter-territorial matrix of cartilage.
CC -!- TISSUE SPECIFICITY: Nasal and articular cartilage, and fetal epiphysis.
CC -!- PTM: After cleavage, the post-translationally modified CHM-I is secreted as a glycoprotein.
CC -!- PTM: Two other smaller nonglycosylated chondromodulin forms (9 kDa and 7kDa) are found either in developing articular cartilage or in chondrocytes. The 9 kDa form could be processed by an extracellular matrix-associated protease as a metalloproteinase and the 7 kDa form could be processed intracellularly.
CC -!- SIMILARITY: BELONGS TO THE CHONDROMODULIN-I FAMILY.
CC
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CC

CC EMBL; M65081; AAA30445.1; -
DR PIR; J0569; J0569.
DR PIR; A33138; A33138.
DR InterPro; IPR001729; Pulm_surfact_AP.
DR SMART; SM00019; SF_P; 1.
KW Cartilage; Glycoprotein; Transmembrane;
KW Cleavage on pair of basic residues.
FT CHAIN 1 210 CHONDROSURFACTANT PROTEIN (POTENTIAL).
FT PROPEP 211 214 POTENTIAL.
FT CHAIN 215 335 CHONDROMODULIN-I.
FT TRANSMEM 45 65 POTENTIAL.
FT DISULFID 283 287 POTENTIAL.
FT DISULFID 284 324 POTENTIAL.
FT CARBOHYD 223 223 O-LINKED.
FT CARBOHYD 236 236 O-LINKED (GLCNAC. :).
FT CARBOHYD 244 244 N-LINKED (GLCNAC. :).
FT VARIANT 221 221 V -> M.
FT CONFLICT 223 224 TT -> NE (IN REF. 2).
FT CONFLICT 256 256 P -> PD (IN REF. 2).
SQ SEQUENCE 335 AA; 37164 MW; 6D72CA8740448441 CRC64;
Query Match 8.6%; Score 85.5; DB 1; Length 335;
Best Local Similarity 22.3%; Pred. NO. 0.71;
Matches 39; Conservative 29; Mismatches 70; Indels 37; Gaps 7;
QY 7 VVCLLLGLLAAPGH-----AYTVNNG--NDGNVDSGGQSVSINGVHNVANIDN 53
DB 52 VLLLLGAIGAFYFWKSDNHHIYNVHTMSINKLOGD-----SMEIDAGNNLETFKM 103
QY 54 NNGWDSWNSIMWYENFAATRLFSKSCIVHRMKNKDAMPSLDLDTWVK-----EQKQK- 107
DB 104 SGAAEEAVEVNDPFGITGIRFAGGKCYKKAQVKARIP---EVGTMTKQSTSELEGI 160
QY 108 GPGCAPPKDLMYSVNTVRVEDLNTFGPKIAGMCRGIPITYVAEEIFCPNPOLYSKK 162
DB 161 MPVKYEENSLIWAGDQPKVNDKNSFLSSKVLLECGDLPIFWL-----KPIYPKE 208
RESULT 7
EFBL_HUMAN STANDARD; PRT; 346 AA.
AC P98172;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ephrin-B1 precursor (EPH-related receptor tyrosine kinase ligand 2) (LERK-2) (ELK ligand) (ELK-L).
GN EFN1 OR EPLG2 OR LERK2 OR EFL-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94349923; PubMed=8070404;
RA Beckmann M.P., Cerretti D.P., Baum P., Vandenbos T., James L., Farrah T., Kozlosky C., Hollingsworth T., Shilling H., Maraskovsky E., Fletcher F.A., Lhotak V., Pawson T., Lyman S.D.;
RT "Molecular characterization of a family of ligands for eph-related tyrosine kinase receptors.";
RN EMBO J. 13:3757-3762(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Davis S., Gale N.W., Aldrich T.H., Maisonnier P.C., Lhotak V., Pawson T., Goldfarb M., Vancopoulos G.D.;
RN Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Fletcher F.A., Huebner K., Shaffer L.G., Monaco A., Mueller U., Kozlosky C., Druck T., Simoneaux D.K., Fairweather N., Chelly J.,

FT CONFLICT 207 207 K -> KANFA (IN REF. 2).
SQ SEQUENCE 334 AA; 37252 MW; DAFDECA3C7D745D6 CRC64;

Query Match 8.5%; Score 84.5; DB 1; Length 334;
Best Local Similarity 20.8%; Pred. No. 0.89;
Matches 31; Conservative 29; Mismatches 64; Indels 25; Gaps 5;

QY 21 YTVNNG--NGNVDSGQSQSVISNGVHNVANIDNNWGSNSLWYDENSEFAATRLFSK 78
DB 78 YMSYNSKGLQDQ-----SWEIDAVNNLETFKMGSCAKAEIEVDFKNGITGIRFAGG 129
QY 79 KSCIVHRMKNKDAMPDLSQDLDTVMKQKCGKPGGAPP-----KDLMSYVNPTRVDELNTFG 133
DB 130 EKCYIKAVKARIP---EVGVTQKSISELEKIMPVNYESNLIWVAVDQPVKDSFSL 186
QY 134 PKIAGMCRGPIYVAEIEIPGNOPLYSKK 162
DB 187 SKILELCLGDLPIFWL-----KPMYPKE 208

RESULT 10
HYSA_PROAC STANDARD; PRT; 752 AA.
AC Q59634;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Hyaluronate lyase precursor (EC 4.2.2.1) (Hyaluronidase) (HYase).
OS Propionibacterium acnes.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Propionibacterineae; Propionibacteriaceae;
OC Propionibacterium.
OX NCBI_TaxID=1747;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=97270208; PubMed=9115089;
RA Steiner B.M., Romero-Steiner S., Cruce D., George R.;
RT "Cloning and sequencing of the hyaluronate lyase gene from
RT Propionibacterium acnes."
RL Can. J. Microbiol. 43:315-321(1997).
CC -1- CATALYTIC ACTIVITY: Hyaluronate = N 3-(4-deoxy-beta-D-gluc-4-
CC enuronosyl)-N-acetyl-D-glucosamine.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: CELL-ASSOCIATED.
CC -1- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 8.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U15927; AAA51650.1;
CC InterPro: IPR003159; Lyase_8.
CC InterPro: IPR004103; Lyase_8_C.
CC Pfam: PF02278; Lyase_8; 1.
CC Pfam: PF02884; Lyase_8_C; 1.
KW Lyase; Signal.
FT SIGNAL 1 32
FT CHAIN 33 752 HYALURONATE LYASE.
SQ SEQUENCE 752 AA; 81910 MW; 60D5DCAA691C41A4 CRC64;

Query Match 8.5%; Score 84; DB 1; Length 752;
Best Local Similarity 24.18; Pred. No. 2.7;
Matches 33; Conservative 18; Mismatches 62; Indels 24; Gaps 6;

QY 15 AAGPFAITVINGNDGNGVDSGQSVISNGVHNVANIDNNWGSNSLWYDENSEFAATR 74
DB 119 ATPGSSY-----HKDPEI-----LSACIEGLRDFCLRYNPQDEYGNWMDWED--GASR 166

ID CHM1_MOUSE STANDARD; PRT; 334 AA.
AC Q921F6; O9CXU5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Chondromodulin-I precursor (CHM-I) (Leukocyte cell-derived chemotaxin
DE 1) [Contains: Chondrosurfactant protein (CH-SP)].
GN CHM1 OR LECT1.
OS Mus musculus (Mouse).
OC Eumetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Hiraki Y., Shukunami C., Inoue H., Suzuki F.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryonic head;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
CC -1- FUNCTION: Bifunctional growth regulator that stimulates the growth
CC of cultured chondrocytes in the presence of basic fibroblast
CC growth factor (FGF) but inhibits the growth of cultured vascular
CC endothelial cells. May contribute to the rapid growth of cartilage by
CC and vascular invasion prior to the replacement of cartilage by
CC bone during endochondral bone development (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and secreted. Accumulated in the
CC interterritorial matrix of cartilage (By similarity).
CC -1- PM: After cleavage, the post-translationally modified CHM-I is
CC secreted as a glycoprotein (By similarity).
CC -1- SIMILARITY: BELONGS TO THE CHONDROMODULIN-I FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U43509; AAD00027.1;
CC EMBL; AK013975; BAB29095.1;
DR MGD; MGI:1341171; Lect1.
KW Cartilage; Glycoprotein; Transmembrane;
KW Cleavage on pair of basic residues.
FT CHAIN 1 210 CHONDROSURFACTANT PROTEIN
FT (BY SIMILARITY).
FT PROPEP 211 214
FT CHAIN 215 334
FT CHONDROMODULIN-I (BY SIMILARITY).
FT TRANSMEM 46 66
FT CARBOHYD 243 243
FT N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 108 109
FT CONFLICT 163 163
FT AK -> RE (IN REF. 2).
FT V -> A (IN REF. 2).

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EMBL: AF045017; AAC24209.1; -.
 EMBL: LI0406; AAA03159.1; -.
 EMBL: X71939; CAA50741.1; -.
 HSSP: Q63245; 2HPH.
 TRANSFAC: T02426; -.
 MGD: MGI:1347466; Foxcl.
 InterPro: IPR001766; Fork_head.
 Pfam: PF00250; Fork_head.1.
 PRINTS: PR00053; FORKHEAD.
 SMART: SM00339; FH; 1.
 PROSITE: PS00657; FORK_HEAD.1; 1.
 PROSITE: PS00658; FORK_HEAD.2; 1.
 PROSITE: PS00039; FORK_HEAD.3; 1.
 DNA-binding; Nuclear protein; Transcription regulation.
 KW DOMAIN 28 33 POLY-ALA.
 FT DNA_BIND 77 168 FORK-HEAD.
 FT DOMAIN 169 173 POLY-ARG.
 FT DOMAIN 194 197 POLY-PRO.
 FT DOMAIN 264 274 POLY-SER.
 FT DOMAIN 375 386 POLY-GLY.
 FT DOMAIN 444 451 POLY-SER.
 FT DOMAIN 453 456 POLY-GLY.
 FT DOMAIN 486 496 POLY-ALA.
 FT CONFLICT 180 187 VKDKEKG -> KKEITFIG (IN REF. 3).
 SQ SEQUENCE 553 AA; 56953 MW; 3CDD12F69CA4F217 CRC64;

Query Match 8.2%; Score 81; DB 1; Length 553;
 Best Local Similarity 19.8%; Pred. No. 3.6;
 Matches 38; Conservative 21; Mismatches 61; Indels 72; Gaps 9;

QY 14 LAAPGFAYTVNINGDGVDSGQSVSINGVHVA-----NIDNNGW-----57
 Db 76 MVKPPYSIALIT---MAIONAPDKKITLNGIYQFIMDRFPFFYEDNKKQGNQNSIRHLSL 132
 QY 58 -----DSWNSLWDYENS--FAATRLFSKKSICIVHRMKNKDM 91
 Db 133 NECFVKVPRDDKKPKGSGYWTLPDPSYNM---FENGSEFLRRRRRPPKKDAVKDKKEKGRL 189
 QY 92 PSLODLTMVKEQKGKPGAPKDLMSV-----NPTRVEDLNTGPKIAGMCRGIPTY 146
 Db 190 ----HLQEPPPPQAGROPAPAPPEQAEGSAPPQPPVRIQDIKTEN-----GTC-----235
 QY 147 VAEIPIGNPL 158
 Db 236 -----PSPQPL 242

RESULT 13
 KDGL_ARATH
 ID KDGL_ARATH STANDARD; PRT; 728 AA.
 AC Q39017;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Diacylglycerol kinase 1 (EC 2.7.1.107) (Diglyceride kinase 1)
 DE (DGL 1) (DAG kinase 1).
 GN DGL1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=96189276; PubMed=8605313;
 RA Katagiri T., Mizoguchi T., Shinozaki K.;

"Molecular cloning of a cDNA encoding diacylglycerol kinase (DGK) in Arabidopsis thaliana".
 Plant Mol. Biol. 30:647-653(1996).
 CC -|- CATALYTIC ACTIVITY: ATP + 1,2-diacylglycerol = ADP + 1,2-diacylglycerol 3-phosphate.
 CC -|- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -|- TISSUE SPECIFICITY: DETECTED IN ROOTS, SHOOTS, AND LEAVES.
 CC -|- SIMILARITY: BELONGS TO THE EUKARYOTIC DIACYLGLYCEROL KINASE FAMILY.
 CC -|- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG BINDING DOMAINS.
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EMBL: D63787; BAA09856.1; -.
 InterPro: IPR000756; DAGKa.
 InterPro: IPR001206; DAGKc.
 InterPro: IPR002219; DAG_PE-bind.
 Pfam: PF00609; DAGKa; 1.
 Pfam: PF00781; DAGKc; 1.
 ProDom: PD002939; DAGKa; 1.
 SMART: SM00109; C1; 2.
 SMART: SM00045; DAGKa; 1.
 SMART: SM00046; DAGKc; 1.
 PROSITE: PS00479; DAG_PE_BIND_DOM.1; FALSE_NEG.
 PROSITE: PS00081; DAG_PE_BIND_DOM.2; 2.
 TRANSFERASE; Kinase; phorbol-ester binding; Transmembrane; Repeat.
 FT TRANSFEM 27 48 POTENTIAL.
 FT DOMAIN 95 137 PHORBOL-ESTER AND DAG BINDING 1.
 FT DOMAIN 169 212 PHORBOL-ESTER AND DAG BINDING 2.
 FT DOMAIN 359 490 CATALYTIC (POTENTIAL).
 FT DOMAIN 507 664 CATALYTIC (POTENTIAL).
 SQ SEQUENCE 728 AA; 79970 MW; 78E4FD2252B76DA8 CRC64;

Query Match 8.1%; Score 80.5; DB 1; Length 728;
 Best Local Similarity 24.1%; Pred. No. 5.7;
 Matches 34; Conservative 27; Mismatches 57; Indels 23; Gaps 7;

QY 27 GNDG-NVDGSGQSV-----SINGVH-----NVANIDNNNGDSWNSLWDYENFAATR 74
 Db 275 GNSGNCDESTESTADTGTVNGAHAVLENSIVNNGSDSDSNGKLEKPSVKRTG 334
 QY 75 LFSKXSCIVHRMKNKDAMPSLODLT-----MVKEQKGKPGGAPPKDLMSVNPTRVE 127
 Db 335 SFGQKE--YHALRSKLKLYELADLPDARPLLVFINKKGAQRGSLRORLHLNLPQVVF 392
 QY 128 DLNTP-GPKIA-GMCRGIPTY 146
 Db 393 ELSSVQGPVEVGLFLFRKVPHF 413

RESULT 14
 F263_RAT
 ID F263_RAT STANDARD; PRT; 555 AA.
 AC O35552; O35553; O35554; O35555; O35556; O35557; O9QWQ6; O9QWQ6;
 AC O35096;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3 (6PF-2-K/Fru-2,6-P2ASE brain-type isozyme) (R6ZK) [Includes: 6-phosphofructo-2-kinase (EC 2.7.1.105); Fructose-2,6-bisphosphatase (EC 3.1.3.46)].
 GN PFKFB3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RP STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RX MEDLINE=97345796; PubMed=9202288;
RA Watanabe F., Sakai A., Furuya E.;
RT "Novel isoforms of rat brain fructose 6-phosphate 2-kinase/fructose
splicing.";
RL J. Neurochem. 69:1-9(1997).
[2]
SEQUENCE OF 61-369 FROM N.A.
RP STRAIN=WISTAR; TISSUE=Placenta;
RA Sakakibara R.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: SYNTHESIS AND DEGRADATION OF FRUCTOSE 2,6-BISPHOSPHATE.
CC -!- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
fructose 2,6-bisphosphate.
CC -!- CATALYTIC ACTIVITY: D-fructose 2,6-bisphosphate + H(2)O = D-
fructose 6-phosphate + phosphate.
CC -!- ALTERNATIVE PRODUCTS: 8 ISOFORMS; 1/RB2K1 (SHOWN HERE), 2/RB2K2,
3/RB2K3, 4/RB2K4, 5/RB2K5, 6/RB2K6, 7/RB2K7 AND 8/RB2K8; ARE
PRODUCED BY ALTERNATIVE SPLICING.
CC -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE
PHOSPHOGLYCERATE MUTASE FAMILY.

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EMBL; D87240; BAA21749.1; -
DR EMBL; D87241; BAA21750.1; -
DR EMBL; D87242; BAA21751.1; -
DR EMBL; D87243; BAA21752.1; -
DR EMBL; D87244; BAA21753.1; -
DR EMBL; D87245; BAA21754.1; -
DR EMBL; D87246; BAA21755.1; -
DR EMBL; D87247; BAA21756.1; -
DR EMBL; AB006710; BAA22048.1; -
DR HSP; P07953; 1PBT.
DR InterPro; IPR000546; 6PF2K.
DR InterPro; IPR003094; 6pfuct_kin.
DR InterPro; IPR001345; PG_mutase.
DR Pfam; PF01591; 6PF2K; 1.
DR Pfam; PF00300; PGAM; 1.
DR PRINTS; PR00991; 6PFUCTKNASE.
DR ProDom; PD002665; 6PF2K; 1.
DR PROSITE; PS00175; PG_MUTASE; 1.
KW Multifunctional enzyme; Transferase; Kinase; Hydrolase; ATP-binding;
KW Phosphorylation; Multigene family; Alternative splicing.
FT DOMAIN 1 245 6-PHOSPHOFRUCTO-2-KINASE.
FT DOMAIN 246 555 FRUCTOSE-2,6-BISPHOSPHATASE.
FT NP_BIND 42 49 ATP (BY SIMILARITY).
FT BINDING 99 99 TO FRU-6-P (BY SIMILARITY).
FT BINDING 190 190 TO FRU-6-P (BY SIMILARITY).
FT ACT_SITE 125 125 POTENTIAL.
FT ACT_SITE 155 155 POTENTIAL.
FT ACT_SITE 254 254 FORMS THE PHOSPHOISTIDINE INTERMEDIATE.
FT ACT_SITE 323 323 POTENTIAL.
FT ACT_SITE 388 388 PROTON DONOR (BY SIMILARITY).
FT VARSPPLIC 448 476 MISSING (IN ISOFORM 4, ISOFORM 5, ISOFORM
6 AND ISOFORM 8).
FT VARSPPLIC 543 555 RTVCHIFSFSY -> T (IN ISOFORM 2 AND
ISOFORM 5).
FT VARSPPLIC 535 555 PLIGRACLRVTVCHIFSFSY -> NMRSPRGAESSQKH
(IN ISOFORM 3 AND ISOFORM 6).
FT VARSPPLIC 543 555 MISSING (IN ISOFORM 7 AND ISOFORM 8).
FT CONFLICT 185 195 D -> H (IN REF. 2).
FT CONFLICT 367 367 V -> L (IN REF. 2).

SQ SEQUENCE 555 AA; 63675 MW; 45B2D090B44FCD8D CRC64;
Query Match 8.1%; Score 80; DB 1; Length 555;
Best Local Similarity 24.8%; Pred. No. 4.5;
Matches 26; Conservative 17; Mismatches 42; Indels 20; Gaps 4;
QY 79 KSCIVHRMKNKAM-----PSLQDLDTM-----VKEQKKGPGGAPPKDL---MYS 120
Db 437 ESVSTHRSEAVKIQHFASVVRPSYITELDFLSVESAKQDAKKGNPLMRNRNVTPLAS 496
QY 121 VNPTRVEDLNTFGPKIAGMCRGIPTVVAEIPG--PNQPLYSKKC 163
Db 497 PETTKPRINSFEHVASTSAALPSCPPEVPTQLFQQLLGKAC 541
RESULT 15
EFB2_MOUSE STANDARD; PRT; 336 AA.
AC P52800;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ephrin-B2 precursor (EPH-related receptor tyrosine kinase ligand 5)
DE (LERK-5) (HTK ligand) (HTK-L) (ELF-2).
GN EFN2 OR EPLG5 OR LERK5 OR HTKL OR ELF2 OR EPL5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96145238; PubMed=8559144;
RA Cerretti D.P., Vanden Bos T., Nelson N., Kozlosky C.J., Reddy P.,
RA Mareskovsky E., Park L.S., Lyman S.D., Copeland N.G.,
RA Gilbert D.J., Jenkins N.A., Fletcher R.A.;
RT "Isolation of LERK-5: a ligand of the eph-related receptor tyrosine
kinases.";
RL Mol. Immunol. 32:1197-1205(1995).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=CB57B1/6J X SJL/J;
RX MEDLINE=95199254; PubMed=7534404;
RA Bennett B.D., Zeigler F.C., Gu Q., Fendly B., Goddard A.D.,
RA Gillett N., Matthews W.;
RT "Molecular cloning of a ligand for the EPH-related receptor protein-
tyrosine kinase Htk";
RL Proc. Natl. Acad. Sci. U.S.A. 92:1866-1870(1995).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Brain;
RX MEDLINE=95379837; PubMed=7651410;
RA Bergemann A.D., Cheng H.J., Brambilla R., Klein R., Flanagan J.G.;
RT "ELF-2, a new member of the EPH ligand family, is segmentally
expressed in mouse embryos in the region of the hindbrain and newly
forming somites.";
RL Mol. Cell. Biol. 15:4921-4929(1995).
[4]
RP FUNCTION.
RX MEDLINE=20171264; PubMed=10704386;
RA Imondi R., Wideman C., Kaprielian Z.;
RT "Complementary expression of transmembrane ephrins and their receptors
in the mouse spinal cord: a possible role in constraining the
orientation of longitudinally projecting axons.";
RL Development 127:1397-1410(2000).
CC -!- FUNCTION: MAY PLAY A ROLE IN CONSTRAINING THE ORIENTATION OF
LONGITUDINALLY PROJECTING AXONS.
CC -!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASE EPHB4.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: EXPRESSED ON LATERAL FLOOR PLATE CELLS,
SPECIFICALLY ON COMMISSURAL AXON SEGMENTS THAT HAVE PASSED THROUGH
THE FLOOR PLATE. EXPRESSED IN CELLS OF THE RETINAL GANGLION CELL
LAYER DURING RETINAL AXON GUIDANCE TO THE OPTIC DISC.

Query Match	8.0%;	Score 79;	DB 1;	Length 336;
Best Local Similarity	24.6%;	Pred. No. 3;		
Matches 34; Conservative 21; Mismatches 47; Indels 36; Gaps 9;				
QY	49	ANIDNNNCWNSLNDYENSFAATRLFS--KKSCIV-----HRMVK	88	
Ddb	209	SSTDGNSAGHSGNMLLGSE-----VALFAGIASGCIIIFVIIITVLLKYYRRRHKHS	263	
QY	89	DAMPSLDLDLTMYKEOKGPGGAPKDLMSVNPTRVEDLNTFGP---KIAGMCRGIPT	145	
Ddb	264	POHTTILSLSTLATPRGGNGNCSFDV---IILPLRTAD-SVFCPHYEKYSG-DYGHPV	318	
QY	146	YVAEEIFGPNQP--LYSK	161	
Ddb	319	VIVOEMP-POSANIYYK	335	

Search completed: September 4, 2002, 17:05:10
Job time: 1136 sec

Page 11

dsr.91

XX DT 11-MAY-2000 (first entry)

XX DE Human signal peptide containing protein HSP-49 SEQ ID NO:49.

XX KW Human: signal peptide-containing protein; HSP; diagnosis; cancer;

XX KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;

XX KW antimicrobial; neutropenic; neuroprotective; cardiovascular; hepatotropic;

XX KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;

XX KW reproductive disorder; developmental disorder; arteriosclerosis;

XX KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;

XX KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;

XX KW Parkinson's disease; Huntington's diseases; ovulatory defect;

XX KW muscular dystrophy.

XX OS Homo sapiens.

XX PN WO200000610-A2.

XX PD 06-JAN-2000.

XX PF 25-JUN-1999; 99WO-US14484.

XX PR 26-JUN-1998; 98US-0090762.

XX PR 31-JUL-1998; 98US-0094983.

XX PR 01-OCT-1998; 98US-0102686.

XX PR 11-DEC-1998; 98US-0112129.

XX PA (INCY-) INCYTE PHARM INC.

XX PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;

XX PI Akarblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;

XX PI Bandman O;

XX DR WPI; 2000-160673/14.

XX DR N-PSDB; AA298157.

XX PT New human signal peptide-containing proteins useful in treatment,

XX PT prevention and diagnosis of e.g. cancer, inflammation and

XX PT cardiovascular disease -

XX PS Claim 1; Page 193-194; 327pp; English.

XX CC AA298109 to AA298242 encode AA298224 to AA2987357 which represent the

XX CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have

XX CC anticancer, anti-inflammatory, antimicrobial, neutropenic, hepatotropic,

XX CC neuroprotective, cardiovascular and antiasthmatic activities, and can

XX CC be used in gene therapy. HSPs can be used to treat or prevent disorders

XX CC associated with decreased activity or function of HSP. Antagonists of

XX CC HSP are used to treat or prevent disorders associated with increased

XX CC activity or function of HSP. Such diseases include cell proliferation

XX CC (including cancer), inflammation, cardiovascular, neurological,

XX CC reproductive or developmental disorders, (e.g. arteriosclerosis,

XX CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,

XX CC asthma, Crohn's disease, microbial or other infections, congestive or

XX CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's

XX CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP

XX CC nucleic acids can be used for the recombinant production of HSP, for

XX CC detecting HSP in standard hybridisation and amplification assays (for

XX CC diagnosis and monitoring), in gene therapy, as antisense,

XX CC triplex-forming or ribozyme therapeutics, for detecting related sequences

XX CC or genetic variations, and for chromosomal mapping. HSP are also used to

XX CC raise specific antibodies (Ab) and to screen for agonists and

XX CC antagonists (potential therapeutic agents). Ab are used to diagnose, or

XX CC monitor, HSP-related diseases (in usual immunoassays), as therapeutic

XX CC antagonists, in competitive drug screens, and for purification of HSP

XX CC from natural sources.

XX SQ Sequence 185 AA;

Query Match 99.0%; Score 984; DB 21; Length 185;

Best Local Similarity 98.9%; Pred. No. 2.6e-93;

Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYNDVDDNNAGSCQSQSVSYNNEHNVANVDDNNNGWDSW 60

DB 1 mkftivfagllgvflapalanyndvddnnnagsgqsgsvsnnehnvanvddnnngwds 60

QY 61 NSIWDYNGGFAATRLFOKKTICIVHKMKKEVMPISQSLDALVREKKLOGKGGPPPKGLM 120

DB 61 nsiwdynggfaatrifqkttcivhkmkempisqsladalvrekklqgkpgpppgkglm 120

QY 121 YSNPNKVDLDSKFGKNIANMCRGIPITYMAEQEASLFFYSGTCYTTSVLWIVDISFCG 180

DB 121 ysnpnkvdldskfkgknianmcrgiptymaeqeasllfysgtcyttsvlwiwdisfcg 180

QY 181 DTVEN 185

DB 181 dtven 185

RESULT 4

AA298109

ID AA298109 standard; protein; 185 AA.

XX AA298109

AC AA298109

XX AA298109

DT 05-APR-2000 (first entry)

XX AA298109

DE Membrane-bound protein PRO1005.

XX AA298109

KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;

KW pharmaceutical; receptor immunoadhesin; gene mapping.

XX Homo sapiens.

XX WO9963088-A2.

XX 09-DEC-1999.

XX 02-JUN-1999; 99WO-US12252.

XX 02-JUN-1999; 98US-0087607.

XX 02-JUN-1999; 98US-0087609.

XX 02-JUN-1999; 98US-0087759.

XX 03-JUN-1998; 98US-0087827.

XX 04-JUN-1998; 98US-0088021.

XX 04-JUN-1998; 98US-0088025.

XX 04-JUN-1998; 98US-0088028.

XX 04-JUN-1998; 98US-0088029.

XX 04-JUN-1998; 98US-0088030.

XX 04-JUN-1998; 98US-0088033.

XX 05-JUN-1998; 98US-0088326.

XX 05-JUN-1998; 98US-0088167.

XX 05-JUN-1998; 98US-0088202.

XX 05-JUN-1998; 98US-0088212.

XX 05-JUN-1998; 98US-0088217.

XX 09-JUN-1998; 98US-0088655.

XX 10-JUN-1998; 98US-0088722.

XX 10-JUN-1998; 98US-0088730.

XX 10-JUN-1998; 98US-0088734.

XX 10-JUN-1998; 98US-0088738.

XX 10-JUN-1998; 98US-0088740.

XX 10-JUN-1998; 98US-0088741.

XX 10-JUN-1998; 98US-0088742.

XX 10-JUN-1998; 98US-0088810.

XX 10-JUN-1998; 98US-0088811.

XX 10-JUN-1998; 98US-0088824.

XX 10-JUN-1998; 98US-0088825.

XX 10-JUN-1998; 98US-0088826.

XX 11-JUN-1998; 98US-0088858.

XX 11-JUN-1998; 98US-0088861.

XX 11-JUN-1998; 98US-0088863.

XX 11-JUN-1998; 98US-0088876.

XX 12-JUN-1998; 98US-0088909.

QY 121 YSNPNKVDLSKFGKNIANMCRGIPTYMAEEMQASLFFYSGTCTTSLVLIWVIDISFCG 180
 Db 121 ysnpnkvadlskfgkniannmcrgiptymaeemqaslfyysgtctttsvlwivdisfcg 180
 QY 181 DTVEN 185
 Db 181 dtven 185
 RESULT 5
 AAB65209
 ID AAB65209 standard; Protein; 185 AA.
 AC AAB65209;
 XX
 XX 02-APR-2001 (first entry)
 XX
 DE Human PRO1005 (UNC489) protein sequence SEQ ID NO:211.
 XX
 XX Human; secreted and transmembrane protein; PRO; cytostatic;
 KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
 KW diagnostic assay.
 XX
 OS Homo sapiens.
 XX
 PN WO200073454-A1.
 XX
 XX 07-DEC-2000.
 XX
 XX 30-MAR-2000; 2000WO-US08439.
 XX
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 07-JUL-1999; 99US-0143048.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 28-JUL-1999; 99US-0146222.
 PR 17-AUG-1999; 99US-0149396.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 08-OCT-1999; 99US-0158663.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;
 XX
 DR WPI; 2001-032160/04.
 DR N-PSDB; AAF44169.
 XX
 XX PRO polynucleotides used to produce polypeptides used to target
 PT bioactive molecules such as toxins, radiolabels or antibodies, to
 PT specific cells, to cause targeted cell death -
 XX
 PS Claim 12; Fig 139; 935pp; English.

CC The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
 CC can be used for targeted delivery of bioactive molecules, such as
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA
 CC and DNA. They may also be used to produce transgenic animals which are
 CC used to develop and screen therapeutically useful reagents. The PRO
 CC nucleotide and protein sequence can be used for tissue typing and in
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
 CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.

XX Sequence 185 AA;

Query Match 99.0%; Score 984; DB 22; Length 185;
 Best Local Similarity 98.9%; Pred. No. 2.6e-93;
 Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYINVDNDNNAGSGQSVSVNNEHHVANYVNDNNNGWDSW 60
 Db 1 mkftivfagllgvflapalanyinvndnnnagsgqsvsvnnhnnvnyvndnnngwdsw 60

QY 61 NSIWDYGNCFATRLFOKKTCIVHKMKKEVMPISIGSLDALVKEKKLOGKGGPPPKGLM 120
 Db 61 nsiwdygnngfaatrifqkktclvkhmkkevmpisigslalvkekklqgkpggpppkglm 120

QY 121 YSNPNKVDLSKFGKNIANMCRGIPTYMAEEMQASLFFYSGTCTTSLVLIWVIDISFCG 180
 Db 121 ysnpnkvadlskfgkniannmcrgiptymaeemqaslfyysgtctttsvlwivdisfcg 180

QY 181 DTVEN 185
 Db 181 dtven 185

RESULT 6

AAB50957
 ID AAB50957 standard; Protein; 185 AA.

XX AAB50957;

XX 21-MAR-2001 (first entry)

XX Human PRO1005 protein.

XX Human; PRO; cytostatic; neurotropic; neuroprotective; respiratory general;
 KW antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
 KW PRO agonist; cancer; inflammatory disorder; immunological disorder.

OS Homo sapiens.

XX WO200073348-A2.

XX 07-DEC-2000.

XX 30-MAY-2000; 2000WO-US14941.

XX 02-JUN-1999; 99WO-US12252.

PR 22-JUN-1999; 99US-0140650.

PR 23-JUN-1999; 99US-0141037.

PR 20-JUL-1999; 99US-0144758.

PR 01-SEP-1999; 99WO-US20111.

PR 08-SEP-1999; 99WO-US20594.

PR 29-OCT-1999; 99US-0162506.

PR 30-NOV-1999; 99WO-US28313.

PR 01-DEC-1999; 99WO-US28634.

PR 02-DEC-1999; 99WO-US28551.

PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30999.

PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000US-0187202.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 XX (GETH) GENENTECH INC.
 XX
 XX Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
 PI Shelton DL, Smith V, Watanabe CK, Wood WI;
 XX WPI; 2001-016509/02.
 DR N-PSDB; AAC91559.
 XX
 XX Twenty eight nucleic acids encoding PRO polypeptides which are useful
 PT for treating various tumors, e.g. breast cancer, and other
 PT inflammatory, angiogenic and immunological disorders -
 XX
 XX Claim 31; Fig 14; 188pp; English.
 XX
 XX The present sequence is one of twenty eight novel PRO polypeptides. The
 CC PRO polypeptides and their agonists, including antibodies, peptides, and
 CC small molecule agonists, may be used to treat various tumours, e.g.,
 CC cancers such as breast cancer, ovarian cancer, renal cancer, colorectal
 CC cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,
 CC central nervous system cancer, melanoma or leukaemia. They are also
 CC useful for treating other disorders such as neuronal, glial, astrocytic,
 CC hypothalamic and other glandular, macrophagal, epithelial, stromal and
 CC blastocoeleic disorders, and inflammatory, angiogenic and immunological
 CC disorders.
 XX
 XX Sequence 185 AA;
 SQ
 Query Match 99.0%; Score 984; DB 22; Length 185;
 Best Local Similarity 98.9%; Pred. No. 2.6e-93;
 Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MKFTIVFAGLLGVFLAPALANYINVDNDNNAGSQSVSVNNEHNVANVDNNGWDSW 60
 DB 1 mkftivfagllgvflapalanyninvndnnagsgqsvsvnnhnavndnnngwds 60
 QY 61 NSIWDYNGNGFAATRLFQKKTCTIVHKMKKEVMPISQSLDALVKEKKLGKGGPPPKGLM 120
 DB 61 nsiwdyngngfaatrifqkktctivhkmknevmpsigsldalvkekklgkpgppkglm 120
 QY 121 YSVNPNKVDLDSKFGKNANMCRGIPTYMAEEMQESLFFYSGTCYTTSVLWIVDISFCG 180
 DB 121 ysvnpnkvdldskfgknanmcrigptymaeemqeslffysgtcyttsvlwiwdisfcg 180
 QY 181 DTVEN 185
 DB 181 dtven 185
 RESULT 7
 AAB38329
 ID AAB38329 standard; Protein; 186 AA.
 XX
 AC AAB38329;
 XX
 DT 31-JAN-2001 (first entry)
 XX
 XX Human secreted protein encoded by gene 9 clone HNSAD53.
 DE
 XX Immunosuppressive; antiarthritic; antirheumatic; antiproliferative;
 KW cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective;
 KW neutropic; antibacterial; virucide; fungicide; ophthalmological; human;

KW vulnery; gene therapy; infection; secreted protein.
 XX Homo sapiens.
 XX W0200061623-A1.
 XX 19-OCT-2000.
 XX 06-APR-2000; 2000WO-US08979.
 XX 09-APR-1999; 99US-0128693.
 PR 26-APR-1999; 99US-0130991.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Ruben SM, Ni J, Komatsoulis GA, Rosen CA, Soppet DR, Shi Y;
 PI Lafleur DW, Olsen HS, Ebner R, Florence KA, Moore PA, Birse CE;
 PI Young PE;
 XX WPI; 2000-647418/62.
 XX New nucleic acid molecules encoding 62 human secreted proteins for
 PT diagnosing, preventing, treating or ameliorating medical conditions and
 PT used as food additives or preservatives -
 XX
 XX Claim 11; Page 598; 716pp; English.
 XX
 XX Sequences AAB38321-B38396 represent the amino acid sequences of 62
 CC human secreted proteins encoded by the genes AAC69512-C69587. The genes
 CC and proteins are useful for preventing, ameliorating or treating medical
 CC conditions, e.g. by protein or gene therapy. The genes are isolated from
 CC a range of human tissues disclosed in the specification. The nucleic
 CC acids, proteins, antibodies and (antagonists are useful in the
 CC diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.
 CC rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms
 CC of the breast or liver; (c) cardiovascular disorders e.g. cardiac
 CC arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e)
 CC angiogenesis; (f) nervous system disorders e.g. Alzheimer's disease; (g)
 CC infections caused by bacteria, viruses and fungi; and (h) ocular
 CC disorders e.g. corneal infection. The polypeptides can also be used to
 CC aid wound healing and epithelial cell proliferation, to prevent skin
 CC aging due to sunburn, to maintain organs before transplantation, for
 CC supporting cell culture of primary tissues, to regenerate tissues and in
 CC chemotaxis.
 XX
 XX Sequence 186 AA;
 SQ
 Query Match 99.0%; Score 984; DB 21; Length 186;
 Best Local Similarity 98.9%; Pred. No. 2.7e-93;
 Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MKFTIVFAGLLGVFLAPALANYINVDNDNNAGSQSVSVNNEHNVANVDNNGWDSW 60
 DB 1 mkftivfagllgvflapalanyninvndnnagsgqsvsvnnhnavndnnngwds 60
 QY 61 NSIWDYNGNGFAATRLFQKKTCTIVHKMKKEVMPISQSLDALVKEKKLGKGGPPPKGLM 120
 DB 61 nsiwdyngngfaatrifqkktctivhkmknevmpsigsldalvkekklgkpgppkglm 120
 QY 121 YSVNPNKVDLDSKFGKNANMCRGIPTYMAEEMQESLFFYSGTCYTTSVLWIVDISFCG 180
 DB 121 ysvnpnkvdldskfgknanmcrigptymaeemqeslffysgtcyttsvlwiwdisfcg 180
 QY 181 DTVEN 185
 DB 181 dtven 185
 RESULT 8
 AAB69974
 ID AAB69974 standard; Protein; 194 AA.
 XX

AAW69974;
16-NOV-1998 (first entry)
Cancer associated protein.
Cancer; PCR; Northern blotting; ribonuclease protection assay;
diagnosis; metastatic cancer.
Synthetic.
WO9837187-A1.
27-AUG-1998.
18-FEB-1998; 98WO-JP00667.
21-FEB-1997; 97JP-0052508.
(TAKI) TAKARA SHUZO CO LTD.
Asada K, Hino F, Kato I, Mukai H, Yoshikawa Y;
WPI; 1998-467552/40.
Detection of cancer cells in tissue samples - by changes in mRNA
expression compared to normal tissue of specific cancer-associated
gene sequences
Claim 14; Page 64-65; 92pp; Japanese.
The cancer associated proteins AAW69974-W69976 where used in the method
of the invention to detect cancer cells in tissue samples or biological
fluids. They are detected by monitoring the change in mRNA expression
as compared to normal tissue of one or more cancer-associated genes
whose cDNA stringently hybridises to cancer associated gene nucleic acid
fragments. The change in expression may be an increase or a decrease
compared to normal tissue. The mRNA expression may be determined by
PCR, Northern blotting or ribonuclease protection assay, or by
determining the change in the amount of protein encoded by the gene(s) as
compared to normal tissue, for example by using a labelled antibody
recognising the protein. Detection of cancer cells for cancer diagnosis,
including detection of metastatic cancer cells in tissues other than the
primary tumour site.
Sequence 194 AA;
Query Match 99.0%; Score 984; DB 19; Length 194;
Best Local Similarity 98.9%; Pred. No. 2.8e-93;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKFTTIVFAGLLGVFLAPALANYINDVNDNNAGSQSQSVSVNNEHNVANVDNNNGWDSW 60
DB 10 mkfttivyagllgvflapalanyninvndnnnagsgqsvsvnnhnvanvndnnngwds 69
QY 61 NSIWDYNGGFAATRLFGKTCIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPPKGLM 120
DB 70 nsiwdynggfaatrllfgkktcivhkmkevmvpsiqslalvkekklogkpgppgpgkglm 129
QY 121 YSVNPNKVDLLSKFGKNIANMCRGIPTYMAEEMQEAISFFYSYTCYTSVLWIVDISFCG 180
DB 130 ysvnpkvddllskfgknianmcrgiptymaeemqeaiffysgcyttsvliwivdisfcg 189
QY 181 DTVEN 185
DB 190 dtven 194
RESULT 9
AAW6591
ID AAY76591 standard; Protein; 194 AA.
XX

AAW76591;
10-APR-2000 (first entry)
Human ovarian tumor EST fragment encoded protein 87.
Expressed sequence tag; EST; human; ovarian tumor; anticancer;
gene therapy; treatment.
Homo sapiens.
DE19817557-A1.
21-OCT-1999.
09-APR-1998; 98DE-1017557.
09-APR-1998; 98DE-1017557.
(META-) METAGEN GES GENOMFORSCHUNG MBH.
Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pillarsky C, Dahl E;
WPI; 1999-591920/51.
N-PSDB; AAZ77487.
New nucleic acid sequences expressed in ovarian, and some other, cancer
tissues, and derived polypeptides, for treatment of ovarian cancer and
identification of therapeutic agents -
Claim 25; Page 279; 310pp; German.
This invention describes novel nucleic acid (cDNA) sequences (A) which
have anticancer activity and are highly expressed in ovarian tumor
tissue (and some also in testis and breast cancer tissue). The products
of the invention can be used for gene therapy. (A) are used (i) for
recombinant expression of polypeptides (B) and (ii) to isolate complete
genes. (B) are used (i) to identify agents suitable for treatment of
ovarian cancer; (ii) directly for treating this form of cancer
(including expression from gene therapy vectors) and (iii) for generation
of specific antibodies. (A) are identified by assembling ESTs (expressed
sequence tags) from a particular tissue type before comparison of
expression patterns. This allows a significantly longer fragment of the
gene to be revealed, so should reduce the number of failures associated
with the fact that ESTs from different libraries may represent different
parts of the same unknown gene, distorting the estimated frequency of
occurrence in a particular tissue. AAY76505-Y76638 represent protein
fragments encoded by the human ovarian tumor cDNA library derived EST
fragments represented in AAZ77450-Z77572.
Sequence 194 AA;
Query Match 99.0%; Score 984; DB 20; Length 194;
Best Local Similarity 98.9%; Pred. No. 2.8e-93;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKFTTIVFAGLLGVFLAPALANYINDVNDNNAGSQSQSVSVNNEHNVANVDNNNGWDSW 60
DB 10 mkfttivyagllgvflapalanyninvndnnnagsgqsvsvnnhnvanvndnnngwds 69
QY 61 NSIWDYNGGFAATRLFGKTCIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPPKGLM 120
DB 70 nsiwdynggfaatrllfgkktcivhkmkevmvpsiqslalvkekklogkpgppgpgkglm 129
QY 121 YSVNPNKVDLLSKFGKNIANMCRGIPTYMAEEMQEAISFFYSYTCYTSVLWIVDISFCG 180
DB 130 ysvnpkvddllskfgknianmcrgiptymaeemqeaiffysgcyttsvliwivdisfcg 189
QY 181 DTVEN 185
DB 190 dtven 194
RESULT 9
AAW76591
ID AAY76591 standard; Protein; 194 AA.
XX

RESULT 10
AA166690
ID AAY66690 standard; protein; 184 AA.
XX
AC AAY66690;
XX
DT 05-APR-2000 (first entry)
XX
DE Membrane-bound protein PRO813.
XX
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW Pharmaceutical; receptor immunoadhesin; gene mapping.
XX
OS Homo sapiens.
XX
PN W09963088-A2.
XX
PD 09-DEC-1999.
XX
PF 02-JUN-1999; 99WO-US12252.
XX
PR 02-JUN-1998; 98US-0087607.
PR 02-JUN-1998; 98US-0087609.
PR 02-JUN-1998; 98US-0087755.
PR 03-JUN-1998; 98US-0087827.
PR 04-JUN-1998; 98US-0088021.
PR 04-JUN-1998; 98US-0088025.
PR 04-JUN-1998; 98US-0088028.
PR 04-JUN-1998; 98US-0088030.
PR 04-JUN-1998; 98US-0088033.
PR 04-JUN-1998; 98US-0088326.
PR 05-JUN-1998; 98US-0088167.
PR 05-JUN-1998; 98US-0088202.
PR 05-JUN-1998; 98US-0088212.
PR 05-JUN-1998; 98US-0088217.
PR 09-JUN-1998; 98US-0088655.
PR 10-JUN-1998; 98US-0088722.
PR 10-JUN-1998; 98US-0088730.
PR 10-JUN-1998; 98US-0088734.
PR 10-JUN-1998; 98US-0088738.
PR 10-JUN-1998; 98US-0088740.
PR 10-JUN-1998; 98US-0088741.
PR 10-JUN-1998; 98US-0088742.
PR 10-JUN-1998; 98US-0088810.
PR 10-JUN-1998; 98US-0088811.
PR 10-JUN-1998; 98US-0088824.
PR 10-JUN-1998; 98US-0088825.
PR 11-JUN-1998; 98US-0088826.
PR 11-JUN-1998; 98US-0088828.
PR 11-JUN-1998; 98US-0088858.
PR 11-JUN-1998; 98US-0088861.
PR 11-JUN-1998; 98US-0088863.
PR 12-JUN-1998; 98US-0088876.
PR 12-JUN-1998; 98US-0089090.
PR 16-JUN-1998; 98US-0089105.
PR 16-JUN-1998; 98US-0089440.
PR 16-JUN-1998; 98US-0089512.
PR 16-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089653.
PR 18-JUN-1998; 98US-0089801.
PR 18-JUN-1998; 98US-0089907.
PR 18-JUN-1998; 98US-0089908.
PR 19-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089948.
PR 19-JUN-1998; 98US-0089952.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090461.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 02-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.

[illegible]

AC	AAE04211;
XX	
DT	09-AUG-2001 (first entry)

Human gene 14 encoded secreted protein HNSAA27, SEQ ID NO:66.

Human: secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; gene therapy; endocrine disorder; infection; wound healing; vulnery; cell culture; chemotaxis; food additive; chromosome 2; binding partner identification.

XX
DN
W0300154177 30

XX
PF 25-JAN-2001; 2001WO-US02687.

PA (HYSE-) HYSEO INC.

WPI: 2001-476164/51

Isolated polypeptide for treatment of diseases, diagnostics, raising

PS Claim 20; Page 814-815; 1275pp; English.

CCC biodiversity and for nutritional purposes. The present sequence is a CCC protein of the invention.

Claim 11; Page 444; 509pp; English.

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Thu Sep 5 11:23:27 2002

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 17:05:07 : Search time 34.18 Seconds
(without alignments)
209.570 Million cell updates/sec

Title: US-09-821-726-13
Perfect score: 994
Sequence: 1 MKFTIVFAGLLGVFLAPALA.....YTTSLVLIWIDISFCGDTVEN 185

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	984	99.0	199	1 CLIP_HUMAN	Q9ns71 homo sapien
2	629	63.3	184	1 CLIP_MOUSE	Q9cr36 mus musculu
3	95.5	9.6	719	1 NRPL_YEAST	P32770 saccharomyc
4	91	9.2	623	1 PNT1_DROME	P51022 drosophila
5	91	9.2	718	1 PNT2_DROME	P51023 drosophila
6	84.5	8.5	189	1 YHCH_BACSU	P54598 bacillus su
7	82.5	8.3	858	1 YHCH_DICDI	Q03101 dictyosteli
8	82	8.2	220	1 NUOB_ECOLI	P33598 escherichia
9	81	8.1	666	1 YEAF_YEAST	P40002 saccharomyc
10	81	8.1	828	1 MRKC_KLEPN	P21647 klebsiella
11	80	8.0	695	1 DVLL_MOUSE	P51141 mus musculu
12	80	8.0	695	1 DVLL_RAT	Q9wvb9 rattus norv
13	80	8.0	749	1 MADL_YEAST	P40957 saccharomyc
14	80	8.0	954	1 XYNA_RUMFL	P29126 ruminococcu
15	79	7.9	535	1 ARSB_FELCA	P37272 felis silve
16	77.5	7.8	1178	1 PH81_YEAST	P17442 saccharomyc
17	77.5	7.8	1341	1 YL78_YEAST	Q05854 saccharomyc
18	77	7.7	1675	1 POL_RTBVP	P27502 rice tungro
19	75.5	7.6	191	1 PSCP_MACMU	P46192 clostridium
20	75.5	7.6	296	1 DPSP_CLOPA	P14164 saccharomyc
21	75.5	7.6	731	1 BAF1_YEAST	Q52657 rickettsia
22	75.5	7.6	2021	1 OMPA_RICCN	P18160 dictyosteli
23	75	7.5	1584	1 KYK1_DICDI	Q9pqy2 ureaplasma
24	74.5	7.5	457	1 YL62_UREPA	P47116 saccharomyc
25	74.5	7.5	818	1 PTK2_YEAST	P36168 saccharomyc
26	74.5	7.5	1195	1 YK76_YEAST	P22335 lycopersico
27	74	7.4	301	1 HSF2_LYCP	Q04956 plasmodium
28	74	7.4	1956	1 ATX1_PLAFA	P15848 homo sapien
29	73.5	7.4	533	1 ARSB_HUMAN	P04931 plasmodium
30	73.5	7.4	537	1 ARP_PLAFA	Q03825 saccharomyc
31	73.5	7.4	758	1 YN38_YEAST	P40467 saccharomyc
32	73.5	7.4	964	1 YIN0_YEAST	P14248 plasmodium
33	73.5	7.4	2452	1 RPBI_PLAFD	

34	73	7.3	1026	1 STAU_DROME	P25159 drosophila
35	72.5	7.3	398	1 LIPG_HUMAN	P07098 homo sapien
36	72.5	7.3	819	1 SWEL_YEAST	P32944 saccharomyc
37	72.5	7.3	920	1 NIA_CICIN	P43101 cichorium i
38	72.5	7.3	1238	1 YN13_YEAST	P53840 saccharomyc
39	72.5	7.3	1858	1 P3K2_DICDI	P54674 dictyosteli
40	72.5	7.3	2249	1 OMPA_RICRI	P15921 rickettsia
41	72	7.2	334	1 CHM1_HUMAN	O75829 homo sapien
42	72	7.2	335	1 CHM1_BOVIN	P17404 bos taurus
43	72	7.2	721	1 GLGX_MYCTU	Q10767 mycobacteri
44	71.5	7.2	340	1 BYRL_SCHPO	P10506 schizosacch
45	71.5	7.2	661	1 WHI3_YEAST	P34761 saccharomyc

ALIGNMENTS

RESULT	1
CLIP_HUMAN	
ID	CLIP_HUMAN
STANDARD:	PRT; 199 AA.
AC	Q9NS71;
DT	01-MAR-2002 (Rel. 41, Created)
DT	01-MAR-2002 (Rel. 41, Last sequence update)
DT	01-MAR-2002 (Rel. 41, Last annotation update)
DE	CAII protein.
GN	CAII.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Stomach;
RX	MEDLINE=20296773; PubMed=10835488;
RA	Yoshikawa Y., Mukai H., Hino F., Asada K., Kato I.;
RT	"Isolation of two novel genes, down-regulated in gastric cancer.";
RL	Jpn. J. Cancer Res. 91:459-463(2000).
CC	-I- TISSUE SPECIFICITY: Expressed in stomach. No expression is
CC	detected in cancer tissue or gastric cancer cell lines.
CC	-----
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL: AB039886; BAA92433.1; -
DR	MTM: 606402; -
SQ	SEQUENCE 199 AA; 21999 MW; C095B8B9A1338D7A CRC64;

Query Match	99.0%;	Score	984;	DB 1;	Length	199;
Best Local Similarity	98.9%;	Pred. No.	4e-84;			
Mismatches	1;	Indels	0;	Gaps	0;	
Matches	183;	Conservative				
Qy	1	MKFTIVFAGLLGVFLAPALANYINVDNDNNAGSGQOSVSVNNEHNVANVDNNGWDSW	60			
Db	15	MKFTIVFAGLLGVFLAPALANYINVDNDNNAGSGQOSVSVNNEHNVANVDNNGWDSW	74			
Qy	61	NSIDWYNGNGFAATRLFOKKTICIVHKMKKEYMPSIQSLDALVKEKKLOGKPGGPPKGLM	120			
Db	75	NSIDWYNGNGFAATRLFOKKTICIVHKMKKEYMPSIQSLDALVKEKKLOGKPGGPPKGLM	134			
Qy	121	YSVNPKNYVDDLKSGKGNKNTANMCRGIPTMYMAEMOEASIFFYSGTCYTTSVLWIVDISFCG	180			
Db	135	YSVNPKNYVDDLKSGKGNKNTANMCRGIPTMYMAEMOEASIFFYSGTCYTTSVLWIVDISFCG	194			
Qy	181	DTVEN 185				
Db	195	DTVEN 199				

RESULT 2
 CLIP_MOUSE
 ID C9CR36; Q9D7K7; Q9CTZ5; PRT; 184 AA.
 AC 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Call protein homolog.
 GN CALI.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC STRAIN=C57BL/6J; TISSUE=Stomach, and Tongue;
 RP MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Konno S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto S.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
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 CC -----
 DR EMBL; AK008990; BAB26010.1;
 DR EMBL; AK008622; BAB25784.1;
 DR EMBL; AK008641; BAB25801.1;
 DR EMBL; AK008647; BAB25805.1;
 DR EMBL; AK008722; BAB25856.1;
 DR EMBL; AK008745; BAB25872.1;
 DR EMBL; AK008933; BAB25975.1;
 DR EMBL; AK008956; BAB25988.1;
 DR EMBL; AK009145; BAB26103.1;
 DR EMBL; AK019050; BAB31525.1;
 FT CONFLICT 113 113 P -> L (IN REF. 1; BAB26103).
 SQ SEQUENCE 184 AA; 20134 MW; 288982F040FFA8B CRC64;

Query Match 63.3%; Score 629; DB 1; Length 184;
 Best Local Similarity 62.7%; Pred. No. 2.6e-51;
 Matches 116; Conservative 25; Mismatches 40; Indels 4; Gaps 3;

QY 1 MKETIVFAGLIGVFLAPALANYLDVNDNNAGSGQSVSNVNEHNVDNNNGWDS 59
 DB 1 MKLTFVVGLLGLAAGFA-YTVNTNGDNGVDGSGQSVSNVNHVNDNNNGWDS 59
 QY 60 WNSWDYNGCFATRLFPQKTCITVHKMKVEYMPSTQSLDALYKVKKLOGKGGPGPPKGL 119
 DB 60 WNSLWDYNSFAATRLFSKKSCIVHRMKNKDAMPSTQLDLDTMTVKEQK--CKGPGGAPPKDL 117

QY 120 MYSVNPKNVDLSKFGKNIANMCRGIPYMAEEMQASLFFYSGTCTYSVLWIVDISPC 179
 DB 118 MYSVNPTRVEDLNTFGPKIAGMCRGIPYVABEIPGNQPLYSKKCYTADILWILMSFC 177
 QY 180 GDIVE 184
 DB 178 GTSVE 182
 RESULT 3
 NRPI_YEAST
 ID NRPI_YEAST STANDARD; PRT; 719 AA.
 AC P32770; Q12228;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Asparagine-rich protein (ARP protein).
 DE NRPI OR ARP1 OR ARP OR YDL167C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RC STRAIN=AH22;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93247548; PubMed=8483449;
 RA Wehner E.P., Rao E., Brendel M.;
 RT "Molecular structure and genetic regulation of SFA, a gene
 RT responsible for resistance to formaldehyde in Saccharomyces
 RT cerevisiae, and characterization of its protein product.";
 RL Mol. Gen. Genet. 237:351-358(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RA Pohl T.M.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: CONTAINS 2 RANBP2-TYPE ZINC FINGERS.
 CC -!- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
 CC -----
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 CC -----
 DR EMBL; X68020; CAA48159.1;
 DR EMBL; Z67750; CAA91579.1;
 DR EMBL; Z74215; CAA98741.1;
 DR PIR; S31139; S31139.
 DR HSPP; P04170; GRXN.
 DR SGD; S0002326; NRPI.
 DR InterPro; IPR000504; RRM.
 DR InterPro; IPR001876; Znf-RanBP.
 DR Pfam; PF00076; rrm; 1.
 DR Pfam; PF00641; zf-RanBP; 2.
 DR SMART; SM00360; RRM; 1.
 DR SMART; SM00547; Znf_RBZ; 2.
 DR PROSITE; PS0102; RRM; 1.
 DR PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.
 DR PROSITE; PS01358; ZF_RANBP2_1; 2.
 DR PROSITE; PS01999; ZF_RANBP2_2; 2.
 KW Nuclear protein; zinc-finger; RNA-binding; Repeat.
 FT DOMAIN 226 322 RNA-BINDING (RRM).
 FT ZN_FING 355 384 RANBP2-TYPE 1.
 FT ZN_FING 581 610 RANBP2-TYPE 2.
 FT DOMAIN 490 564 ASN-RICH.
 FT CONFLICT 493 493 I -> N (IN REF. 1).
 SQ SEQUENCE 719 AA; 79299 MW; ADA9BC09FD582669 CRC64;

Query Match 9.6%; Score 95.5; DB 1; Length 719;

[illegible]

RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke K., Davenport L.B., Davies P.,
RA De Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K.A., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kimons I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RL The genome sequence of *Drosophila melanogaster*.
RN [3]
RP SEQUENCE OF 551-708 FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL
STAGE.
RC STRAIN=CANTON-S; TISSUE=Larva;
RX MEDLINE=92249640; PubMed=1577186;
RA Chen T., Bunting M., Karim F.D., Thummel C.S.;
RT "Isolation and characterization of five *Drosophila* genes that encode
RL an ets-related DNA binding domain."
RL Dev. Biol. 151:176-191(1992).
CC -!- FUNCTION: REQUIRED FOR GLIAL-NEURONAL CELL INTERACTIONS AT THE
CC VENTRAL MIDLINE WHICH ARE NECESSARY FOR THE PROPER ELABORATION OF
CC COMMISSURES IN THE EMBRYONIC CNS.
CC -!- SUBCELLULAR LOCATION: Nuclear (potential).
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; P1 (AC P51022) AND P2 (SHOWN
CC HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN A COMPLEX DYNAMIC PATTERN IN
CC EARLY EMBRYOS, INCLUDING THE MIDLINE AND MIDLINE GLIAL CELLS.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT DEVELOPMENT WITH LOWER
CC LEVELS DURING LARVAL DEVELOPMENT.
CC -!- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC -!- SIMILARITY: CONTAINS 1 POINTED (PNT) DOMAIN.

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CC or send an email to license@isb-sib.ch).

CC EMBL; X69167; CAA48917.1;
CC EMBL; AE003742; AAF56125.1; --

DR EMBL; M88472; AAC34200.1; --
DR HSSP; P14921; 2STT.
DR FlyBase; FBgn0003118; pnt.
DR InterPro; IPR000418; ETS.
DR InterPro; IPR003341; HSF_ETs.
DR Pfam; PF00178; Ets; 1.
DR Pfam; PF02198; SAM_PNT; 1.
DR PRINTS; PR00454; ETSDOMAIN.
DR SMART; SM00413; ETS; 1.
DR SMART; SM00251; SAM_PNT; 1.
DR PROSITE; PS00345; ETS_DOMAIN_1; 1.
DR PROSITE; PS00346; ETS_DOMAIN_2; 1.
DR PROSITE; PS00061; ETS_DOMAIN_3; 1.
KW DNA-binding; Nuclear protein; Developmental protein;
KW Alternative splicing.
FT DOMAIN 166 250 POINTED.
FT DOMAIN 341 347 POLY-GLN.
FT DOMAIN 359 362 POLY-ASN.
FT DOMAIN 389 393 POLY-ASN.
FT DOMAIN 405 415 POLY-ASN.
FT DOMAIN 418 421 POLY-ALA.
FT DOMAIN 481 484 POLY-GLY.
FT DNA_BIND 610 690 ETS-DOMAIN.
FT CONFLICT 133 135 DIS -> VYP (IN REF. 1).
SQ SEQUENCE 718 AA; 77683 MW; FD6AFD0F4BCD69C5 CRC64;

Query Match 9.2%; Score 91; DB 1; Length 718;
Best Local Similarity 27.1%; Pred. No. 0.85;
Matches 38; Conservative 21; Mismatches 37; Indels 44; Gaps 8;

QY 15 LAPALANYINDVNDNNAGSGQGSVSVNEH-----NVANVDNNNGDSWNSIWDYNGNF 70
Db 365 LPFAVQSN--NENNTSSNTNNSSNNNNSSNGGNNNNNNNNNNI-----NEM 417
QY 71 AATRLFKKTCIVHKMKKEVMPISQIDALVKEKLGKGGPPPKGLMYSVNPKNKVD 130
Db 418 AAAAIFQ-----HLLKEE--PQTQN-----GNIGGGGG-----SNSQNDPTD 453
QY 131 LSKFGKNIAMCRGIPTMYA 150
Db 454 LSSY-----GLPAHLA 464

RESULT 6
YHCN.BACSU
ID YHCN.BACSU STANDARD; PRT; 189 AA.
AC P54598;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical lipoprotein yhcN precursor.
GN YHCN
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=97124185; PubMed=8969498;
RA Noback M.A., Terpstra P., Holsappel S., Venema G., Bron S.;
RT "A 22 kb DNA sequence in the *cspB*-*glpP*PKD region at 75 degrees on the
RL Bacillus subtilis chromosome."
RL Microbiology 142:3021-3026(1996).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (Probable).

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CC use by non-profit institutions as long as its content is in no way

InterPro; IPR000591; DEP.
DR InterPro; IPR001158; DIX.
DR InterPro; IPR001478; PDZ.
DR Pfam; PF00610; DEP; 1.
DR Pfam; PF00778; DIX; 1.
DR ProDom; PD003639; DIX; 1.
DR SMART; SM00021; DAX; 1.
DR SMART; SM00049; DEP; 1.
DR PROSITE; PS00186; DEP; 1.
DR PROSITE; PSS0106; PDZ; PARTIAL.
DR Developmental protein.
KW DOMAIN
FT DOMAIN 251 323 PDZ.
FT DOMAIN 425 499 DEP.
SQ SEQUENCE 695 AA; 75684 MW; BDEA252B41E87601 CRC64;

Query Match 8.0%; Score 80; DB 1; Length 695;
Best Local Similarity 25.7%; Pred.No. 8.5;
Matches 28; Conservative 14; Mismatches 49; Indels 18; Gaps 5;

OY 34 GSGQSSVANEHNVANVDNNNGWSDNWSNIWDYNGGFAATRLFKTKTCIVHKMKKEVMPS 93
||||| :||| :||| :||| :||| :||| :||| :|||
D b 598 GSGSES-----DHTVPGSGSTGW-----WER----PVSQLSRGSS--PRSQASAVAPG 640

OY 94 IQSLDALVKKKLGKGGPPPKGLMYSNPNKVDDLSPFGKNIANWC 142
||||| :||| :||| :||| :||| :||| :||| :|||
D b 641 LPPLHLPTKAYAVVGPPGVPRELA-AVPPELTGRSQSFQKAMGNPC 688

RESULT 13
MADL YEAST STANDARD; PRT; 749 AA.

ID MADL_YEAST STANDARD; PRT; 749 AA.
AC F40957; 1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Spindle assembly checkpoint component MAD1 (Mitotic MAD1 protein).
GN MAD1 OR YGI086W,
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
ON NCBI_TaxID=4932;
RX [1]
RN [1] SEQUENCE FROM N.A.
RC STRAIN=W303;
RP MEDLINE=96042315; PubMed=7593191;
RA Hardwick K.G., Murray A.W.;
RT "Mad1, a phosphoprotein component of the spindle assembly checkpoint
in budding yeast.",
RT J. Cell Biol. 131:709-720(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=97435481; PubMed=9290212;
RA Rieger M., Brueckner M., Schaefer M., Mueller-Auer S.;
RT "Sequence analysis of 203 kilobases from Saccharomyces cerevisiae
chromosome VII.",
RT Yeast 13:1077-1090(1997).
RN [3]
RP INTERACTIONS.
RX MEDLINE=98128031; PubMed=9461437;
RA Hwang L.H., Lau L.F., Smith D.L., Mistrot C.A., Hardwick K.G.,
Hwang E.S., Anon A., Murray A.W.;
RT "Budding yeast Cdc20: a target of the spindle checkpoint.";
RT Science 279:1041-1044(1998).
CC -! FUNCTION: CENTRAL COMPONENT OF THE SPINDLE ASSEMBLY CHECKPOINT.
CC -! SUBUNIT: THE SPINDLE CHECKPOINT COMPLEX IS COMPOSED OF MAD1, MAD2
AND MAD3. IT INTERACTS WITH CDC20.
CC -! SUBCELLULAR LOCATION: Nuclear.
CC -! PTM: BECOMES HYPERPHOSPHORYLATED WHEN WILD-TYPE CELLS ARE ARRESTED
IN MITOSIS.
CC -! SIMILARITY: SOME, TO S.POMBE SPBC3D5.04C.
CC -----

CC SYNDROME; ALSO KNOWN AS MUCOPOLYSACCHARIDOSIS TYPE VI (MPS-VI).
CC MPS-VI HAS BEEN DESCRIBED IN SIAMESE CATS.
CC -!- SIMILARITY: BELONGS TO THE SULFATASE FAMILY.
CC -----
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CC -----

DR EMBL; S48472; AAB23941.1; -.
DR PIR; A44475; A44475.
DR HSPP; P15848; IFSU.
DR InterPro: IPR000917; Sulfatase.
DR Pfam; PF00884; Sulfatase; 1.
DR PROSITE; PS00523; SULFATASE_1; 1.
DR PROSITE; PS00149; SULFATASE_2; 1.
KW Hydrolase; Signal; Glycoprotein; Lysosome; Mucopolysaccharidosis.
FT SIGNAL 1 41 POTENTIAL.
FT CHAIN 42 535 ARYL SULFATASE B.
FT ACT_SITE 149 149 POTENTIAL.
FT MOD_RES 93 93 2-AMINO-3-OXOPROPIONIC ACID
FT (BY SIMILARITY).
FT DISULFID 119 523 BY SIMILARITY.
FT DISULFID 123 157 BY SIMILARITY.
FT DISULFID 183 194 BY SIMILARITY.
FT DISULFID 407 449 BY SIMILARITY.
FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 281 281 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 428 428 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 460 460 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 535 AA; 59753 MW; 43A527886A9983C4 CRC64;

Query Match 7.9%; Score 79; DB 1; Length 535;
Best Local Similarity 27.0%; Pred. No. 7.7;
Matches 34; Conservative 18; Mismatches 40; Indels 34; Gaps 7;
Qy 43 NNEHNVANVDN-----NNGWD-----SWNSIWD---YGNQFAATRLFQKKTCTIVHKMK 88
|| : : || : : || : : || : : || : : || : : || : : || : :
Db 293 NNTVFIFSTDNGGOTLAGGNWPLRGKW-SLWEGGIRGVGFVAPLLKOKGV----KNR 347
| : : ||| : || : : || : : || : : || : : || : : || : :
Qy 89 EVMPISQSLDALVKEKKLOGK-----PGGPPP-KGLMYSVNPKNVDDLSK 133
| : : ||| : || : : || : : || : : || : : || : : || : :
Db 348 ELIHSDWLPVLVLRGSKTKPLDGFVWKTISEGSFSPRKELHNDPFDISPC 407
Qy 134 FGKNIA 139
| : : || : : || : : || : : || : : || : : || : :
Db 408 PGKSLA 413

Search completed: September 4, 2002, 17:05:09
Job time: 1135 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2002, 16:45:04 ; Search time 158.52 Seconds
(without alignments)
129.628 Million cell updates/sec

Title: US-09-821-726-13

Perfect score: 994

Sequence: 1 MKFTIVFAGILGVFLAPALA.....YTTSLWIVDISFCGDTVEN 185

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues 747574

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

- Database : A_Geneseq_032802.*
- 1: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
 - 2: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
 - 3: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
 - 4: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
 - 5: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
 - 6: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
 - 7: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
 - 8: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
 - 9: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
 - 10: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
 - 11: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
 - 12: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
 - 13: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
 - 14: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
 - 15: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
 - 16: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
 - 17: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
 - 18: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
 - 19: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
 - 20: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
 - 21: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
 - 22: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	984	99.0	185	20	AAW99667 Human secreted pro
2	984	99.0	185	21	AAW99667 Human secreted pro
3	984	99.0	185	21	AAW99667 Human signal pepti
4	984	99.0	185	21	AAW99667 Membrane-bound pro
5	984	99.0	185	22	AAW99667 Human PRO1005 (UNQ
6	984	99.0	185	22	AAW99667 Human PRO1005 prot
7	984	99.0	186	21	AAW99667 Human secreted pro
8	984	99.0	194	19	AAW99667 Cancer associated
9	984	99.0	194	20	AAW99667 Human ovarian tumo
10	189	19.0	184	21	AAW99667 Membrane-bound pro
11	189	19.0	184	22	AAW99667 Human PRO813 (UNQ4

12	188	18.9	184	22	AAW23556 Human EST encoded
13	188	18.9	184	22	AAW23556 Human gene 14 enco
14	188	18.9	184	22	AAW23556 Human gene 14 enco
15	178	17.9	176	22	AAW23556 Human PRO polypept
16	154.5	15.5	147	22	AAW23556 Human gene 14 enco
17	95.5	9.6	719	22	AAW23556 S cerevisiae apopt
18	93	9.4	764	21	AAW23556 plasmodium falcipa
19	93	9.4	1176	21	AAW23556 plasmodium falcipa
20	91	9.2	718	22	AAW23556 Drosophila melanog
21	90	9.1	1245	21	AAW23556 plasmodium falcipa
22	88	8.9	286	22	AAW23556 Dictyostelium disc
23	84.5	8.5	2188	22	AAW23556 Drosophila melanog
24	84	8.5	1817	21	AAW23556 plasmodium falcipa
25	83.5	8.4	1979	21	AAW23556 plasmodium falcipa
26	81.5	8.2	537	7	AAW23556 Sequence of the As
27	80.5	8.1	447	17	AAW23556 Oyster pearl prote
28	80.5	8.1	652	18	AAW23556 plasmodium falcipa
29	80	8.0	280	21	AAW23556 Gene 21 human secr
30	80	8.0	695	22	AAW23556 Mouse Dishevelled-
31	80	8.0	954	21	AAW23556 Ruminococcus flave
32	79.5	8.0	943	22	AAW23556 Drosophila melanog
33	78	7.8	540	21	AAW23556 plasmodium falcipa
34	78	7.8	2539	21	AAW23556 plasmodium falcipa
35	77.5	7.8	1714	21	AAW23556 plasmodium falcipa
36	77	7.7	1316	21	AAW23556 A calcium-dependen
37	77	7.7	1337	21	AAW23556 A calcium-dependen
38	77	7.7	2010	21	AAW23556 plasmodium falcipa
39	76.5	7.7	642	22	AAW23556 Drosophila melanog
40	76.5	7.7	794	22	AAW23556 P. falciparum telo
41	76	7.6	429	20	AAW23556 Potato isoamylase
42	76	7.6	477	22	AAW23556 Amino acid sequenc
43	75	7.5	289	17	AAW23556 Mature Pseudomonas
44	75	7.5	289	17	AAW23556 Mature Pseudomonas
45	75	7.5	289	17	AAW23556 Mature Pseudomonas

ALIGNMENTS

RESULT 1

AAW99667

ID AAW99667 standard; Protein; 185 AA.

AC AAW99667;

DT 07-JUN-1999 (first entry)

Human secreted protein clone ej90_5 protein.

Human; secreted protein; nutritional; cytokine; cell proliferation;
differentiation; immune stimulating; vaccine; haematopoiesis regulation;
tissue growth; chemotactic; chemokinetic; haemostatic; thrombolytic;
anti-inflammatory; cadherin; tumour invasion suppressor;
tumour inhibition; gene therapy.

OS Homo sapiens.

PN WC9907840-A1.

PD 18-FEB-1999.

PF 06-AUG-1998; 98WO-US16318.

PR 04-AUG-1998; 98US-0130189.

XX 06-AUG-1997; 97US-0906708.

(GEM) GENETICS INST INC.

PI Agostino MJ, Evans C, Jacobs K, Lavallie ER, McCoy JM;

PI Werberg D, Racie LA, Steininger RJ, Treacy M;

XX WPI; 1999-167419/14.

DR N-PSDB; AAX19493.

SEARCHING
Human genes

OM protein - protein search, using sw model
Run on: September 4, 2002, 16:45:05 ; Search time 158.52 Seconds
(without alignments)
128.927 Million cell updates/sec

Title: US-09-821-726-16
Perfect score: 993
Sequence: 1 MKLTFMVVGLGLAAPGFA.....TADILWILRMSFCGTSVETY 184
Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues 747574
Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :	A_Geneseq_032802.*
1:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
4:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
5:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
6:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
7:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
8:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
9:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
10:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
11:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
12:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
13:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
14:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
15:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
16:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
17:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
18:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
19:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Result No.	Score	Query Match	Length	ID	Description
1	640	64.5	185	20	AAW99667 Human secreted pro
2	640	64.5	185	21	AAW99667 Human PRO1005 prot
3	640	64.5	185	21	AAW99667 Human signal pepti
4	640	64.5	185	21	AAW99667 Membrane-bound pro
5	640	64.5	185	21	AAW99667 Human PRO1005 (UNQ
6	640	64.5	185	22	AAW99667 Human PRO1005 prot
7	640	64.5	185	22	AAW99667 Human secreted pro
8	640	64.5	194	19	AAW99667 Cancer associated
9	640	64.5	194	19	AAW99667 Human ovarian tumo
10	161	16.2	184	22	AAW99667 Human EST encoded
11	161	16.2	184	22	AAW99667 Human gene 14 enco

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Human gene 14 enco
Membrane-bound pro
Human PRO1005 (UNQ)
Human PRO1005 prot
Human signal pepti
Membrane-bound pro
Human PRO1005 (UNQ)
Human PRO1005 prot
Human secreted pro
Cancer associated
Human ovarian tumo
Human EST encoded
Human gene 14 enco

Handwritten notes: "1800000000" and "1800000000" with arrows pointing to the sequence and scoring table.

ALIGNMENTS

RESULT 1	AAW99667	AAW99667 standard; Protein; 185 AA.
ID	AAW99667	AAW99667 standard; Protein; 185 AA.
AC	AAW99667	AAW99667 standard; Protein; 185 AA.
DT	07-JUN-1999	(first entry)
DE	Human secreted protein clone ej90_5 protein.	
KW	Human; secreted protein; nutritional; cytokine; cell proliferation; differentiation; immune stimulating; vaccine; haematopoiesis regulation; tissue growth; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; cadherin; tumour invasion suppressor;	
KW	tumour inhibition; gene therapy.	
OS	Homo sapiens.	
PN	WO9907840-A1.	
XX	18-FEB-1999.	
XX	06-AUG-1998;	98WO-US16318.
XX	04-AUG-1998;	98US-0130189.
XX	06-AUG-1997;	97US-0906708.
XX	(GEM) GENETICS INST INC.	
PI	Agostino MJ, Evans CA, Jacobs K, Lavallie ER, McCoy JM;	
PI	Merberg D, Racie LA, Steininger RJ, Treacy M;	
XX	WPI: 1999-167419/14.	
DR	N-PSDB: AAX19493.	

134 roAsnLysValAspLeuSerLysPheGlyLysAsnIleAlaAsnMet 150
463 TCGAAGGGATTCCACATACATGCTGAAGAGATTCAAGGACCAACCT 512
151 CysArgGlyIleProThrTyrMetAlaGluMetGlnGluAlaSerLe 167
513 GATTTCGTACTCAGAAAGTCATCAGTCGCAATATATCTCTGGATTCTTA 562
167 uPhePheTyrSerGlyThrCysTyrThrThrSerValLeuTrpIleValA 184
563 ACATTTCCTCTCTGGAGGAATACGGAGAAC 594
184 spIleSerPheCysGlyAspThrValGluAsn 194

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT:AAW99667

seq_documentation_block:
ID AAW99667 standard; Protein; 185 AA.

AC AAW99667;

DT 07-JUN-1999 (first entry)

DE Human secreted protein clone ej90_5 protein.

XX Human; secreted protein; nutritional; cytokine; cell proliferation;
KW differentiation; immune stimulating; vaccine; haematopoiesis regulation;
KW tissue growth; chemotactic; chemokinetic; haemostatic; thrombolytic;
KW anti-inflammatory; cadherin; tumour invasion suppressor;
KW tumour inhibition; gene therapy.

OS Homo sapiens.

XX W09907840-A1.

XX 18-FEB-1999.

XX 06-AUG-1998; 98WO-US16318.

XX 04-AUG-1998; 98US-0130189.

XX 06-AUG-1997; 97US-0906708.

XX (GEM) J GENETICS INST INC.

XX Agostino MJ, Evans C, Jacobs K, Lavallie ER, McCoy JM;

XX Merberg D, Racie LA, Steininger RJ, Treacy M;

XX WPI; 1999-167419/14.

XX New polynucleotides encoding secreted human proteins - derived from

XX fetal kidney, adult testes, adult brain, adult heart, adult placenta

XX or adult retina cDNA libraries

XX Claim 34; Page 98-99; 107pp; English.

XX The present sequence represents a human secreted protein. The secreted
XX protein can have activities such as: nutritional activity, cytokine and
XX cell proliferation/differentiation activity, immune stimulating (e.g. as
XX vaccines) or suppressing activity, haematopoiesis regulating activity,
XX tissue growth activity, activin/inhibin activity, chemotactic/
XX chemokinetic activity, haemostatic and thrombolytic activity, receptor/
XX ligand activity, anti-inflammatory activity, cadherin/tumour invasion
XX suppressor activity, and tumour inhibition activity. The secreted
XX protein polynucleotides and proteins are predicted to have biological
XX activities which would make them suitable for treating, preventing or
XX ameliorating medical conditions in humans and animals. The
XX polynucleotides are also stated to be useful for gene therapy.

XX Sequence 185 AA;

alignment_scores:

77 Encodes SEQ ID 18

Quality: 775.00 Length: 185
Ratio: 4.429 Gaps: 0
Percent Similarity: 94.595 Percent Identity: 75.135
alignment_block:
US-09-821-726-17 x AAW99667 ..

Align seg 1/1 to: AAW99667 from: 1 to: 185

40 ATGAAGCTTCACAAATTCCTTGTGCTGACCTCTTGGTGTCTCTCTGACTCC 89
1 MetCysPheThrIleValPheAlaGlyLeuGluGlyValPheLeuAlaPr 17
90 TGCCTTGTCTGACTATAGTATCAGTGTCAACGACGACGCGCAACAGTGGTG 139
17 oAlaLeuAlaAsnTyrAsnIleAsnValAsnAspAsnAsnAlaG 34
140 GAAGTGGGAGCAGTCAGTGTGCTCAACAATGAACACACACGTCGGCAAC 189
34 lySerGlyGlnGlnSerValSerValAsnAsnGluHisAsnValAlaAsn 50
190 GTTGACAATAACAATGGATGGAATCTCTGGAATCTCTGGACTATAG 239
51 ValAspAsnAsnGlyTrpAspSerTrpAsnSerIleTrpAspTyrGl 67
240 AACTGCTTGTGTGTAAACGAGCTCTTCGAGAAGAGTCAATGCTGTGC 289
67 yAsnGlyPheAlaAlaThrArgLeuPheGlnLysLysThrCysIleValH 84
290 ACAAATGAAGAGGAGCCATCCCTCTCTCAAGCCCTTGTATGCGCTG 339
84 isLysMetAsnLysGluValMetProSerIleGlnSerLeuAspAlaLeu 100
340 GTCAAGAAAAGAGCTTCAGGCTAAGGCGCCAGGGGAGCCACTCCCAA 389
101 ValLysGluLysLysLeuGlnGlyLysGlyProGlyGlyProProPol 117
390 GAGCCTCAGTACTCAGTCAACCCCAACAGAGTCGACAACTGGACAAGT 439
117 sGlyLeuMetTyrSerValAsnProAsnLysValAspAspLeuSerLysP 134
440 TTGGAATAATCCATCGTGTCCATGTGCAAGGGGATTCACACATACATGCT 489
134 heGlyLysAsnIleAlaAsnMetCysArgGlyIleProThrTyrMetAla 150
490 GAAGAGATTCAAGGAGCAACCTGATTTCGTACTCTCAGAAAAGTGCATCAG 539
151 GluGluMetGlnGluAlaSerLeuPhePheTyrSerGlyThrCysTyrTh 167
540 TGCCAATATCTCTGGAATCTTAAACATTTCTCTGTGGAGGAATACCGG 589
167 rThrSerValLeuTrpIleValAspIleSerPheCysGlyAspThrValG 184
590 AGAAC 594
184 luAsn 185

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:AAAB24067

seq_documentation_block:
ID AAB24067 standard; Protein; 185 AA.

XX AAB24067;

XX AC

XX DT 29-JAN-2001 (first entry)

XX Human PR01005 protein sequence SEQ ID NO:34.

XX Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;

XX proliferation; tumourigenesis; identification; cancer; cytostatic;

XX neutropenic; neuroprotective; antiinflammatory; immunosuppressive;

XX immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;

XX neuronal disorder; glial disorder; astrocytal disorder; angiogenic;

